

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 19:09:18 ; Search time 8.49515 Seconds
(without alignments)
79.283 Million cell updates/sec

Title: US-10-774-928A-1

Perfect score: 38

Sequence: 1 YEDEINK 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	310	2 S43865	cyto keratin 8, typ
2	38	100.0	384	2 I61769	keratin 6d, type I
3	38	100.0	390	2 A60093	cyto keratin, type
4	38	100.0	419	1 KRXL2B	keratin, 64K type
5	38	100.0	425	1 KRXL2A	keratin, 64K type
6	38	100.0	461	2 A43782	keratin, type II -
7	38	100.0	483	2 A34720	keratin 8, type II
8	38	100.0	487	2 JTO407	keratin 8, type II
9	38	100.0	490	2 JS0658	cyto keratin EndoA
10	38	100.0	513	2 S08381	keratin, 58K type
11	38	100.0	520	2 JS0291	intermediate filam
12	38	100.0	523	2 I99009	epidermal keratin
13	38	100.0	564	1 KRHUEA	keratin 6a, type I
14	38	100.0	564	1 KRHUEB	keratin 6b, type I
15	38	100.0	564	2 I61770	keratin 6e, type I
16	38	100.0	564	2 I61768	keratin 6c, type I
17	38	100.0	564	2 I61771	keratin 6f, type I
18	38	100.0	581	1 KRWS2	keratin, type II C
19	38	100.0	590	2 A29904	keratin 5, type II
20	38	100.0	629	2 A29666	keratin, 65K type
21	38	100.0	629	2 S42629	keratin K3 - rabbi
22	38	100.0	638	2 I53169	cyto keratin 2 - hu
23	38	100.0	643	1 KRHD2	keratin 1, type II
24	38	100.0	645	2 A44861	keratin, 67K type
25	36	94.7	681	2 T14903	NADPH-ferrihemopro
26	35	92.1	94	2 C59094	hypothetical prote
27	35	92.1	224	2 S00959	hypothetical prote
28	35	92.1	469	2 S05602	keratin K7, type I
29	35	92.1	489	2 B24177	keratin, 55K type

ALIGNMENTS

RESULT 1

S43865

Cyto keratin 8, type II - potorooc (fragment)

C:Species: Potorous tridactylus (potoroo, long-nosed rat kangaroo)

C:Date: 20-Feb-1995 #sequence_revision 06-Dec-1996 #text_change 09-Jul-2004

C:Accession: S43865; S40172

R:Boettger, V.; Lane, E.B.

J. Mol. Biol. 235, 61-67, 1994

A:Title: A monoclonal antibody epitope on keratin 8 identified using a phage peptide lib

A:Reference number: S43865; MUID:94118290; PMID:7507169

A:Accession: S43865

A:Molecule type: mRNA

A:Residues: 1-310 <BOE>

A:Cross-references: UNIPROT:Q28810; UNIPARC:UPI0000086BF0; EMBL:X70987; NID:9437902; PIDN:

A:Experimental source: kidney epithelium cells

C:Superfamily: cytoskeletal keratin

C:Keywords: coiled coil

Query Match 100.0%; Score 38; DB 2; Length 310;

Best Local Similarity 100.0%; Pred. No. 4.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7

Db 180 YEDEINK 186

RESULT 2

I61769

keratin 6d, type II - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004

C:Accession: I61769

R:Takahashi, K.; Paladini, R.D.; Coulombe, P.A.

J. Biol. Chem. 270, 18581-18592, 1995

A:Title: Cloning and characterization of multiple human genes and cDNAs encoding highly

A:Reference number: A57398; MUID:95355491; PMID:7543104

A:Accession: I61769

A:Molecule type: DNA

A:Residues: 1-384 <RES>

A:Cross-references: UNIPROT:P48667; UNIPARC:UPI000012DB17; GB:L42602; NID:9914823; GB:L42

28; GB:L42608; NID:9914829; GB:L42609; NID:9914830; GB:L42610; NID:91488252; PIDN:AAB606

C:Genetics:

A:Gene: KRT6D

A:Introns: 72/2; 92/3; 124/3; 179/3; 221/3; 295/2; 307/1

C:Superfamily: cytoskeletal keratin

C:Keywords: coiled coil

Query Match

Best Local Similarity 100.0%; Score 38; DB 2; Length 384;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 YEDEINK 7
Db      73 YEDEINK 79

RESULT 3
A60093
cyto keratin, type II, early ectodermal - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993
C:Accession: A60093
R:Charlebois, T.S.; Spencer, D.H.; Tarkington, S.K.; Henry, J.J.; Grainger, R.M.
Development 108, 33-45, 1990
A:Title: Isolation of a chick cyto keratin cDNA clone indicative of regional specialization
A:Reference number: A60093; MUID:90276238; PMID:1693557
A:Accession: A60093
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-390 <CHA>
A:Cross-references: UNIPARC:UPI00001774C6
C:Superfamily: cytoskeletal keratin
C:Keywords: intermediate filament

Query Match      100.0%; Score 38; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 5.3; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Qy      1 YEDEINK 7
Db     100 YEDEINK 106

RESULT 4
KRXL2B
keratin, 64K type II cytoskeletal (clone pUF164) - African clawed frog (fragment)
N:Alternate names: 64-kDa type II keratin
C:Species: Xenopus laevis (African clawed frog)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C:Accession: A02952
R:Hoffmann, W.; Franz, J.K.; Franke, W.W.
J. Mol. Biol. 184, 713-724, 1985
A:Title: Amino acid sequence microheterogeneities of basic (type II) cyto keratins of xenopus
A:Reference number: A92914; MUID:86011576; PMID:2413219
A:Accession: A02952
A:Molecule type: mRNA
A:Residues: 1-419 <HOF>
A:Cross-references: UNIPROT:P04265; UNIPARC:UPI000012DB07; GB:X02895; GB:M13954; NID:G64
A:Experimental source: clone pUF164
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament
F:1-275/Domain: rod (fragment) <ROD>
F:1-9/Region: linker 1
F:10-110/Region: coil 1B
F:111-127/Region: linker 12
F:128-146/Region: coil 2A
F:147-154/Region: linker 2
F:155-275/Region: coil 2B
F:213/Region: stutter
F:276-419/Domain: tail <END>
F:276-399/Region: H2 and V2 subdomains
F:400-419/Region: E2 subdomain

Query Match      100.0%; Score 38; DB 1; Length 419;
Best Local Similarity 100.0%; Pred. No. 5.7; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Qy      1 YEDEINK 7
Db     52 YEDEINK 58

RESULT 5

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KRXL2A
keratin, 64K type II cytoskeletal (clone pUF23) - African clawed frog (fragment)
N:Alternate names: 64-kDa type II keratin
C:Species: Xenopus laevis (African clawed frog)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C:Accession: A02953
R:Hoffmann, W.; Franz, J.K.; Franke, W.W.
J. Mol. Biol. 184, 713-724, 1985
A:Title: Amino acid sequence microheterogeneities of basic (type II) cyto keratins of xenopus
A:Reference number: A92914; MUID:86011576; PMID:2413219
A:Accession: A02953
A:Molecule type: mRNA
A:Residues: 1-425 <HOF>
A:Cross-references: UNIPROT:P04266; UNIPARC:UPI000012DB06; GB:X02894; GB:M13956; NID:G64
A:Experimental source: clone pUF23
C:Comment: The cyto keratin IF proteins appear to be obligate heteropolymers, composed of
types of proteins is low and restricted to specific isolated regions within the rod domain,
C:Comment: Three subdomains, each characterized by a distinctive amino acid composition,
d length among the intermediate filament proteins, the arrangement of its subdomains pres
ally distant species, suggests functional significance.
C:Comment: There is only one group of closely related type II amphibian cyto keratins. Thi
ate of differentiation of the amphibian epidermis, which lacks a true stratum corneum.
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament
F:1-296/Domain: rod (fragment) <ROD>
F:1-16/Region: coil 1A (fragment)
F:17-30/Region: linker 1
F:31-131/Region: coil 1B
F:132-148/Region: linker 12
F:149-167/Region: coil 2A
F:168-175/Region: linker 2
F:176-296/Region: coil 2B
F:234/Region: stutter
F:297-425/Domain: tail <END>
F:297-405/Region: H2 and V2 subdomains
F:406-425/Region: E2 subdomain

Query Match      100.0%; Score 38; DB 1; Length 425;
Best Local Similarity 100.0%; Pred. No. 5.8; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Qy      1 YEDEINK 7
Db     73 YEDEINK 79

RESULT 6
A43782
keratin, type II - eastern newt (fragment)
C:Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C:Accession: A43782
R:Ferretti, P.; Brockes, J.P.; Brown, R.
Development 111, 497-507, 1991
A:Title: A new type II keratin restricted to normal and regenerating limbs and tails is
A:Reference number: A43782; MUID:91372147; PMID:1716554
A:Accession: A43782
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <FER>
A:Cross-references: UNIPROT:O42435; UNIPARC:UPI00001774C4; GB:X57671
C:Superfamily: cytoskeletal keratin

Query Match      100.0%; Score 38; DB 2; Length 461;
Best Local Similarity 100.0%; Pred. No. 6.3; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Qy      1 YEDEINK 7
Db     134 YEDEINK 140

RESULT 7

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A34720
keratin 8, type II cytoskeletal - human
C:Species: Homo sapiens (man)
C:Date: 06-Jul-1990 #sequence revision 06-Jul-1990 #text change 09-Jul-2004
C:Accession: A34720; S06888; S12479; I37982; I37983; JS0487; A31942
R:Yanamoto, R.; Kao, L.C.; McKnight, C.E.; Strauss III, J.F.
Mol. Endocrinol. 4, 370-374, 1990
A:Title: Cloning and sequence of cDNA for human placental cytokeratin 8. Regulation of
A:Reference number: A34720; MUID:90258929; PMID:1692965
A:Accession: A34720
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-483 <YAM>
A:Cross-references: UNIPROT:P05787; UNIPARC:UPI00001774C3; GB:M34225
R:Leube, R.E.; Bosch, F.X.; Romano, V.; Zimbelmann, R.; Hosfeler, H.; Franke, W.W.
Differentiation 33, 69-85, 1986
A:Title: Cytokeratin expression in simple epithelia.
A:Reference number: S06888; MUID:87134779; PMID:2434381
A:Accession: S06888
A:Molecule type: mRNA
A:Residues: 205-483 <LEU>
A:Cross-references: UNIPARC:UPI000016ABAI; EMBL:X12882
R:Franke, W.W.
submitted to the EMBL Data Library, September 1988
A:Reference number: S12479
A:Accession: S12479
A:Molecule type: mRNA
A:Residues: 205-309, '1', 311-483 <FRA>
A:Cross-references: UNIPARC:UPI000016A769; EMBL:X12882; NID:G30312; PIDN:CAA31376.1; PID
R:Waseem, A.; Alexander, C.M.; Steel, J.B.; Lane, E.B.
New Biol. 2, 464-478, 1990
A:Title: Embryonic simple epithelial keratins 8 and 18: chromosomal location emphasizes
A:Reference number: I37982; MUID:91145351; PMID:1705144
A:Accession: I37982
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-76, 'V', 78-428, 'G', 430-431, 'S', 433-483 <RES>
A:Cross-references: UNIPARC:UPI0000161B3E; EMBL:X74929; NID:G400415; PIDN:CAAS2882.1; PI
A:Accession: I37983
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 151-201, 'VD', 202-271 <RE2>
A:Cross-references: UNIPARC:UPI000016ABCF; EMBL:X74981; NID:G400417; PIDN:CAAS2916.1; PI
R:Krauss, S.; Franke, W.W.
Gene 86, 241-249, 1990
A:Title: Organization and sequence of the human gene encoding cytokeratin 8.
A:Reference number: JS0487; MUID:90215304; PMID:1691124
A:Accession: JS0487
A:Molecule type: DNA
A:Residues: 1-76, 'V', 78-428, 'G', 'SQ', 434-483 <KRA>
A:Cross-references: UNIPARC:UPI000016AG2B; GB:M34482; NID:G181572; PIDN:AAA35763.1; PID:
R:Kulesh, D.A.; Cecena, G.; Darmon, Y.M.; Vasseur, M.; Oshima, R.G.
Mol. Cell. Biol. 9, 1553-1565, 1989
A:Title: Posttranslational regulation of keratins: degradation of mouse and human keratin
A:Reference number: A31942; MUID:89261783; PMID:2471065
A:Accession: A31942
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-76, 'V', 78-231 <KUL>
A:Cross-references: UNIPARC:UPI000016A354; GB:M26512; NID:G177796; PIDN:AAA51542.1; PID:
A:Comment: This protein is one of the type II cytokeratins.
C:Genetics:
A:Gene: GDB:KRT8
A:Cross-references: GDB:118830; OMIM:148060
A:Map position: 12p13.2-12q24.1
A:Introns: 108/3; 178/2; 198/3; 230/3; 327/3; 401/2; 421/1
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament

Query Match 100.0%; Score 38; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
|||||
DB 179 YEDEINK 185

RESULT 8

JS0407
keratin 8, type II cytoskeletal, embryonic - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: J70407; A22078
R:Ouillet, T.; Levac, P.; Royal, A.
Gene 70, 75-84, 1988
A:Title: Complete sequence of the mouse type-II keratin EndoA: its amino-terminal region
A:Reference number: J70407; MUID:89196919; PMID:2467842
A:Accession: J70407
A:Molecule type: mRNA
A:Residues: 1-487 <OUE>
A:Cross-references: UNIPROT:Q61518; UNIPARC:UPI00000E6EE0; GB:M22831; NID:G511653; PIDN:
A:Experimental source: carcinoma cell line F9-21
R:Vasseur, M.; Duprey, P.; Brulet, P.; Jacob, F.
Proc. Natl. Acad. Sci. U.S.A. 82, 1155-1159, 1985
A:Title: One gene and one pseudogene for the cytokeratin endo A.
A:Reference number: A22078; MUID:85140247; PMID:2579387
A:Accession: A22078
A:Molecule type: DNA
A:Residues: 1-13 <VAS>
A:Cross-references: UNIPARC:UPI000016CD31; GB:K02783; NID:G193019; PIDN:AAA37549.1; PID:
C:Genetics:
A:Gene: EndoA
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament
F:1-94/Domain: head <HED>
F:95-406/Domain: rod <ROD>
F:95-128/Region: coil 1A
F:129-146/Region: linker 1
F:147-235/Region: coil 1B
F:236-260/Region: linker 12
F:261-406/Region: coil 2
F:407-487/Domain: tail <TAI>

Query Match 100.0%; Score 38; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
|||||
DB 182 YEDEINK 188

RESULT 9

JS0658
cytokeratin EndoA - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: JS0658
R:Tamai, Y.; Takemoto, Y.; Matsumoto, M.; Morita, T.; Matsushiro, A.; Nozaki, M.
Gene 104, 169-176, 1991
A:Title: Sequence of the EndoA gene encoding mouse cytokeratin and its methylation state
A:Reference number: JS0658; MUID:92009210; PMID:1717348
A:Accession: JS0658
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-490 <TAM>
A:Cross-references: UNIPROT:Q61463; UNIPARC:UPI00000220F8; GB:D90360; NID:G220391; PIDN:
A:Comment: This type-II cytokeratin forms intermediate filaments together with type-I cy
C:Genetics:
A:Gene: EndoA
A:Introns: 114/3; 184/2; 204/3; 236/3; 291/3; 333/3; 407/2; 427/1
C:Superfamily: cytoskeletal keratin

Query Match 100.0%; Score 38; DB 2; Length 490;
Best Local Similarity 100.0%; Pred. No. 6.7;

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Matches      7;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      1 YEDEINK 7
      |||||
Db      185 YEDEINK 191

RESULT 10
S08381
keratin, 58K type II, cytoskeletal (clone pXenCK55(5/6)) - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
C:Accession: S08381
R:Fouquet, B.; Herrmann, H.; Franz, J.K.; Franke, W.W.
Development 104, 533-548, 1988
A:Title: Expression of intermediate filament proteins during development of Xenopus laevis
A:Reference number: S08381; MUID:90032362; PMID:2478354
A:Accession: S08381
A:Molecule type: mRNA
A:Residues: 1-513 <FOU>
A:Cross-references: UNIPROT:P16978; UNIPARC:UPI000017151D; EMBL:X14427; NID:G64625; PIDN:
C:Superfamily: cytoskeletal keratin

Query Match      100.0%; Score 38; DB 2; Length 513;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches      7;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      1 YEDEINK 7
      |||||
Db      217 YEDEINK 223

RESULT 11
JS0291
intermediate filament protein ON3 - goldfish
C:Species: Carassius auratus (goldfish)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: JS0291
R:Giordano, S.; Glasgow, E.; Tesser, P.; Schechter, N.
Neuron 2, 1507-1516, 1989
A:Title: A type II keratin is expressed in glial cells of the goldfish visual pathway.
A:Reference number: JS0291; MUID:90180470; PMID:2483326
A:Accession: JS0291
A:Molecule type: mRNA
A:Residues: 1-520 <GIO>
A:Cross-references: UNIPROT:P18520; UNIPARC:UPI000012D74A
A:Experimental source: glial cell
C:Comment: This protein is one of the nonneuronal predominant intermediate filament proteins
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; optic nerve; visual pathway
F:1-108/Domain: head <HEA>
F:109-144/Region: coil 1A
F:145-157/Region: linker
F:158-253/Region: coil 1B
F:254-273/Region: linker
F:274-420/Region: coil 2
F:421-520/Domain: tail <TAI>

Query Match      100.0%; Score 38; DB 2; Length 520;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches      7;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      1 YEDEINK 7
      |||||
Db      197 YEDEINK 203

RESULT 12
I59009
epidermal keratin subunit II - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I59009; A61205

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R:Steinert, P.M.; Parry, D.A.D.; Racoosin, E.L.; Idler, W.W.; Steven, A.C.; Trus, B.L.;
Proc. Natl. Acad. Sci. U.S.A. 81, 5709-5713, 1984
A:Title: The complete cDNA and deduced amino acid sequence of a type II mouse epidermal
A:Reference number: I59009; MUID:85014838; PMID:6207530
A:Accession: I59009
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-553 <RES>
A:Cross-references: UNIPROT:P50446; UNIPARC:UPI000016CE87; GB:K02108; NID:G198634; PIDN:I
R:Finch, J.; Andrews, K.; Krieg, P.; Fuerstenberger, G.; Slaga, T.; Ootsuyama, A.; Tanook
Carcinogenesis 12, 1519-1522, 1991
A:Title: Identification of a cloned sequence activated during multi-stage carcinogenesis
A:Reference number: A61205; MUID:91316763; PMID:1713533
A:Accession: A61205
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 528-553 <FIN>
A:Cross-references: UNIPARC:UPI00001774C8
C:Genetics:
A:Gene: KER2
C:Superfamily: cytoskeletal keratin

Query Match      100.0%; Score 38; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches      7;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      1 YEDEINK 7
      |||||
Db      242 YEDEINK 248

RESULT 13
KHUEA
keratin 6a, type II - human
N:Alternate names: 56-kDa type II keratin; keratin cytoskeletal
C:Species: Homo sapiens (man)
C:Date: 15-Nov-1984 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: A57398; A02944
R:Takahashi, K.; Paladini, R.D.; Coulombe, P.A.
J. Biol. Chem. 270, 18581-18592, 1995
A:Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
A:Reference number: A57398; MUID:95355491; PMID:7543104
A:Accession: A57398
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-564 <TAK>
A:Cross-references: UNIPROT:P02538; UNIPARC:UPI000013CD4C; GB:L42575; NID:G908769; GB:L4
74; GB:L42581; NID:G908775; GB:L42582; NID:G908776; GB:L42583; NID:G908777; PIDN:AAC4176;
R:Hanukoglu, I.; Fuchs, E.
Cell 33, 915-924, 1983
A:Title: The cDNA sequence of a type II cytoskeletal keratin reveals constant and variab
A:Reference number: A02944; MUID:83259278; PMID:6191871
A:Accession: A02944
A:Molecule type: mRNA
A:Residues: 208-394, 'S', 396-564 <HAN>
A:Cross-references: UNIPARC:UPI000016AB87; GB:J00269; NID:G34068; PIDN:CAA24760.1; PID:G
C:Comment: The cytoskeletal and microfibrillar keratins are classified into two types, t
atin IF protein subunit appears to be a heterotetramer of two type I and two type II prot
C:Genetics:
A:Gene: GDB:KRT6A
A:Cross-references: GDB:128111; OMIM:148041
A:Map position: 12q12-12q21
A:Introns: 180/3; 252/2; 272/3; 304/3; 359/3; 401/3; 475/2; 487/1
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament
F:2-163/Domain: head <HED>
F:2-126/Region: E1 and V1 subdomains
F:127-163/Region: H1 subdomain
F:162-476/Domain: rod <ROD>
F:199-210/Region: linker 1
F:211-311/Region: coil 1B
F:312-328/Region: linker 12
F:329-347/Region: coil 2A

```

F:348-355/Region: linker 2
F:356-476/Region: coil 2B
F:414/Region: stutter
F:477-564/Domain: tail <END>
F:477-496/Region: H2 subdomain
F:497-564/Region: V2 and E2 subdomains

Query Match 100.0%; Score 38; DB 1; Length 564;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
|||
DB 253 YEDEINK 259

RESULT 14

KRHUEB

keratin 6b, type II - human
N:Alternate names: 56K type II keratin; keratin, cytoskeletal
C:Species: Homo sapiens (man)
C>Date: 04-Dec-1986 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: I61767; A02945
R:Takahashi, K.; Paladini, R.D.; Coulombe, P.A.
J. Biol. Chem. 270, 18581-18592, 1995
A:Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
A:Reference number: A57398; MUID:95355491; PMID:7543104
A:Accession: I61767
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-564 <RES>
A:Cross-references: UNIPROT:P04259; UNIPARC:UPI0000167B38; GB:L42584; NID:908780; GB:L4
85; GB:L42590; NID:908786; GB:L42591; NID:908787; GB:L42592; NID:908788; PIDN:RAC4176
R:Tyner, A.L.; Eichman, M.J.; Fuchs, E.
Proc. Natl. Acad. Sci. U.S.A. 82, 4683-4687, 1985
A:Title: The sequence of a type II keratin gene expressed in human skin: conservation of
A:Reference number: A02945; MUID:85270392; PMID:2410904
A:Accession: A02945
A:Molecule type: DNA
A:Residues: 2-88, 'AG', '91-115, 'PA', '118, 'LC', '122-158, 'IG', '161-254, 'V', '256-564 <TYN>
A:Cross-references: UNIPARC:UPI0000173D58; GB:M11229; NID:900205; PIDN:AAA59

A:Note: initiator Met not shown
C:Comment: There are two types of cytoskeletal and microfibrillar keratin, I (acidic) and
biligate heteropolymers, composed of complexes formed by the aggregation of at least one
C:Genetics:
A:Gene: GDB:KRT6B
A:Cross-references: GDB:128113; OMIM:148042
A:Map position: 12pter-12qter
A:Introns: 180/3; 252/2; 272/3; 304/3; 359/3; 401/3; 475/2; 487/1
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament
F:2-163/Domain: head <HED>
F:2-127/Region: E1 and V1 subdomains
F:128-163/Region: H1 subdomain
F:164-476/Domain: rod <ROD>
F:164-198/Region: coil 1A
F:199-210/Region: linker 1
F:211-311/Region: coil 1B
F:312-328/Region: linker 12
F:329-347/Region: coil 2A
F:348-355/Region: linker 2
F:356-476/Region: coil 2B
F:414/Region: stutter
F:477-564/Domain: tail <END>
F:477-496/Region: H2 subdomain
F:497-564/Region: V2 and E2 subdomains

Query Match 100.0%; Score 38; DB 1; Length 564;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
|||
DB 253 YEDEINK 259

DB 253 YEDEINK 259

RESULT 15

I61770

keratin 6e, type II - human
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: I61770
R:Takahashi, K.; Paladini, R.D.; Coulombe, P.A.
J. Biol. Chem. 270, 18581-18592, 1995
A:Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
A:Reference number: A57398; MUID:95355491; PMID:7543104
A:Accession: I61770
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-564 <RES>
A:Cross-references: UNIPROT:P48668; UNIPARC:UPI0000167E31; GB:L42611; NID:908802; PIDN:7

C:Genetics:

A:Gene: KRT6E

A:Note: this may not be a distinct gene

C:Superfamily: cytoskeletal keratin

C:Keywords: coiled coil

Query Match 100.0%; Score 38; DB 2; Length 564;

Best Local Similarity 100.0%; Pred. No. 7.8;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7

|||
DB 253 YEDEINK 259

Search completed: July 5, 2006, 19:20:30

Job time : 8.49515 secs

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GenCore version 5.1.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 18:28:56 ; Search time 71.6311 Seconds
(without alignments)
90.395 Million cell updates/sec

Title: US-10-774-928A-1
Perfect score: 38
Sequence: 1 YEDEINK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	38	100.0	176	2	Q4JI23 ICTPU	Q4ji23 ictalurus p
2	38	100.0	222	2	Q4LOE7 MOUSE	Q4loE7 mus musculus
3	38	100.0	224	2	Q678L1 MOUSE	Q678l1 mus musculus
4	38	100.0	310	2	Q28810 POTTR	Q28810 pottorus tr
5	38	100.0	324	2	Q80VP7 MOUSE	Q80vp7 mus musculus
6	38	100.0	346	2	Q4QV72 SPAAU	Q4qv72 sparus aura
7	38	100.0	365	2	Q69I10 HUMAN	Q69i10 homo sapien
8	38	100.0	381	2	Q99MH7 MOUSE	Q99mh7 mus musculus
9	38	100.0	384	1	K2C6D HUMAN	P48667 homo sapien
10	38	100.0	417	2	Q4SRP0 TETNG	Q4srp0 tetraodon n
11	38	100.0	419	1	K2C2 XENLA	P04265 xenopus lae
12	38	100.0	425	1	K2C1 XENLA	P04266 xenopus lae
13	38	100.0	461	2	Q42435 NOTVI	Q42435 notophthalm
14	38	100.0	482	1	K2C8 HUMAN	P05787 homo sapien
15	38	100.0	482	1	K2C8 RAT	Q10758 rattus norv
16	38	100.0	483	2	Q53GJ0 HUMAN	Q53gj0 homo sapien
17	38	100.0	483	2	Q6DHW5 HUMAN	Q6dhw5 homo sapien
18	38	100.0	483	2	Q6GMY0 HUMAN	Q6gmy0 homo sapien
19	38	100.0	483	2	Q5RB34 PONPY	Q5rb34 pongo pygma
20	38	100.0	483	2	Q80WH8 SMURI	Q80wh8 rattus sp.
21	38	100.0	486	2	Q9YH07 9CHON	Q9yh07 scylliorhinu
22	38	100.0	487	2	Q61518 MOUSE	Q61518 mus musculus
23	38	100.0	487	2	Q7SYF6 ACIBE	Q7syf6 acipenser b
24	38	100.0	490	2	Q3KQK5 MOUSE	Q3kqk5 mus musculus
25	38	100.0	490	2	Q3TG11 MOUSE	Q3tg11 mus musculus
26	38	100.0	490	2	Q3TJEL MOUSE	Q3tjel mus musculus
27	38	100.0	490	2	Q3TKY7 MOUSE	Q3tky7 m blastocys
28	38	100.0	490	2	Q61463 MOUSE	Q61463 m cytokerat
29	38	100.0	492	1	K2CO CHICK	Q93532 gallus gall
30	38	100.0	496	2	Q42434 NOTVI	Q42434 notophthalm
31	38	100.0	497	2	Q5K2N3 PROAT	Q5k2n3 prototerp

32	38	100.0	497	2	Q6NY60 BRARE	Q6ny60 brachydanio
33	38	100.0	498	2	Q9PV92 BRARE	Q9pv92 brachydanio
34	38	100.0	499	2	Q9H552 HUMAN	Q9h552 homo sapien
35	38	100.0	499	2	Q7ZT78 BRARE	Q7zt78 brachydanio
36	38	100.0	505	2	Q6P4C7 HUMAN	Q6p4c7 homo sapien
37	38	100.0	508	2	Q6NVR6 XENTR	Q6nvr6 xenopus tro
38	38	100.0	511	2	Q90ZF7 XANCA	Q90zf7 rana catesb
39	38	100.0	512	1	K2C5 XENLA	P16878 xenopus lae
40	38	100.0	515	2	Q8JFG4 ONCMY	Q8jfg4 oncorhynchu
41	38	100.0	519	1	K2C1B RAT	Q6i901 rattus norv
42	38	100.0	520	1	ION3 CARAU	P18520 carassius a
43	38	100.0	520	2	Q6NWF6 BRARE	Q6nwf6 brachydanio
44	38	100.0	521	2	Q5K2N4 PROAT	Q5k2n4 prototerp
45	38	100.0	521	2	Q5K2N5 PROAT	Q5k2n5 prototerp

ALIGNMENTS

RESULT 1
Q4JI23 ICTPU PRELIMINARY; PRT; 176 AA.
AC Q4JI23;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Keratin 8 (Fragment).
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yeh H.-Y., Klesius P.H.;
RT "Differential gene expression of Ictalurus punctatus after
RT Edwardsiella ictaluri infection."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
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EMBL; DQ086174; AAY86957.1; -; mRNA.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002957; Keratin I.
DR InterPro; IPR003054; Keratin II.
DR PANTHER; PTHR18893:SP5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
KW Keratin.
FT NON_TER 1
FT NON_TER 176 176
SQ SEQUENCE 176 AA; 20651 MW; 8EE3A88097529C33 CRC64;

Query Match 100.0%; Score 38; DB 2; Length 176;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
DB 70 YEDEINK 76

RESULT 2
Q4LOE7 MOUSE PRELIMINARY; PRT; 222 AA.
ID Q4LOE7;
AC Q4LOE7;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Type II cytokeratin Kb39 (Fragment).

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GN Name=4732484G22Rik;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=NMRI; TISSUE=Tail skin;
RA Zinek A., Hesse M.;
RT "Cornea-specific cytochrome B3 seems to be absent in the rodent
lineage.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL; AY651826; AAV85505.1; -; mRNA.
DR MGI; MGI:3588209; 4732484G22Rik.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002957; Keratin_1.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
KW Keratin.
FT NON TER 1
FT NON TER 222
FT NON TER 222
SQ SEQUENCE 222 AA; 25801 MW; 483B4F589032C1D1 CRC64;

Query Match 100.0%; Score 38; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINK 7
Db 70 YEDEINK 76

RESULT 3
Q678L1 MOUSE
ID Q678L1 MOUSE PRELIMINARY; PRT; 224 AA.
AC Q678L1.
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Keratin 1b (Fragment).
GN Name=4732484G22Rik;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=NMRI; TISSUE=Tail skin;
RA Zinek A., Hesse M., Magin T., Weber K.;
RT "Homologies between the human, mouse and rat keratin-clusters.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL; AY379112; AAR23930.1; -; mRNA.
DR Ensembl; ENSMUSG0000067594; Mus musculus.
DR MGI; MGI:3588209; 4732484G22Rik.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR InterPro; IPR003054; Keratin_II.

Name=4732484G22Rik;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=NMRI; TISSUE=Tail skin;
RA Zinek A., Hesse M., Magin T., Weber K.;
RT "Homologies between the human, mouse and rat keratin-clusters.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL; AY379112; AAR23930.1; -; mRNA.
DR Ensembl; ENSMUSG0000067594; Mus musculus.
DR MGI; MGI:3588209; 4732484G22Rik.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR InterPro; IPR003054; Keratin_II.
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DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
KW Keratin.
FT NON TER 1
FT NON TER 224
FT NON TER 224
SQ SEQUENCE 224 AA; 25995 MW; DD6F783B4F589032 CRC64;

Query Match 100.0%; Score 38; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINK 7
Db 70 YEDEINK 76

RESULT 4
Q28810 POTTR
ID Q28810 POTTR PRELIMINARY; PRT; 310 AA.
AC Q28810.
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 27.
DE Keratin 8 (Fragment).
OS Potorous tridactylus (Potoroo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Potoroidae; Potorous.
OX NCBI_TaxID=9310;
RN [1]
RP NUCLEOTIDE SEQUENCE
RC MEDLINE=94118290; PubMed=7507169;
RA Boettger V., Lane E.B.;
RT "A monoclonal antibody Epitope on Keratin 8 identified using a phage
peptide library.";
RL J. Mol. Biol. 235:61-67 (1994).
CC
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CC
CC EMBL; X70987; CAA50316.1; -; mRNA.
DR PIR; S43865; S43865.
DR HSP; P08670; 1GK7.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
KW Keratin.
FT NON TER 1
FT NON TER 310
FT NON TER 310
SQ SEQUENCE 310 AA; 35170 MW; 31D37E0BC63BFA85 CRC64;

Query Match 100.0%; Score 38; DB 2; Length 310;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINK 7
Db 180 YEDEINK 186

RESULT 5
Q80VP7 MOUSE
ID Q80VP7 MOUSE PRELIMINARY; PRT; 324 AA.
AC Q80VP7.
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
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DT 07-FEB-2006, entry version 20.
DE Hypothetical protein MGC54654;
GN Name=MGC54654;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Villalón D.K., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL [2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RG NIH MGC Project;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; BC046626; AAH46626.1; -; mRNA.
DR HSSP; P08670; 1GK7.
DR Ensembl; ENSMUSG00000046162; Mus musculus.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
DR Hypothetical protein.
SQ SEQUENCE 324 AA; 35165 MW; 0E4D7E25144435DD CRC64;
KW Hypothetical protein.
Query Match 100.0%; Score 38; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEDEINK 7
Db 203 YEDEINK 209
|||||
RESULT 6
Q4QY72 SPAAU PRELIMINARY; PRT; 346 AA.
ID Q4QY72;
AC Q4QY72;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Type II keratin (Gilthead sea bream).
OS Sparus aurata (Gilthead sea bream).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Sparus.
OX NCBI_TaxID=8175;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sarrapoulou E., Power D.M., Magoulas A., Geisler R., Kotoulas G.;
RT "Comparative analysis and characterization of expressed sequence tags
in gilthead sea bream (Sparus aurata) liver and embryos.";
RL Aquaculture 243:69-81 (2005).
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----
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CC -----
CC EMBL; AY50955; AAT44423.1; -; mRNA.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
SQ SEQUENCE 346 AA; 38624 MW; 75468AFCEB8048F5 CRC64;
Query Match 100.0%; Score 38; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEDEINK 7
Db 62 YEDEINK 68
|||||
RESULT 7
Q96910 HUMAN PRELIMINARY; PRT; 365 AA.
ID Q96910;
AC Q96910;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 2.
DT 07-FEB-2006, entry version 23.
DE KRT8 protein (fragment).
GN Name=KRT8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

```
RT and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
RC [2]
RP NUCLEOTIDE SEQUENCE.
RG TISSUE=Placenta;
RL NIH MGC Project;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BC011373; AAH11373.2; -; mRNA.
DR Ensembl; ENSG00000170421; Homo sapiens.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893:SP5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament.
FT NON TER 1
SQ SEQUENCE 365 AA; 41108 MW; 57CD83091D0635E8 CRC64;

Query Match 100.0%; Score 38; DB 2; Length 365;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINK 7
Db 61 YEDEINK 67

RESULT 8
Q99MH7 MOUSE PRELIMINARY; PRT; 381 AA.
AC Q99MH7;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Cytokeratin KRT2-6HF (Fragment).
GN Name=Krtcap1; Synonyms=Krt2-6hf;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C3H/HeN;
RX MEDLINE=22286385; PubMed=12399393;
RA Polier C., Yoshiki A., Fujiwara K., Guenet J.-L., Kusakabe M.;
RT "Hague (Hag): a new mouse hair mutation with an unstable semidominant
RT allele.";
RL Genetics 162:831-840 (2002).
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF343088; AAK17206.1; -; mRNA.
DR HSSP; P08670; IKG4.
DR Ensembl; ENSMUSG0000022986; Mus musculus.
DR MGI; MGI:1923500; Krtcap1.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR InterPro; IPR003054; Keratin_II.
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DR PANTHER; PTHR1893:SP5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
FT NON TER 1
SQ SEQUENCE 381 AA; 42383 MW; 4143A882F7F6E9A1 CRC64;

Query Match 100.0%; Score 38; DB 2; Length 381;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINK 7
Db 70 YEDEINK 76

RESULT 9
K2C6D HUMAN STANDARD; PRT; 384 AA.
AC K2C6D;
DT 01-FEB-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-FEB-1996, sequence version 1.
DT 07-FEB-2006, entry version 44.
DE Keratin, type II cytoskeletal 6D (Cytokeratin-6D) (CK 6D) (K6d
DE keratin) (Fragment).
GN Name=KRT6D;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC TISSUE=Skin;
RX MEDLINE=95355491; PubMed=7543104; DOI=10.1074/jbc.270.31.18581;
RA Takahashi K., Paladini R.D., Coulombe P.A.;
RT "Cloning and characterization of multiple human genes and CDNAs
RT encoding highly related type II keratin 6 isoforms.";
RL J. Biol. Chem. 270:18581-18592 (1995).
CC -!- FUNCTION: There are two types of cytoskeletal and microfibrillar
CC keratin: I (acidic; 40-55 kDa) [K9 to K20] and II (neutral to
CC basic; 56-70 kDa) [K1 to K8]. Both a basic and an acidic keratin
CC are required for filament assembly.
CC -!- SUBUNIT: Heterodimer of a type I and a type II keratin. KRT6
CC isomers associate with KRT16 and/or KRT17.
CC -!- TISSUE SPECIFICITY: Constitutively expressed in distinct types of
CC epithelia such as those in oral mucosa, esophagus, papillae of
CC tongue and hair follicle outer root sheath.
CC -!- MISCELLANEOUS: There are at least six isoforms of human type II
CC keratin 6 (K6).
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; L42610; AAB60696.1; -; Genomic_DNA.
DR EMBL; L42603; AAB60696.1; JOINED; Genomic_DNA.
DR EMBL; L42604; AAB60696.1; JOINED; Genomic_DNA.
DR EMBL; L42605; AAB60696.1; JOINED; Genomic_DNA.
DR EMBL; L42606; AAB60696.1; JOINED; Genomic_DNA.
DR EMBL; L42607; AAB60696.1; JOINED; Genomic_DNA.
DR EMBL; L42608; AAB60696.1; JOINED; Genomic_DNA.
DR EMBL; L42609; AAB60696.1; JOINED; Genomic_DNA.
DR PIR; I61769; I61769.
DR HSSP; P08670; IKG4.
DR Ensembl; ENSG00000170465; Homo sapiens.
DR HGNC; HGNC:20405; KRT6D.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; NAS.
DR GO; GO:0030154; P:cell differentiation; NAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; NAS.
DR InterPro; IPR001664; IF.
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DR InterPro; IPR003054; Keratin II.
DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Coiled coil; Intermediate filament; Keratin.
FT CHAIN <1 384 Keratin, type II cytoskeletal 6D.
FT REGION <1 292 Rod.
FT REGION <1 18 Coil 1A.
FT REGION 19 37 Linker 1.
FT REGION 19 37 Linker 1B.
FT REGION 38 129 Coil 1B.
FT REGION 130 153 Linker 12.
FT REGION 154 292 Coil 2.
FT REGION 293 384 Tail.
FT SITE 234 234 Stutter.
FT NON TER 1 1
SQ SEQUENCE 384 AA; 42468 MW; D69DCF808C94E91 CRC64;

Query Match 100.0%; Score 38; DB 1; Length 384;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
Db 73 YEDEINK 79

RESULT 10
O4SRP0_TETNG PRELIMINARY; PRT; 417 AA.
ID O4SRP0_TETNG
AC O4SRP0_TETNG
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Chromosome undetermined SCAR14505, whole genome shotgun sequence.
GN ORFNames=GSTENG00013917001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphia; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segreus B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poullain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schacherer V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
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DR EMBL; CAAE01014505; CAF96692.1; -; Genomic DNA.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR003054; Keratin II.
DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament.
SQ SEQUENCE 417 AA; 46557 MW; B2F4D4E29B625589 CRC64;

Query Match 100.0%; Score 38; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
Db 222 YEDEINK 228

RESULT 11
K2C2_XENLA STANDARD; PRT; 419 AA.
ID K2C2_XENLA
AC P04265;
DT 20-MAR-1987, integrated into UniProtKB/Swiss-Prot.
DT 20-MAR-1987, sequence version 1.
DT 07-FEB-2006, entry version 39.
DE Keratin, type II cytoskeletal I (Clone PUF164) (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=86011576; PubMed=2413219;
RA Hoffmann W., Franz J.K., Franke W.W.;
RT "Amino acid sequence microheterogeneities of basic (type II)
RT cytokeratins of Xenopus laevis epidermis and evolutionary
RT conservativity of helical and non-helical domains.";
RL J. Mol. Biol. 184:713-724(1985).
CC -!- SUBUNIT: Heterotrimer of two type I and two type II keratins.
CC -!- MISCELLANEOUS: There are two types of cytoskeletal and
CC microfibrillar keratin, I (acidic) and II (neutral to basic) (40-
CC 55 and 56-70 kilodaltons, respectively).
CC -!- SIMILARITY: Belongs to the intermediate filament family.
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EMBL; X02895; CAA26654.1; -; mRNA.
DR PIR; A02952; KRXL2B.
DR HSP; P08670; 1GK4.
DR InterPro; IPR001664; IF.
DR InterPro; IPR003054; Keratin II.
DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Coiled coil; Intermediate filament; Keratin.
FT CHAIN <1 419 Keratin, type II cytoskeletal I.
FT REGION <1 271 Rod.
FT REGION <1 16 Linker 1.
FT REGION 17 108 Coil 1B.
FT REGION 109 132 Linker 12.
FT REGION 133 271 Coil 2.
FT REGION 272 419 Tail.
FT SITE 215 215 Stutter.
FT NON TER 1 1
SQ SEQUENCE 419 AA; 44595 MW; 15D79584FC31DF15 CRC64;
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Query Match 100.0%; Score 38; DB 1; Length 419;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINK 7
 |||||
 Db 52 YEDEINK 58

RESULT 12
 K2C1 XENLA STANDARD; PRT; 425 AA.
 AC P04266;
 DT 20-MAR-1987, integrated into UniProtKB/Swiss-Prot.
 DT 20-MAR-1987, sequence version 1.
 DT 07-FEB-2006, entry version 39.
 DE Keratin, type II cytoskeletal I (Clone PUF23) (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [mRNA].
 RX MEDLINE=86011576; PubMed=2413219;
 RA Hoffmann W., Franz J.K., Franke W.W.
 RT "Amino acid sequence microheterogeneities of basic (type II) cyokeratins of Xenopus laevis epidermis and evolutionary conservativity of helical and non-helical domains."
 J. Mol. Biol. 184:713-724 (1985).
 CC -!- SUBUNIT: Heterotetramer of two type I and two type II keratins.
 CC -!- MISCELLANEOUS: There are two types of cytoskeletal and microfibrillar keratin, I (acidic) and II (neutral to basic) (40-55 and 56-70 kilodaltons, respectively).
 CC -!- SIMILARITY: Belongs to the intermediate filament family.
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 EMBL; X02894; CAA26653.1; -; mRNA.
 PIR; A02953; KRXL2A.
 HSSP; P08670; 1GK4.
 DR InterPro; IPR001664; IF.
 DR InterPro; IPR002957; Keratin_I.
 DR InterPro; IPR003054; Keratin_II.
 DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
 DR Pfam; PF00036; Filament; 1.
 DR PRINTS; PR01248; TYPE1KERATIN.
 DR PROSITE; PS00226; IF; 1.
 KW Coiled coil; Intermediate filament; Keratin.
 FT CHAIN <1 425 Keratin, type II cytoskeletal I.
 FT REGION <1 292 Rod.
 FT REGION <1 16 Coil 1A.
 FT REGION 17 37 Linker 1.
 FT REGION 38 129 Coil 1B.
 FT REGION 130 153 Linker 12.
 FT REGION 154 292 Coil 2.
 FT REGION 293 425 Tail.
 FT SITE 236 236 Stutter.
 FT NON TER 1
 SQ SEQUENCE 425 AA; 45725 MW; D58D15DEC8C1C4E3 CRC64;

Query Match 100.0%; Score 38; DB 1; Length 425;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINK 7
 |||||
 Db 73 YEDEINK 79

RESULT 13
 O42435 NOTVI PRELIMINARY; PRT; 461 AA.
 AC O42435;
 DT 01-JAN-1998, integrated into UniProtKB/TREMBL.
 DT 01-JAN-1998, sequence version 1.
 DT 07-FEB-2006, entry version 27.
 DE Cytokeratin type II (Fragment).
 GN Name=K11;
 OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
 OC Notophthalmus.
 OX NCBI_TaxID=8316;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Limb blastema;
 RA MEDLINE=91372147; PubMed=1716554;
 RX Ferretti P., Brookes J.P., Brown R.;
 RT "A new type II keratin restricted to normal and regenerating limbs and tails is responsive to retinoic acid."
 Development 111:497-507 (1991).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Limb blastema;
 RA Ferretti P.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the intermediate filament family.
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 EMBL; AJ001295; CAA04655.1; -; mRNA.
 PIR; A43782; A43782.
 HSSP; P08670; 1GK7.
 DR GO; GO:0005882; C:intermediate filament; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR001664; IF.
 DR InterPro; IPR003054; Keratin_II.
 DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
 DR Pfam; PF00036; Filament; 1.
 DR PRINTS; PR01276; TYPE2KERATIN.
 DR PROSITE; PS00226; IF; 1.
 KW Intermediate filament; Keratin.
 FT NON TER 1
 SQ SEQUENCE 461 AA; 50638 MW; F3A018A7C10CA0FD CRC64;
 Query Match 100.0%; Score 38; DB 2; Length 461;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINK 7
 |||||
 Db 134 YEDEINK 140

RESULT 14
 K2C8 HUMAN STANDARD; PRT; 482 AA.
 AC P05787; Q14099; Q14716; Q14717; Q96J60;
 DT 01-NOV-1988, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1997, sequence version 5.
 DT 07-FEB-2006, entry version 72.
 DE Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8).
 GN Name=KRT8; Synonyms=CYK8;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=90258929; PubMed=1692965;
RA Yamamoto R., Kao L.C., McKnight C.E., Strauss J.F. III;
RT "Cloning and sequence of cDNA for human placental cytokeratin 8.
RT Regulation of the mRNA in trophoblastic cells by cAMP.";
RL Mol. Endocrinol. 4:370-374(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=90215304; PubMed=1691124; DOI=10.1016/0378-1119(90)90285-Y;
RA Krauss S., Franke W.W.;
RT "Organization and sequence of the human gene encoding cytokeratin 8.";
RL Gene 86:241-249(1990).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91145351; PubMed=1705144;
RA Wassem A., Alexander C.M., Steel J.B., Lane E.B.;
RT "Embryonic simple epithelial keratins 8 and 18: chromosomal location
RT emphasizes difference from other keratin pairs.";
RL New Biol. 2:464-478(1990).
RN [4]
RP NUCLEOTIDE SEQUENCE, AND PHOSPHORYLATION SITES SER-23 AND SER-431.
RX MEDLINE=97207326; PubMed=9054461; DOI=10.1074/jbc.272.11.7556;
RA Ku N.-O., Omary M.B.;
RT "Phosphorylation of human keratin 8 in vivo at conserved head domain
RT serine 23 and at epidermal growth factor-stimulated tail domain serine
RT 431.";
RL J. Biol. Chem. 272:7556-7564(1997).
RN [5]
RP TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP NUCLEOTIDE SEQUENCE OF 1-230.
RX MEDLINE=89261783; PubMed=2471065;
RA Kulesh D.A., Cecena G., Darmon Y.M., Vasseur M., Oshima R.G.;
RT "Posttranslational regulation of keratins: degradation of mouse and
RT human keratins 18 and 8.";
RL Mol. Cell. Biol. 9:1553-1565(1989).
RN [7]
RP NUCLEOTIDE SEQUENCE OF 204-482.
RX MEDLINE=87134779; PubMed=2434381;
RA Leube R.E., Bosch F.X., Romano V., Zimbelmann R., Hofler H.,
RA Franke W.W.;
RT "Cytokeratin expression in simple epithelia. III. Detection of mRNAs
RT encoding human cytokeratins nos. 8 and 18 in normal and tumor cells by
RT hybridization with cDNA sequences in vitro and in situ.";
RL Differentiation 33:69-85(1986).
RN [8]
RP PARTIAL PROTEIN SEQUENCE.
RX MEDLINE=97295306; PubMed=9150948;
RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
RT "A two-dimensional gel database of human colon carcinoma proteins.";
RT Electrophoresis 18:605-613(1997).
RN [9]
RP INTERACTION WITH PNN.
RX PubMed=10809736; DOI=10.1074/jbc.275.20.14910;
RA Shi J., Sugrue S.P.;
RT "Dissection of protein linkage between keratins and pinin, a protein
RT with dual location at desmosome-intermediate filament complex and in
RT the nucleus.";
RL J. Biol. Chem. 275:14910-14915(2000).
RN [10]
RP PHOSPHORYLATION SITE SER-73.
RX MEDLINE=21909496; PubMed=11781324; DOI=10.1074/jbc.M111436200;
RA He T., Stepulak A., Holmstrom T.H., Omary M.B., Eriksson J.E.;
RT "The intermediate filament protein keratin 8 is a novel cytoplasmic
RT substrate for c-Jun N-terminal kinase.";
RL J. Biol. Chem. 277:10767-10774(2002).
RN [11]
RP PHOSPHORYLATION SITE SER-73, AND MUTAGENESIS OF LEU-71 AND SER-73.
RX MEDLINE=21909510; PubMed=11788583; DOI=10.1074/jbc.M107623200;
RA Ku N.O., Azhar S., Omary M.B.;
RT "Keratin 8 phosphorylation by p38 kinase regulates cellular keratin
RT filament reorganization: modulation by a keratin 1-like disease
RT causing mutation.";
RL J. Biol. Chem. 277:10775-10782(2002).
RN [12]
RP INTERACTION WITH HCV CORE PROTEIN.
RX PubMed=15846844; DOI=10.1002/pmic.200401093;
RA Kang S.-M., Shin M.-J., Kim J.-H., Oh J.-W.;
RT "Proteomic profiling of cellular proteins interacting with the
RT hepatitis C virus core protein.";
RL Proteomics 5:2227-2237(2005).
RN [13]
RP VARIANTS CRYPTOGENIC CIRRHOSIS VAL-52; CYS-53 AND CYS-61, AND VARIANT
RP VAL-62.
RX PubMed=1274528; DOI=10.1073/pnas.0936165100;
RA Ku N.-O., Darling J.M., Krams S.M., Esquivel C.O., Keefe E.B.,
RA Sibley R.K., Lee Y.M., Wright T.L., Omary M.B.;
RT "Keratin 8 and 18 mutations are risk factors for developing liver
RT disease of multiple etiologies.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:6063-6068(2003).
CC -!- SUBUNIT: Heterotrimer of two type I and two type II keratins.
CC Keratin 8 associates with keratin 18. Interacts with HCV core
CC protein and PNN.
CC -!- PTM: Phosphorylation on serine residues is enhanced during EGF
CC stimulation and mitosis. Ser-73 phosphorylation plays an important
CC role in keratin filament reorganization.
CC -!- DISEASE: Defects in KRT8 are a cause of cryptogenic cirrhosis
CC [MIM:215600].
CC -!- MISCELLANEOUS: There are two types of cytoskeletal and
CC microfibrillar keratin: I (acidic; 40-55 kDa) [K9 to K20] and II
CC (neutral to basic; 56-70 kDa) [K1 to K8].
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -!- DATABASE: NAME=Human Intermediate Filament Mutation Database;
CC WWW="http://www.interfil.org".
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; M34225; AAA35748.1; -; mRNA.
DR EMBL; M34482; AAA35763.1; -; Genomic_DNA.
DR EMBL; X74929; CAA52882.1; -; mRNA.
DR EMBL; U76549; AAB18966.1; -; mRNA.
DR EMBL; X98614; CAA67203.1; -; mRNA.
DR EMBL; M26512; AAA51542.1; -; mRNA.
DR EMBL; BC00654; AAH00654.2; ALT INIT; mRNA.
DR EMBL; X12882; CAA31376.1; -; mRNA.
DR EMBL; X74981; CAA52916.1; -; Genomic_DNA.
DR PIR; A34720; A34720.
DR HSP; P08670; IGK7.
DR IntAct; P05787; -.
DR GlycoSuiteDB; P05787; -.
DR SWISS-2DPAGE; P05787; HUMAN.
DR Sienaa-2DPAGE; P05787; -.
DR Ensembl; ENSG00000170421; Homo sapiens.

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DR HGNC; HGNC:6446; KRT8.
DR MIM; 148060; Gene.
DR MIM; 215600; Phenotype.
DR LinkHub; P05787; -.
DR GO; GO:0005882; C:intermediate filament; NAS.
DR GO; GO:0005198; P:structural molecule activity; NAS.
DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; NAS.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
DR Coiled coil; Direct protein sequencing; Disease mutation;
KW Intermediate filament; Keratin; Phosphorylation; Polymorphism.
FT INIT_MET 0 0
FT CHAIN 1 482 Keratin, type II cytoskeletal 8.
FT REGION 1 89 Head.
FT REGION 90 397 Rod.
FT REGION 90 125 Coil 1A.
FT REGION 126 142 Linker 1.
FT REGION 143 234 Coil 1B.
FT REGION 235 258 Linker 12.
FT REGION 259 397 Coil 2.
FT REGION 260 381 Necessary for interaction with PNN.
FT REGION 398 482 Tail.
FT SITE 341 341 Stutter.
FT MOD_RES 23 23 Phosphoserine.
FT MOD_RES 73 73 Phosphoserine (by MAPK).
FT MOD_RES 431 431 Phosphoserine (by CaMK2 and MAPK).
FT VARIANT 52 52 G -> V (in cryptogenic cirrhosis).
FT VARIANT 53 53 Y -> C (in cryptogenic cirrhosis).
FT VARIANT 61 61 G -> C (in cryptogenic cirrhosis).
FT VARIANT 61 61 /FTID=VAR_023060.

Query Match 100.0%; Score 38; DB 1; Length 482;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YEDEINK 7
Db 178 YEDEINK 184
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RESULT 15
K2C8_RAT
ID K2C8_RAT STANDARD; PRT; 482 AA.
AC Q10758; Q5WPB3;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997, sequence version 2.
DE 07-FEB-2006, entry version 40.
DE Keratin, type II cytoskeletal 8 (Cytokeratin-8) (Keraton-8)
DE (K8) (Cytokeratin endo A).
GN Name=Krt8; Synonyms=Krt2-8;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Sprague-Dawley; TISSUE=Prostate;
RA MEDLINE=92129104; PubMed=1370816;
RA Hsieh J.-T., Zhou H.E., Wang X.-H., Liew C.-C., Chung L.W.K.;
RT "Regulation of basal and luminal cell-specific cytokeratin expression
in rat accessory sex organs. Evidence for a new class of androgen-
repressed genes and insight into their pairwise control.";
RL J. Biol. Chem. 267:2303-2310(1992).

[2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=95042924; PubMed=7525090;
RA Wang X., Hsieh J.-T., Zhou H.E.;
RT "Cloning and characterization of a specific cytokeratin-8 cDNA from
rat prostatic epithelium.";
RL Zhongguo Yi Xue Ke Xue Yuan Xue Bao 16:1-7(1994).
[3]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Heart muscle;
RX PubMed=15247274; DOI=10.1074/jbc.M400128200;
RA Ursitti J.A., Lee P.C., Resneck W.G., McNally M.M., Bowman A.L.,
O'Neill A., Stone M.R., Bloch R.J.;
RT "Cloning and characterization of cytokeratins 8 and 19 in adult rat
striated muscle. Interaction with the dystrophin glycoprotein
complex.";
RL J. Biol. Chem. 279:41830-41838(2004).
[4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Placenta, and Thymus;
RG NIH - Mammalian Gene Collection (MGC) project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
[5]
RP PROTEIN SEQUENCE OF 8-17; 23-74 AND 414-451.
RX MEDLINE=96220159; PubMed=8660345; DOI=10.1006/bbrc.1996.0546;
RA Ando S., Tokui T., Yano T., Inagaki M.;
RT "Keratin 8 phosphorylation in vitro by cAMP-dependent protein kinase
occurs within the amino- and carboxyl-terminal end domains.";
RL Biochem. Biophys. Res. Commun. 221:67-71(1996).
[6]
RP PROTEIN SEQUENCE OF 264-272, AND SUBCELLULAR LOCATION.
RC TISSUE=Liver;
RX PubMed=16128803; DOI=10.1111/j.1742-4658.2005.04847.x;
RA Segawa M., Niino K., Mineki R., Kaga N., Murayama K., Sugimoto K.,
Watanabe Y., Furukawa K., Horigome T.;
RT "Proteome analysis of a rat liver nuclear insoluble protein fraction
and localization of a novel protein, ISP36, to compartments in the
interchromatin space.";
RL FEBS J. 272:4327-4338(2005).
-!- SUBUNIT: Heterotrimer of two type I and two type II keratins.
CC Keratin 8 associates with keratin 18. Interacts with PNN (By
similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear matrix.
-!- MISCELLANEOUS: There are two types of cytoskeletal and
microfibrillar keratin, I (acidic) and II (neutral to basic) (40-
55 and 56-70 kilodaltons, respectively).
-!- SIMILARITY: Belongs to the intermediate filament family.
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-----
EMBL; M63482; AAA19667.1; -; mRNA.
EMBL; M63482; AAA19668.1; ALT INIT; mRNA.
EMBL; S76054; -; NOT_ANNOTATED_CDS; mRNA.
EMBL; AY464139; AAK36875.1; -; mRNA.
EMBL; BC091106; AAH91106.1; -; mRNA.
EMBL; BC097497; AAH97497.1; -; mRNA.
HSSP; P08670; 1GK7.
Ensembl; ENSRNOG0000009779; Rattus norvegicus.
RG; 2984; Krt2-8.
LinkHub; Q10758; -.
GO; GO:0045095; C:Keratin filament; IDA.
InterPro; IPR001664; IF.
InterPro; IPR002957; Keratin_I.
InterPro; IPR003054; Keratin_II.
PANTHER; PTHR1893:SF5; Keratin_II; 1.
Pfam; PF00038; Filament; 1.
PRINTS; PR01248; TYPE1KERATIN.
PRINTS; PR01276; TYPE2KERATIN.
PROSITE; PS00226; IF; 1.
Coiled coil; Direct protein sequencing; Intermediate filament;
Keratin; Nuclear protein; Phosphorylation.
INIT_MET 0 0 By similarity.
INIT_MET 0 0 By similarity.

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FT CHAIN      1  482      Keratin, type II cytoskeletal 8.  
FT REGION    1  89      /FTId=PRO_0000063742.  
FT REGION    90 397      Head.  
FT REGION    90 125      Rod.  
FT REGION    126 142      Coil 1A.  
FT REGION    143 234      Linker 1.  
FT REGION    235 258      Coil 1B.  
FT REGION    259 397      Linker 12.  
FT REGION    260 381      Coil 2.  
FT REGION    398 482      Necessary for interaction with PNN (By  
FT SITE      341 341      similarity).  
FT SITE      341 341      Tail.  
FT MOD_RES   23 23      Stutter.  
FT MOD_RES   431 431      Phosphoserine (By similarity).  
SQ SEQUENCE  482 AA; 53888 MW; C4DD2FE25CB2C18B CRC64;  
Phosphoserine (By similarity).  
Query Match      100.0%; Score 38; DB 1; Length 482;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY      1 YEDEINK 7  
Db      178 YEDEINK 184
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Job time : 72.7311 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 18:28:26 ; Search time 60.8252 Seconds
(without alignments)
52.618 Million cell updates/sec

Title: US-10-774-928a-1

Perfect score: 38

Sequence: 1 YEDEINK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*
10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	7	6	Aao26381 Psoriasis
2	38	100.0	7	9	Adv04406 Leishmania
3	38	100.0	8	6	Aao26392 Psoriasis
4	38	100.0	8	9	Adv04417 Leishmania
5	38	100.0	113	6	Abg74871 Human cyt
6	38	100.0	132	8	Adr98929 Lung spec
7	38	100.0	180	8	Adn99441 Novel hum
8	38	100.0	186	4	Aam16318 Peptide #
9	38	100.0	186	4	Aam16310 Peptide #
10	38	100.0	186	4	Aam28813 Peptide #
11	38	100.0	186	4	Abb30140 Peptide #
12	38	100.0	186	4	Abb20752 Protein #
13	38	100.0	186	4	Aam68514 Human bon
14	38	100.0	186	4	Aam56141 Human bra
15	38	100.0	186	4	Abg50183 Human liv
16	38	100.0	186	4	Aam04056 Peptide #
17	38	100.0	186	4	Abg09410 Novel hum
18	38	100.0	186	5	Abg38095 Human pep
19	38	100.0	233	8	Adr98930 Lung spec
20	38	100.0	273	4	Abg26376 Novel hum
21	38	100.0	275	4	Abg15282 Novel hum
22	38	100.0	278	8	Abm81219 Tumour-as
23	38	100.0	282	8	Abm80614 Tumour-as

24	38	100.0	328	7	ADC31601	Adc31601 Human nov
25	38	100.0	342	7	Ade15641	Ade15641 Human str
26	38	100.0	347	4	Abg15636	Abg15636 Novel hum
27	38	100.0	347	4	Abg09411	Abg09411 Novel hum
28	38	100.0	394	4	Abg26375	Abg26375 Novel hum
29	38	100.0	398	6	Abg38086	Abg38086 Human cyt
30	38	100.0	401	8	Abm80365	Abm80365 Tumour-as
31	38	100.0	403	8	Abm81640	Abm81640 Tumour-as
32	38	100.0	416	4	Abg23034	Abg23034 Novel hum
33	38	100.0	420	8	Adp29879	Adp29879 Human sec
34	38	100.0	429	4	Abg19547	Abg19547 Novel hum
35	38	100.0	429	4	Abg19546	Abg19546 Novel hum
36	38	100.0	476	8	Adr66033	Adr66033 Human pro
37	38	100.0	476	8	Adr66931	Adr66931 Human pro
38	38	100.0	477	4	AAU06112	AAU06112 Novel hum
39	38	100.0	480	10	AEF92273	AEF92273 Human cyt
40	38	100.0	481	6	ABU52604	ABU52604 Human NOV
41	38	100.0	482	4	ABG08132	ABG08132 Novel hum
42	38	100.0	482	6	AAE38082	AAE38082 Human cyt
43	38	100.0	482	8	ADT51418	ADT51418 Human ker
44	38	100.0	482	8	ADT51421	ADT51421 Human ker
45	38	100.0	482	8	ADT51419	ADT51419 Human ker

ALIGNMENTS

RESULT 1
AAO26381
ID AAO26381 standard; peptide; 7 AA.
XX
AC AAO26381;
XX
DT 30-JAN-2003 (first entry)
XX
DE Psoriasis treating immunotherapeutic peptide, SEQ ID No 1.
XX
KW Antipsoriatic; immunostimulant; gene therapy; pharmaceutical composition;
KW vaccine; immunogenic variant; immunotherapeutic agent; psoriasis;
KW gene therapy.
XX
OS Leishmania sp.
XX
PN WO200274239-A2.
XX
PD 26-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006496.
XX
PR 16-MAR-2001; 2001US-00809003.
XX
PA (AKIV-) AKIVA LLC.
XX
PI O'daly JA;
XX
DR WPI; 2003-018763/01.
XX
PT New polypeptide and immunogenic variants comprising amino acid sequences of particulate antigens, useful for the treatment and clinical remission of psoriasis.
XX
PS Claim 1; Page 43; 56pp; English.
XX
CC The invention relates to a polypeptide comprising an isolated amino acid sequence or immunogenic variants selected from any of 14 fully defined sequences of 7-16 amino acids, given in the specification. The immunotherapeutic agents and a pharmaceutical compositions comprising polynucleotides and vectors of the invention are useful for the treatment and clinical remission of psoriasis. The isolated nucleic acids are useful as probes. The sequences of the invention can be used in the treatment of disorders by gene therapy. This sequence represents one of the 14 immunotherapeutic peptides of the invention

```
SQ Sequence 7 AA;
Query Match 100.0%; Score 38; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. NO. 2.1e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEDEINK 7
Db 1 YEDEINK 7
RESULT 2
ADV04406
ID ADV04406 standard; peptide; 7 AA.
XX
AC ADV04406;
XX
DT 24-FEB-2005 (first entry)
XX
DE Leishmania immunotherapeutic peptide SEQ ID NO:1.
XX
KW T-lymphocyte; immunogenicity; antigen; antipsoriatic; immunostimulant;
KW psoriasis.
XX
OS Leishmania sp.
XX
PN US2004241168-A1.
XX
PD 02-DEC-2004.
XX
PF 09-FEB-2004; 2004US-00774928.
XX
PR 16-MAR-2001; 2001US-00809003.
PR 17-OCT-2003; 2003US-00687892.
XX
PA (ODAL/) ODALY J A.
XX
PI Odaly JA;
XX
DR WPT; 2005-011563/01.
XX
PT Inhibiting selectively T-cell rolling in human, by administering compound
PT interfering with cutaneous lymphocyte antigen-E selectin interaction and
PT leukocyte function associated antigen-1 interaction.
XX
PS Claim 9; SEQ ID NO 1; 21pp; English.
XX
CC The invention relates to a novel method for selectively inhibiting T-cell
CC rolling in a human host, comprising administering a compound that
CC selectively interferes with the cutaneous lymphocyte antigen (CLA)-E
CC selectin interaction and leukocyte function associated antigen (LFA) -
CC 1/intercellular adhesion molecule (ICAM) and very late antigen
CC (VLA)/vascular cell adhesion molecule (VCAM) interactions. The compound
CC includes an immunotherapeutic agent, which comprises a purified protein
CC extract that is isolated by diethylaminoethyl Sephadex chromatography of
CC a Nonidet P-40 insoluble particulate antigen fraction derived from
CC isolated killed cells of amastigotes from one or more species of the
CC Leishmania genus, where the particulate antigen fraction is solubilized
CC with 8M urea and 0.025 M Tris(hydroxymethyl)aminomethane pH 8.3, and
CC to diethylaminoethyl Sephadex and is eluted with a solution comprising
CC 0.1 M sodium chloride, 8 M urea and 0.025 M
CC Tris(hydroxymethyl)aminomethane pH 8.3, and the purified protein extract
CC includes polypeptides having apparent molecular weights of 73, 80 and 82
CC kDa, after total reduction and alkylation. The species is Leishmaniosis,
CC L. venezuelensis, L. brasiliensis and/or L. chagasi. A compound of the
CC invention has antipsoriatic and immunostimulant activity, and inhibits T-
CC cell rolling by interfering with CLA-E selectin interaction and LFA-
CC 1/ICAM and VLA/VCAM interactions. The method is useful for selectively
CC inhibiting T-cell rolling in a human host, and for treating psoriasis.
CC The present sequence represents a Leishmania peptide used in the
CC invention.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 38; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. NO. 2.1e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEDEINK 7
Db 1 YEDEINK 7
RESULT 3
AAO26392
ID AAO26392 standard; peptide; 8 AA.
XX
AC AAO26392;
XX
DT 30-JAN-2003 (first entry)
XX
DE Psoriasis treating immunotherapeutic peptide, SEQ ID NO 12.
XX
KW Antipsoriatic; immunostimulant; gene therapy; pharmaceutical composition;
KW vaccine; immunogenic variant; immunotherapeutic agent; psoriasis;
KW gene therapy.
XX
OS Leishmania sp.
XX
PN WO200274239-A2.
XX
PD 26-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006496.
XX
PR 16-MAR-2001; 2001US-00809003.
XX
PA (AKIV-) AKIVA LLC.
XX
PI O'daly JA;
XX
DR WPI; 2003-018763/01.
XX
PT New polypeptide and immunogenic variants comprising amino acid sequences
PT of particulate antigens, useful for the treatment and clinical remission
PT of psoriasis.
XX
PS Claim 1; Page 43; 56pp; English.
XX
CC The invention relates to a polypeptide comprising an isolated amino acid
CC sequence or immunogenic variants selected from any of 14 fully defined
CC sequences of 7-16 amino acids, given in the specification. The
CC immunotherapeutic agents and a pharmaceutical compositions comprising
CC polynucleotides and vectors of the invention are useful for the treatment
CC and clinical remission of psoriasis. The isolated nucleic acids are
CC useful as probes. The sequences of the invention can be used in the
CC treatment of disorders by gene therapy. This sequence represents one of
CC the 14 immunotherapeutic peptides of the invention
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 38; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. NO. 2.1e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEDEINK 7
Db 2 YEDEINK 8
RESULT 4
ADV04417
ID ADV04417 standard; peptide; 8 AA.
XX
AC ADV04417;
XX
```


XX	Human cytokera	1 protein frag	
XX	DE	XX	
XX	Cytokeratin-1	inflammation	infection; soluble; sepsis; veterinary;
KW	sepsis-like	systemic infection	human.
XX	Homo sapiens.		
OS	WO2003002600-A1.		
PN	09-JAN-2003.		
XX	12-JUN-2002;	2002WO-EP006473.	
XX	27-JUN-2001;	2001DE-01030985.	
XX	(BRAH-) BRAHMS AG.		
PA	Bergmann A, Struck J, Uehlein M;		
XX	WPI; 2003-201491/19.		
XX	New use of soluble cytokera	1 fragments from body fluid	are tissue as
PT	marker peptides or to provide	therapeutics for the diagnosis,	prognosis
PT	and treatment of inflammatory	disease and infection, including	systemic
PT	inflammation.		
XX	Claim 4;	Page 41; 51pp;	German.
PS	This invention describes a novel	use of soluble cytokera	1 fragments
CC	from body fluid or tissue as	marker peptides for the	detection, prognosis
CC	and control of inflammation	and infection or as a	therapeutic target for
CC	inflammation and infection.	The invention also	describes a method of
CC	producing a soluble cytokera	1 fragment in rich or	pure form from a
CC	human material rich in	cytokera	1 by enzymatically
CC	splitting the		
CC	cytokera	1 with endoprotease to	obtain the hydrolysis
CC	purifying the resulting	fragments. The novel	cytokera
CC	useful for the differential	diagnosis, early	recognition and
CC	evaluation of severity of	sepsis and heavy	infection, particularly
CC	sepsis		
CC	therapy, particularly the	fragment or it's	specific antibody is
CC	treat inflammatory	disease or infection.	This sequence
CC	human cytokera	1 protein	fragment described
CC	invention		
XX	Sequence 113	AA;	
SQ	Query Match	100.0%;	Score 38; DB 6; Length 113;
	Best Local Similarity	100.0%;	Pred. No. 11;
	Matches 7; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1 YEDEINK 7		
DB	85 YEDEINK 91		
RESULT 6			
ADR98929			
ID	ADR98929	standard; protein;	132 AA.
XX	AC	ADR98929;	
XX	18-NOV-2004	(first entry)	
DE	Lung specific gene	splice variant	encoded protein #101.
XX	cytostatic; gene	therapy; vaccine; lung;	diagnosis; cancer;
KW	non-cancerous lung	disease; lung tissue;	antagonist; gene
KW	transgenic animal;	splice variant.	
XX	Homo sapiens.		
XX	WO2004074430-A2.		

XX PD 02-SEP-2004.
 XX PF 08-DEC-2003; 2003WO-US038896.
 XX PR 06-DEC-2002; 2002US-0431307P.
 XX PR 06-DEC-2002; 2002US-0431510P.
 XX PR 06-DEC-2002; 2002US-0431516P.
 XX PA (DIAD-) DIADEXUS INC.
 XX PI Macina RA, Turner LR, Sun Y, Liu S;
 XX DR WPI; 2004-635553/61.
 XX DR N-PSDB; ADR98791.
 XX PT New isolated human lung specific nucleic acid molecule, useful for
 PT identifying, diagnosing, monitoring, staging, imaging and treating lung
 PT cancer and non-cancerous diseases of the lung.
 XX PS Claim 1; SEQ ID NO 214; 542pp; English.
 XX CC The invention relates to a new isolated lung specific nucleic acid
 CC molecule (I) comprising any of 113 fully defined nucleotide sequences
 CC given in the specification, their encoded protein sequences, sequences
 CC selectively hybridizing to the nucleotide sequences or a sequence having
 CC at least 60% identity to the nucleotide sequences. The methods and
 CC compositions of the present invention are useful for identifying,
 CC diagnosing, monitoring, staging, imaging and treating lung cancer and non
 CC cancerous diseases of the lung. They are also used for identifying lung
 CC tissue, monitoring and identifying and/or designing antagonists of the
 CC polypeptide of the invention, gene therapy, production of transgenic
 CC animals and production of engineered lung tissue for treatment and
 CC research. Lung specific genes (LSEs) were identified by a systematic
 CC analysis of gene expression data in the LIFESEQ Gold database using the
 CC data mining software package candidate lead automatic search program
 CC (CLASP). Genes were grouped into gene bins where each bin is a cluster of
 CC sequences grouped together where they share a common contig.
 CC Differentially expressed tissue-specific genes were selected based on the
 CC percentage level in the targeted tissue versus all the other tissues. The
 CC expression levels for each gene in libraries of normal tissues or non-
 CC tumour tissues from cancer patients were compared with the expression
 CC levels in tissue libraries associated with tumour or disease. This
 CC sequence represents a protein of the invention.
 XX SQ Sequence 132 AA;
 Query Match 100.0%; Score 38; DB 8; Length 132;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEDEINK 7
 DB 47 YEDEINK 53
 RESULT 7
 ADN99441
 ID ADN99441 standard; protein; 180 AA.
 XX AC ADN99441;
 XX DT 29-JUL-2004 (first entry)
 XX DE Novel human protein sequence #257.
 XX KW anti-inflammatory; dermatological; neuroprotective; immunomodulator;
 KW antibacterial; virucide; antiparasitic; cytostatic; gene therapy;
 KW vaccine; inflammatory; CNS; immune disorder; cancer; psoriasis; diabetes;
 KW early aging; hormonal imbalance; ischemic heart disease;
 KW ulcerative colitis.
 XX PA Homo sapiens.
 XX OS

XX PN WO2004038003-A2.
 XX PD 06-MAY-2004.
 XX XX 24-OCT-2003; 2003WO-US0333947.
 XX PR 25-OCT-2002; 2002US-0421061P.
 XX PR 25-OCT-2002; 2002US-0421080P.
 XX PR 25-OCT-2002; 2002US-0421552P.
 XX PR 30-OCT-2002; 2002US-0421614P.
 XX PR 30-OCT-2002; 2002US-0422177P.
 XX PR 30-OCT-2002; 2002US-0422178P.
 XX PR 15-NOV-2002; 2002US-0426355P.
 XX PR 15-NOV-2002; 2002US-0426384P.
 XX PR 15-NOV-2002; 2002US-0426394P.
 XX PR 15-NOV-2002; 2002US-0426430P.
 XX PR 15-NOV-2002; 2002US-0426916P.
 XX PR 27-NOV-2002; 2002US-0429224P.
 XX PR 27-NOV-2002; 2002US-0429275P.
 XX PR 27-NOV-2002; 2002US-0429302P.
 XX PR 27-NOV-2002; 2002US-0429326P.
 XX PR 27-NOV-2002; 2002US-0429651P.
 XX PR 04-DEC-2002; 2002US-0430645P.
 XX PR 04-DEC-2002; 2002US-0430651P.
 XX PR 04-DEC-2002; 2002US-0430657P.
 XX PR 04-DEC-2002; 2002US-0430663P.
 XX PR 04-DEC-2002; 2002US-0430688P.
 XX PR 04-DEC-2002; 2002US-0430684P.
 XX PR 05-DEC-2002; 2002US-0430937P.
 XX PR 05-DEC-2002; 2002US-0430965P.
 XX PR 12-DEC-2002; 2002US-0431458P.
 XX PR 12-DEC-2002; 2002US-0433251P.
 XX PR 13-DEC-2002; 2002US-0433316P.
 XX PR 13-DEC-2002; 2002US-0433318P.
 XX PR 23-DEC-2002; 2002US-0436236P.
 XX PR 03-JAN-2003; 2003US-0437914P.
 XX PR 17-JAN-2003; 2003US-0440820P.
 XX PR 18-APR-2003; 2003US-0463700P.
 XX PR 18-APR-2003; 2003US-0463708P.
 XX PR 18-APR-2003; 2003US-0463716P.
 XX PR 18-APR-2003; 2003US-0463732P.
 XX PR 02-MAY-2003; 2003US-0467199P.
 XX PR 02-MAY-2003; 2003US-0467201P.
 XX PR 02-MAY-2003; 2003US-0467203P.
 XX PR 02-MAY-2003; 2003US-0467230P.
 XX PR 19-MAY-2003; 2003US-0471306P.
 XX PR 19-MAY-2003; 2003US-0471336P.
 XX PR 22-MAY-2003; 2003US-0472420P.
 XX PR 22-MAY-2003; 2003US-0472430P.
 XX PR 09-JUN-2003; 2003US-0476609P.
 XX PR 09-JUN-2003; 2003US-0476621P.
 XX PR 09-JUN-2003; 2003US-0476632P.
 XX PR 09-JUN-2003; 2003US-0476641P.
 XX PR 08-JUL-2003; 2003US-0485217P.
 XX PR 08-JUL-2003; 2003US-0485218P.
 XX PR 08-JUL-2003; 2003US-0485223P.
 XX PR 08-JUL-2003; 2003US-0485224P.
 XX PR 08-JUL-2003; 2003US-0485325P.
 XX PR 08-JUL-2003; 2003US-0485359P.
 XX PR 14-JUL-2003; 2003US-0486446P.
 XX PR 14-JUL-2003; 2003US-0486480P.
 XX PR 15-JUL-2003; 2003US-0486891P.
 XX PR 15-JUL-2003; 2003US-0486960P.
 XX PR 08-AUG-2003; 2003US-0493341P.
 XX PR 08-AUG-2003; 2003US-0493370P.
 XX PR 08-AUG-2003; 2003US-0493573P.
 XX PR 08-AUG-2003; 2003US-0493577P.
 XX PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 XX XX

PI Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RF, Kothakota S, Lin H, Linnemann T, Pierce K, Wang Y;
PI Wong JGP, Wu G, Zhang H, Zeng C;
XX
DR WPI: 2004-365511/34.
DR N-PSDB; ADN98657.
XX
PT New nucleic acid molecules, useful in preparing a composition for
PT treating or preventing e.g. inflammatory, CNS, bacterial or viral
PT disorders, cancer, psoriasis, diabetes, ischemic heart disease or
PT ulcerative colitis.
XX
XX
PS Claim 14; SEQ ID NO 1041; 532pp; English.
XX
CC The invention relates to a nucleic acid molecule comprising a
CC polynucleotide sequence or its complement that encodes a polypeptide. The
CC nucleic acid is useful in preparing a composition for treating or
CC preventing inflammatory, CNS, immune, bacterial or viral disorder,
CC cancer, psoriasis, diabetes, early aging, hormonal imbalance, ischemic
CC heart disease or ulcerative colitis. This sequence corresponds to a
CC protein of the invention.
XX
XX
SQ Sequence 180 AA;
Query Match 100.0%; Score 38; DB 8; Length 180;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEDEINK 7
DB 41 YEDEINK 47
RESULT 8
AAM16318
ID AAM16318 standard; protein; 186 AA.
XX
AC AAM16318;
XX
DT 12-OCT-2001 (first entry)
XX
DE Peptide #2752 encoded by probe for measuring cervical gene expression.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer.
XX
OS Homo sapiens.
XX
XX WO200157278-A2.
PN
PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000670.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI: 2001-488901/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human cervical epithelial cells.
PS Claim 27; SEQ ID NO 21144; 487pp; English.

CC The present invention relates to human single exon nucleic acid probes
CC (SENP: see AA110068-AA128459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 186 AA;
Query Match 100.0%; Score 38; DB 4; Length 186;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEDEINK 7
DB 174 YEDEINK 180
RESULT 9
ABB35310
ID ABB35310 standard; peptide; 186 AA.
XX
AC ABB35310;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #2816 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
XX WO200157277-A2.
PN
PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000669.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI: 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human fetal liver.
PS Claim 27; SEQ ID NO 27945; 639pp + Sequence Listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for measuring
XX human gene expression in a sample derived from human foetal liver. The
XX single exon nucleic acid probes may be used for predicting, measuring and
XX displaying gene expression in samples derived from human fetal liver. The
XX present sequence is a peptide encoded by a single exon nucleic acid probe
XX of the invention. Note: The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 186 AA;
Query Match 100.0%; Score 38; DB 4; Length 186;

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Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINK 7
Db 174 YEDEINK 180

RESULT 10
AAM28813
ID AAM28813 standard; protein; 186 AA.
XX
AC AAM28813;
XX
XX 17-OCT-2001 (first entry)
XX
DE Peptide #2850 encoded by probe for measuring placental gene expression.
XX
XX Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
OS Homo sapiens.
XX
XX WO200157272-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488997/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
XX Claim 27; SEQ ID NO 29082; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP:
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
XX Sequence 186 AA;
SQ
Query Match 100.0%; Score 38; DB 4; Length 186;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINK 7
Db 174 YEDEINK 180

RESULT 11
ABB30140
ID ABB30140 standard; peptide; 186 AA.
XX
XX ABB30140;
XX
XX 01-FEB-2002 (first entry)
DT

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XX Peptide #2791 encoded by breast cell single exon nucleic acid probe.
DE
XX
XX Human; microarray; single exon probe; gene expression; breast; disease;
KW cancer.
XX
XX Homo sapiens.
XX
XX WO200157271-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000662.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-496933/54.
XX
XX New spatially-addressable set of single exon nucleic acid probes, useful
PT for measuring gene expression in sample derived from human breast,
PT comprises number of single exon nucleic acid probes.
XX
XX Claim 27; SEQ ID NO 13108; 327pp + Sequence Listing; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and Br 474 cells. The method involves contacting the
CC probes with a collection of detectably labelled nucleic acids derived
CC from mRNA of human breast, and then measuring the label bound to each
CC probe of the microarray. The probes are useful for verifying the
CC expression of regions of genomic DNA predicted to encode proteins. They
CC are useful for gene discovery, and for determining predisposition and/or
CC prognosing breast disease. Gene expression analysis is useful for
CC assessing the toxicity of chemical agents on cells. The microarray of
CC this invention presents a far greater diversity of probes for measuring
CC gene expression, with far less bias than expressed sequence tag
CC microarrays. The method is suitable for rapid production of functional
CC information from genomic sequence. The present sequence is a peptide
CC encoded by a single exon nucleic acid probe of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 186 AA;
SQ
Query Match 100.0%; Score 38; DB 4; Length 186;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINK 7
Db 174 YEDEINK 180

RESULT 12
ABB20752
ID ABB20752 standard; protein; 186 AA.
XX
XX ABB20752;
XX
XX 23-JAN-2002 (first entry)
DT
XX
XX Protein #2751 encoded by probe for measuring heart cell gene expression.
DE

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XX KW Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX OS Homo sapiens.
XX PN WO200157274-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000666.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488999/53.
XX DR Single exon nucleic acid probes for analyzing gene expression in human
XX PT hearts.
XX PT hearts.
XX PS Claim 15; SEQ ID NO 22522; 530pp; English.
XX CC The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart (see
XX CCA21535-ABA41305). The present sequence is a protein encoded by one such
XX probe. The probes may be used for predicting, measuring and displaying
XX gene expression in samples derived from the human heart via microarrays.
XX By measuring gene expression, the probes are useful for predicting,
XX diagnosing, grading, staging, monitoring and prognosing diseases of the
XX human heart and vascular system e.g. cardiovascular disease,
XX hypertension, cardiac arrhythmias and congenital heart disease. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 186 AA;

Query Match 100.0%; Score 38; DB 4; Length 186;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
Db 174 YEDEINK 180

RESULT 13
AAM68514
ID AAM68514 standard; protein; 186 AA.
XX AC AAM68514;
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28820.
XX DE Human bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX KW Homo sapiens.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

Query Match 100.0%; Score 38; DB 4; Length 186;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
Db 174 YEDEINK 180

RESULT 14
AAM56141
ID AAM56141 standard; protein; 186 AA.
XX AC AAM56141;
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe encoded protein SEQ ID NO: 28246.
XX DE Human; brain expressed exon; gene expression analysis; probe; microarray;
XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX KW Homo sapiens.
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000667.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
```

XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX Example 4; SEQ ID NO 28246; 650pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention
XX
SQ Sequence 186 AA;
Query Match 100.0%; Score 38; DB 4; Length 186;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YEDEINK 7
Db 174 YEDEINK 180
RESULT 15
ABG50183
ID ABG50183 standard; peptide; 186 AA.
AC ABG50183;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver peptide, SEQ ID NO 28831.
XX
KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW hypercholesterolaemia; coronary heart disease.
XX
OS Homo sapiens.
XX
PN WO200157273-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000664.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488898/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX
PS Claim 27; SEQ ID NO 28831; 658pp; English.
XX
CC The invention relates to a single exon nucleic acid probe (SEN) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression

CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG5930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence
CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 186 AA;
Query Match 100.0%; Score 38; DB 4; Length 186;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YEDEINK 7
Db 174 YEDEINK 180
Search completed: July 5, 2006, 18:43:53
Job time : 60.8252 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 20:38:52 ; Search time 51.2427 Seconds
(without alignments)
63.277 Million cell updates/sec

Title: US-10-774-928A-1

Perfect score: 38

Sequence: 1 YEDEINK 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	38	100.0	7	5	US-10-774-928-1	Sequence 1, Appli
2	38	100.0	8	5	US-10-774-928-12	Sequence 12, Appl
3	38	100.0	113	5	US-10-480-848A-5	Sequence 5, Appli
4	38	100.0	186	3	US-09-864-761-36050	Sequence 36050, A
5	38	100.0	186	5	US-10-450-763-39769	Sequence 39769, A
6	38	100.0	273	5	US-10-450-763-56735	Sequence 56735, A
7	38	100.0	275	5	US-10-450-763-45641	Sequence 45641, A
8	38	100.0	347	5	US-10-450-763-39770	Sequence 39770, A
9	38	100.0	347	5	US-10-450-763-45995	Sequence 45995, A
10	38	100.0	394	5	US-10-450-763-56734	Sequence 56734, A
11	38	100.0	398	5	US-10-883-020-5	Sequence 5, Appli
12	38	100.0	416	5	US-10-450-763-53393	Sequence 53393, A
13	38	100.0	422	3	US-09-779-307-18	Sequence 18, Appl
14	38	100.0	422	3	US-09-779-307-20	Sequence 20, Appl
15	38	100.0	429	5	US-10-450-763-49905	Sequence 49905, A
16	38	100.0	429	5	US-10-450-763-49906	Sequence 49906, A
17	38	100.0	430	3	US-09-779-307-19	Sequence 19, Appl
18	38	100.0	476	3	US-09-779-307-16	Sequence 16, Appl
19	38	100.0	477	3	US-09-779-307-4	Sequence 4, Appli
20	38	100.0	481	4	US-10-080-334-54	Sequence 54, Appl
21	38	100.0	481	6	US-11-156-300-24	Sequence 24, Appl
22	38	100.0	482	3	US-09-779-307-17	Sequence 17, Appl
23	38	100.0	482	4	US-10-080-334-187	Sequence 187, Appl
24	38	100.0	482	5	US-10-883-020-1	Sequence 1, Appli
25	38	100.0	482	5	US-10-450-763-38491	Sequence 38491, A
26	38	100.0	483	3	US-09-919-497-79	Sequence 79, Appl
27	38	100.0	483	3	US-09-974-298-41	Sequence 41, Appl

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28 38 100.0 483 3 US-09-981-353-158 Sequence 158, App
29 38 100.0 483 4 US-10-177-293-258 Sequence 258, App
30 38 100.0 483 4 US-10-080-334-183 Sequence 183, App
31 38 100.0 483 4 US-10-080-334-184 Sequence 184, App
32 38 100.0 483 4 US-10-080-334-185 Sequence 185, App
33 38 100.0 483 4 US-10-080-334-186 Sequence 186, App
34 38 100.0 483 4 US-10-734-564-116 Sequence 116, App
35 38 100.0 483 6 US-11-037-713-9 Sequence 2, Appli
36 38 100.0 498 4 US-10-605-708A-2 Sequence 2, Appli
37 38 100.0 500 5 US-10-450-763-39773 Sequence 39773, A
38 38 100.0 513 5 US-10-450-763-38492 Sequence 38492, A
39 38 100.0 521 3 US-09-976-782-8 Sequence 8, Appli
40 38 100.0 523 3 US-09-976-782-6 Sequence 6, Appli
41 38 100.0 541 5 US-10-450-763-55674 Sequence 55674, A
42 38 100.0 551 3 US-09-976-782-89 Sequence 89, Appl
43 38 100.0 551 3 US-09-976-782-90 Sequence 90, Appl
44 38 100.0 551 4 US-10-015-115-127 Sequence 127, App
45 38 100.0 551 4 US-10-231-913-116 Sequence 116, App

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ALIGNMENTS

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RESULT 1
US-10-774-928-1
; Sequence 1, Application US/10774928
; Publication No. US20040241168A1
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 302178
; CURRENT APPLICATION NUMBER: US/10/774,928
; CURRENT FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Leishmania
US-10-774-928-1

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Query Match      100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 YEDEINK 7
Db 1 YEDEINK 7

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RESULT 2
US-10-774-928-12
; Sequence 12, Application US/10774928
; Publication No. US20040241168A1
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 302178
; CURRENT APPLICATION NUMBER: US/10/774,928
; CURRENT FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Leishmania
US-10-774-928-12

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Query Match      100.0%; Score 38; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 YEDEINK 7
      |||||
Db      2 YEDEINK 8

RESULT 3
US-10-480-848A-5
; Sequence 5, Application US/10480848A
; Publication No. US20040219597A1
; GENERAL INFORMATION:
; APPLICANT: B.R.A.H.M.S Aktiengesellschaft
; TITLE OF INVENTION: Use of soluble cytochrome c in diagnosis and
; FILE REFERENCE: 3537PCTNAT
; CURRENT APPLICATION NUMBER: US/10/480,848A
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: DE 101 30 985.6
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-480-848A-5

Query Match      100.0%; Score 38; DB 5; Length 113;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YEDEINK 7
      |||||
Db      85 YEDEINK 91

RESULT 4
US-09-864-761-36050
; Sequence 36050, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36050
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011309.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 72
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 59
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 7.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.8
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 44
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 16
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5e+02
; OTHER INFORMATION: EST HUMAN HIT: BE870853.1, EVALUE 9.00e-68
; OTHER INFORMATION: SWISSPROT HIT: P05787, EVALUE 1.00e-68
US-09-864-761-36050

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Query Match      100.0%; Score 38; DB 3; Length 186;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 YEDEINK 7
      |||||
Db      174 YEDEINK 180

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RESULT 5
US-10-450-763-39769
; Sequence 39769, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 39769
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (124)..(171)
; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL00226D, p-value=7.000e-38, raw score of 19.10
; FEATURE:
; NAME/KEY: DOMAIN

```



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; LOCATION: (1)..(169)
; OTHER INFORMATION: Intermediate filament proteins domain identified by Pfam,
; OTHER INFORMATION: accession name filament, E-value=4.3e-71, Pfam score of 249.6
US-10-450-763-39769

Query Match      100.0%; Score 38; DB 5; Length 186;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
Db 12 YEDEINK 18

RESULT 6
US-10-450-763-56735
; Sequence 56735, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56735
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (177)..(225)
; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL00226B, p-value=3.348e-35, raw score of 23.86
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (78)..(271)
; OTHER INFORMATION: Intermediate filament proteins domain identified by Pfam,
; OTHER INFORMATION: accession name filament, E-value=8.6e-101, Pfam score of 348.3
US-10-450-763-56735

Query Match      100.0%; Score 38; DB 5; Length 273;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
Db 167 YEDEINK 173

RESULT 7
US-10-450-763-45641
; Sequence 45641, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
```

```
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 45641
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (179)..(227)
; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL00226B, p-value=3.348e-35, raw score of 23.86
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (87)..(273)
; OTHER INFORMATION: Intermediate filament proteins domain identified by Pfam,
; OTHER INFORMATION: accession name filament, E-value=3.2e-89, Pfam score of 309.8
US-10-450-763-45641

Query Match      100.0%; Score 38; DB 5; Length 275;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
Db 169 YEDEINK 175

RESULT 8
US-10-450-763-39770
; Sequence 39770, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 39770
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (180)..(228)
; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL00226B, p-value=1.643e-31, raw score of 23.86
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (77)..(342)
; OTHER INFORMATION: Intermediate filament proteins domain identified by Pfam,
; OTHER INFORMATION: accession name filament, E-value=1.1e-78, Pfam score of 274.8
US-10-450-763-39770

Query Match      100.0%; Score 38; DB 5; Length 347;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
Db 170 YEDEINK 176

RESULT 9
US-10-450-763-45995
; Sequence 45995, Application US/10450763
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; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 45995
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (180)..(228)
; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
; accession number BL00226B, p-value=1.643e-31, raw score of 23.86
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (77)..(342)
; OTHER INFORMATION: Intermediate filament proteins domain identified by PFam,
; accession name filament, E-value=1.1e-78, PFam score of 274.8
US-10-450-763-45995

Query Match      100.0%; Score 38; DB 5; Length 347;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YEDEINK 7
      |||||
Db      170 YEDEINK 176

RESULT 10
US-10-450-763-56734
; Sequence 56734, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56734
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (164)..(212)
; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
; accession number BL00226B, p-value=4.656e-29, raw score of 23.86
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (80)..(312)
; OTHER INFORMATION: Intermediate filament proteins domain identified by PFam,
; accession name filament, E-value=4e-88, PFam score of 306.2
; FEATURE:
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; NAME/KEY: misc feature
; LOCATION: (1)..(394)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-56734

Query Match      100.0%; Score 38; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YEDEINK 7
      |||||
Db      154 YEDEINK 160

RESULT 11
US-10-883-020-5
; Sequence 5, Application US/10883020
; Publication No. US20050048070A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, Henrik
; APPLICANT: Jensenius, Jens
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: Cancer-Associated Epitope
; FILE REFERENCE: 1361.017US1
; CURRENT APPLICATION NUMBER: US/10/883,020
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: PCT/US03/00297
; PRIOR FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,208
; PRIOR FILING DATE: 2002-01-03
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-883-020-5

Query Match      100.0%; Score 38; DB 5; Length 398;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YEDEINK 7
      |||||
Db      94 YEDEINK 100

RESULT 12
US-10-450-763-53393
; Sequence 53393, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 53393
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (122)..(137)
; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
```

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; OTHER INFORMATION: accession number BL00226A, p-value=4.600e-14, raw score of 12.77
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (125)..(346)
; OTHER INFORMATION: Intermediate filament proteins domain identified by Pfam.
; OTHER INFORMATION: accession name filament, E-value=2e-54, Pfam score of 194.2
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(416)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-53393

Query Match          100.0%; Score 38; DB 5; Length 416;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
DB 212 YEDEINK 218

RESULT 13
US-09-779-307-18
; Sequence 18, Application US/09779307
; Patent No. US20020137675A1
; GENERAL INFORMATION:
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Majumder, Kumud
; APPLICANT: Vernet, Corine
; APPLICANT: Pravaga, Sudhirdas
; TITLE OF INVENTION: Polynucleotides and Polypeptides Encoded Thereby
; FILE REFERENCE: 15966-662 US
; CURRENT APPLICATION NUMBER: US/09/779,307
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/180,880
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/181,044
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/181,656
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/182,795
; PRIOR FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-307-18

Query Match          100.0%; Score 38; DB 3; Length 422;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
DB 178 YEDEINK 184

RESULT 14
US-09-779-307-20
; Sequence 20, Application US/09779307
; Patent No. US20020137675A1
; GENERAL INFORMATION:
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Majumder, Kumud
; APPLICANT: Vernet, Corine
; APPLICANT: Pravaga, Sudhirdas
; TITLE OF INVENTION: Polynucleotides and Polypeptides Encoded Thereby
; FILE REFERENCE: 15966-662 US
; CURRENT APPLICATION NUMBER: US/09/779,307
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/180,880
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; OTHER INFORMATION: accession number BL00226B, p-value=2.714e-23, raw score of 23.86
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (107)..(348)
; OTHER INFORMATION: Intermediate filament proteins domain identified by Pfam.
; OTHER INFORMATION: accession name filament, E-value=4.2e-90, Pfam score of 312.7
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(429)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-49905

Query Match          100.0%; Score 38; DB 5; Length 429;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
DB 173 YEDEINK 179

RESULT 15
US-10-450-763-49905
; Sequence 49905, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 49905
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (183)..(231)
; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL00226B, p-value=2.714e-23, raw score of 23.86
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (107)..(348)
; OTHER INFORMATION: Intermediate filament proteins domain identified by Pfam.
; OTHER INFORMATION: accession name filament, E-value=4.2e-90, Pfam score of 312.7
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(429)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-49905

Query Match          100.0%; Score 38; DB 5; Length 429;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
DB 173 YEDEINK 179

Search completed: July 5, 2006, 20:52:00
Job time : 52.2427 secs
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OM protein - protein search, using sw model

Run on: July 5, 2006, 20:39:32 ; Search time 4.00971 Seconds
(without alignments)
46.842 Million cell updates/sec

Title: US-10-774-928A-1

Perfect score: 38

Sequence: 1 YEDEINK 7

Scoring table: BLOSUM62

Gapop 10:0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 112942

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New.*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pap.*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pap.*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	483	7	US-11-105-233-180
2	35	92.1	469	6	US-10-505-928-457
3	34	89.5	140	6	US-10-953-349-1458
4	34	89.5	147	6	US-10-953-349-1457
5	34	89.5	164	6	US-10-953-349-1456
6	34	89.5	940	6	US-10-449-902-45238
7	34	89.5	940	6	US-10-449-902-45669
8	33	86.8	242	6	US-10-449-902-46212
9	33	86.8	256	7	US-11-174-307B-4514
10	33	86.8	758	6	US-10-449-902-51086
11	33	86.8	799	6	US-10-449-902-47602
12	33	86.8	964	7	US-11-289-102-392
13	32	84.2	33	7	US-11-134-871-915
14	32	84.2	225	6	US-10-471-571A-5244
15	31	81.6	107	6	US-10-953-349-13561
16	31	81.6	158	6	US-10-953-349-13560
17	31	81.6	247	6	US-10-449-902-54216
18	31	81.6	568	6	US-10-449-902-46926
19	31	81.6	568	6	US-10-449-902-47019
20	31	81.6	591	6	US-10-953-349-1322
21	31	81.6	705	6	US-10-953-349-1321
22	31	81.6	713	6	US-10-953-349-1320
23	31	81.6	714	6	US-10-449-902-54951
24	31	81.6	723	6	US-10-449-902-53379
25	30	78.9	196	6	US-10-953-349-19059

26	30	78.9	228	6	US-10-449-902-50750	Sequence 50750, A
27	30	78.9	238	6	US-10-953-349-19058	Sequence 19058, A
28	30	78.9	350	6	US-10-449-902-55155	Sequence 55155, A
29	30	78.9	586	6	US-10-505-928-314	Sequence 314, App
30	29	76.3	158	6	US-10-953-349-13251	Sequence 13251, A
31	29	76.3	183	6	US-10-953-349-13250	Sequence 13250, A
32	29	76.3	246	6	US-10-449-902-35293	Sequence 35293, A
33	29	76.3	256	6	US-10-449-902-37092	Sequence 37092, A
34	29	76.3	407	6	US-10-449-902-51903	Sequence 51903, A
35	29	76.3	471	6	US-10-449-902-36733	Sequence 36733, A
36	29	76.3	471	6	US-10-449-902-49633	Sequence 49633, A
37	29	76.3	471	6	US-10-449-902-54344	Sequence 54344, A
38	29	76.3	531	6	US-10-953-349-27961	Sequence 27961, A
39	29	76.3	533	6	US-10-953-349-27960	Sequence 27960, A
40	29	76.3	557	6	US-10-953-349-27959	Sequence 27959, A
41	29	76.3	600	6	US-10-449-902-38563	Sequence 38563, A
42	29	76.3	600	6	US-10-449-902-54061	Sequence 54061, A
43	28	73.7	68	6	US-10-471-571A-5136	Sequence 5136, Ap
44	28	73.7	107	6	US-10-471-571A-1754	Sequence 1754, Ap
45	28	73.7	219	6	US-10-953-349-2869	Sequence 2869, Ap

ALIGNMENTS

RESULT 1
US-11-105-233-180
; Sequence 180, Application US/11105233
; Publication No. US20060134653A1
; GENERAL INFORMATION:
; APPLICANT: Thiagalingam et al
; TITLE OF INVENTION: Differential Expression of Genes in MSI
; FILE OF INVENTION: Tumors
; FILE REFERENCE: 1657/2001
; CURRENT APPLICATION NUMBER: US/11/105,233
; CURRENT FILING DATE: 2005-04-13
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 180
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-233-180

Query Match 100.0%; Score 38; DB 7; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
DB 179 YEDEINK 185

RESULT 2
US-10-505-928-457
; Sequence 457, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 457
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-457

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Query Match      92.1%; Score 35; DB 6; Length 469;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YEDEINK 7
Db      180 YEDEINK 186

RESULT 3
US-10-953-349-1458
; Sequence 1458, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1458
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1458

Query Match      89.5%; Score 34; DB 6; Length 140;
Best Local Similarity 85.7%; Pred. No. 5.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YEDEINK 7
Db      56 FEDEINK 62

RESULT 4
US-10-953-349-1457
; Sequence 1457, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1457
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1457

Query Match      89.5%; Score 34; DB 6; Length 147;
Best Local Similarity 85.7%; Pred. No. 5.9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YEDEINK 7
Db      63 FEDEINK 69

RESULT 5
US-10-953-349-1456
; Sequence 1456, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1456
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1456

Query Match      89.5%; Score 34; DB 6; Length 164;
Best Local Similarity 85.7%; Pred. No. 6.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YEDEINK 7
Db      80 FEDEINK 86

RESULT 6
US-10-449-902-45238
; Sequence 45238, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45238
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-45238

Query Match      89.5%; Score 34; DB 6; Length 940;
Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YEDEINK 7
Db      413 YEDEINK 419

RESULT 7
US-10-449-902-45669
; Sequence 45669, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 45669
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-45669

Query Match 89.5%; Score 34; DB 6; Length 940;
Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEDEINK 7
|||||
Db 413 YEDEINE 419

RESULT 8
US-10-449-902-46212
; Sequence 46212, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46212
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-46212

Query Match 86.8%; Score 33; DB 6; Length 242;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YEDEINK 7
|||||
Db 84 YEDEANK 90

RESULT 9
US-11-174-307B-4514
; Sequence 4514, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 4514
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:

; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 50947575; NR Description: thylakoid lumen protein,
; OTHER INFORMATION: chloroplast precursor-like [Oryza sativa (japonica cultivar-group)]
; OTHER INFORMATION: >gi|42408803|dbj|BAD10064.1| thylakoid lumen protein, chloroplast
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 21537211; NR Description: thylakoid lumen protein,
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 32815945; NR Description: Atlg76450 [Arabidopsis
; OTHER INFORMATION: thaliana] >gi|18203439|sp|Q9S720|THL1_ARATH Unknown thylakoid lume
; OTHER INFORMATION: protein, chloroplast precursor >gi|18411110|ref|NP_565131.1|
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 61826057; NR Description: PREDICTED: similar to
; OTHER INFORMATION: serine/arginine repetitive matrix 1, partial [Bos taurus]
; OTHER INFORMATION: gi|61818041|ref|XP_593433.1| PREDICTED: similar to serine/arginin
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 7949115; NR Description: Ser/Arg-related nuclear
; OTHER INFORMATION: matrix protein; plenty-of-prolines-101; serine/arginine repetitive
; OTHER INFORMATION: matrix protein 1 [Mus musculus] >gi|3153821|gb|AAC17422.1|
US-11-174-307B-4514

Query Match 86.8%; Score 33; DB 7; Length 256;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YEDEINK 7
|||||
Db 98 YEDEANK 104

RESULT 10
US-10-449-902-51086
; Sequence 51086, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51086
; LENGTH: 758
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-51086

Query Match 86.8%; Score 33; DB 6; Length 758;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEDEIN 6
|||||
Db 230 YEDEIN 235

RESULT 11

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US-10-449-902-47602
; Sequence 47602, Application US/10449902
; Publication No. US20060123503A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0203Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47602
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-47602

Query Match      86.8%; Score 33; DB 6; Length 799;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEIN 6
| | | | |
Db 349 YEDEIN 354

RESULT 12
US-11-289-102-392
; Sequence 392, Application US/11289102
; Publication No. US20060121511A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Hyerim
; APPLICANT: Shaw, Peter M.
; APPLICANT: Clark, Edwin
; TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO
; TITLE OF INVENTION: MICROTUBULE-STABILIZING AGENTS
; FILE REFERENCE: 10338 NP
; CURRENT APPLICATION NUMBER: US/11/289,102
; CURRENT FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US 60/631,993
; PRIOR FILING DATE: 2004-11-30
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 392
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-289-102-392

Query Match      86.8%; Score 33; DB 7; Length 964;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINK 7
| | | | |
Db 524 YEDEVNQ 530

RESULT 13
US-11-134-871-915
; Sequence 915, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
```

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; TITLE OF INVENTION: Quatification of Serum Glycoproteins
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 915
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-915

Query Match      84.2%; Score 32; DB 7; Length 33;
Best Local Similarity 83.3%; Pred. No. 2.9;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEIN 6
| | | | |
Db 20 YEDEVN 25

RESULT 14
US-10-471-571A-5244
; Sequence 5244, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927W0
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 5244
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(225)
; OTHER INFORMATION: hypothetical protein
US-10-471-571A-5244

Query Match      84.2%; Score 32; DB 6; Length 225;
Best Local Similarity 71.4%; Pred. No. 23;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINK 7
| | | | |
Db 172 YDQINK 178

RESULT 15
US-10-953-349-13561
; Sequence 13561, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED
; TITLE OF INVENTION: ENCODED THERAPY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13561
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Glycine max
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US-10-953-349-13561

Query Match 81.6%; Score 31; DB 6; Length 107;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
|:|||||:
Db 26 YQDEINE 32

Search completed: July 5, 2006, 20:53:03
Job time : 4.00971 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 5, 2006, 19:18:42 ; Search time 15.767 Seconds
(without alignments)
38.861 Million cell updates/sec

Title: US-10-774-928A-1
Perfect score: 38
Sequence: 1 YEDEINK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /EMC_Celerra_SID33/ptodata/2/iaa/6 COMB.pcp:*
3: /EMC_Celerra_SID33/ptodata/2/iaa/7 COMB.pcp:*
4: /EMC_Celerra_SID33/ptodata/2/iaa/H COMB.pcp:*
5: /EMC_Celerra_SID33/ptodata/2/iaa/PCTUS COMB.pcp:*
6: /EMC_Celerra_SID33/ptodata/2/iaa/RE COMB.pcp:*
7: /EMC_Celerra_SID33/ptodata/2/iaa/backfiles1.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	100.0	7	US-09-809-003A-1	Sequence 1, Appli
2	38	100.0	8	US-09-809-003A-12	Sequence 12, Appl
3	38	100.0	384	US-09-949-016-11034	Sequence 11034, A
4	38	100.0	443	US-09-949-016-10582	Sequence 10582, A
5	38	100.0	482	US-09-538-092-858	Sequence 858, App
6	38	100.0	483	US-09-919-497-79	Sequence 79, Appl
7	38	100.0	502	US-09-949-016-11033	Sequence 11033, A
8	38	100.0	551	US-09-067-351-2	Sequence 2, Appli
9	38	100.0	551	US-09-360-490-2	Sequence 2, Appli
10	38	100.0	564	US-09-949-016-6628	Sequence 6628, Ap
11	38	100.0	567	US-10-104-047-3772	Sequence 3772, Ap
12	38	100.0	569	US-09-949-016-11035	Sequence 11035, A
13	38	100.0	569	US-09-949-016-11036	Sequence 11036, A
14	38	100.0	637	US-09-949-016-8152	Sequence 8152, Ap
15	38	100.0	643	US-09-538-092-844	Sequence 844, App
16	38	100.0	645	US-09-919-172-41	Sequence 41, Appl
17	35	92.1	469	US-09-077-606-3	Sequence 3, Appli
18	35	92.1	476	US-09-949-016-9096	Sequence 9096, Ap
19	34	89.5	608	US-10-094-749-2446	Sequence 2446, Ap
20	33	86.8	8	US-09-809-003A-11	Sequence 11, Appl
21	33	86.8	216	US-09-248-796A-14967	Sequence 14967, A
22	33	86.8	546	US-09-067-351-1	Sequence 1, Appli
23	33	86.8	546	US-09-360-490-1	Sequence 1, Appli
24	32	84.2	369	US-09-248-796A-18582	Sequence 18582, A
25	32	84.2	652	US-08-559-896B-2	Sequence 2, Appli
26	32	84.2	652	US-09-351-794A-2	Sequence 2, Appli

27	32	84.2	1348	2	US-09-949-002-517	Sequence 517, App
28	32	84.2	2196	2	US-10-360-101-259	Sequence 259, App
29	32	84.2	2224	2	US-09-054-272-38	Sequence 38, Appl
30	32	84.2	2224	2	US-09-949-002-292	Sequence 292, App
31	31	81.6	27	2	US-09-270-767-59516	Sequence 59516, A
32	31	81.6	82	2	US-09-270-767-44099	Sequence 44099, A
33	31	81.6	234	2	US-09-270-767-32857	Sequence 32857, A
34	31	81.6	234	2	US-09-270-767-48074	Sequence 48074, A
35	31	81.6	277	2	US-09-538-092-485	Sequence 485, App
36	31	81.6	284	2	US-09-248-796A-17686	Sequence 17686, A
37	31	81.6	286	2	US-09-248-796A-19241	Sequence 19241, A
38	31	81.6	289	2	US-09-248-796A-27946	Sequence 27946, A
39	31	81.6	439	2	US-09-465-558-38	Sequence 38, Appl
40	31	81.6	608	2	US-09-270-767-32937	Sequence 32937, A
41	31	81.6	608	2	US-09-270-767-48154	Sequence 48154, A
42	31	81.6	676	2	US-09-151-189-2	Sequence 2, Appli
43	31	81.6	676	2	US-09-596-794-2	Sequence 2, Appli
44	31	81.6	676	2	US-09-840-762A-2	Sequence 2, Appli
45	31	81.6	676	2	US-10-691-383-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-809-003A-1
; Sequence 1, Application US/09809003A
; Patent No. 6673351
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; FILE REFERENCE: 302178
; CURRENT APPLICATION NUMBER: US/09/809,003A
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Leishmania
US-09-809-003A-1

Query Match 100.0%; Score 38; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
DB 1 YEDEINK 7

RESULT 2
US-09-809-003A-12
; Sequence 12, Application US/09809003A
; Patent No. 6673351
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; FILE REFERENCE: 302178
; CURRENT APPLICATION NUMBER: US/09/809,003A
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Leishmania
US-09-809-003A-12

Query Match 100.0%; Score 38; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINK 7
Db 2 YEDEINK 8

RESULT 3
US-09-949-016-11034
; Sequence 11034, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11034
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11034

Query Match 100.0%; Score 38; DB 2; Length 384;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINK 7
Db 276 YEDEINK 282

RESULT 4
US-09-949-016-10582
; Sequence 10582, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10582
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10582

Query Match 100.0%; Score 38; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINK 7
Db 139 YEDEINK 145

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 5
US-09-538-092-858
; Sequence 858, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapSeqFormer Version 0.9
; SEQ ID NO 858
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (0)_(0)
; OTHER INFORMATION: Polypeptide Accession Number P05787
US-09-538-092-858

Query Match 100.0%; Score 38; DB 2; Length 482;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINK 7
Db 178 YEDEINK 184

RESULT 6
US-09-919-497-79
; Sequence 79, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-79

Query Match 100.0%; Score 38; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINK 7
Db 179 YEDEINK 185

RESULT 7
US-09-949-016-11033
; Sequence 11033, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
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;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 11033
;; LENGTH: 502
;; TYPE: PRT
;; ORGANISM: Human
US-09-949-016-11033

Query Match 100.0%; Score 38; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
DB 198 YEDEINK 204

RESULT 8
US-09-067-351-2
; Sequence 2, Application US/09067351
; Patent No. 5994081
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN KERATINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,351
FILING DATE: Herewith

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0511 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 551 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KERANOT02
CLONE: 2029060
US-09-067-351-2

Query Match 100.0%; Score 38; DB 1; Length 551;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
DB 239 YEDEINK 245

RESULT 9
US-09-360-490-2
; Sequence 2, Application US/09360490
; Patent No. 6221843
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN KERATINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/360,490
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/067,351
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0511 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 551 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KERANOT02
CLONE: 2029060
US-09-360-490-2

Query Match 100.0%; Score 38; DB 2; Length 551;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINK 7
DB 239 YEDEINK 245

RESULT 10
US-09-949-016-6628
; Sequence 6628, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6628
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6628

Query Match 100.0%; Score 38; DB 2; Length 564;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINK 7
Db 253 YEDEINK 259

RESULT 11
US-10-104-047-3772
; Sequence 3772, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. 6943241el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 3772
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3772

Query Match 100.0%; Score 38; DB 2; Length 567;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINK 7
Db 235 YEDEINK 241

RESULT 12
US-09-949-016-11035
; Sequence 11035, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11035
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11035

Query Match 100.0%; Score 38; DB 2; Length 569;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINK 7
Db 259 YEDEINK 265

RESULT 13
US-09-949-016-11036
; Sequence 11036, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11036
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11036

Query Match 100.0%; Score 38; DB 2; Length 569;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINK 7
Db 259 YEDEINK 265

RESULT 14
US-09-949-016-8152
; Sequence 8152, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8152
; LENGTH: 637
; TYPE: PRT

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; ORGANISM: Human
US-09-949-016-8152

Query Match      100.0%; Score 38; DB 2; Length 637;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YEDEINK 7
DB      270 YEDEINK 276

RESULT 15
US-09-538-092-844
; Sequence 844, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 844
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)-(0)
; OTHER INFORMATION: Polypeptide Accession Number P04264
US-09-538-092-844

Query Match      100.0%; Score 38; DB 2; Length 643;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YEDEINK 7
DB      269 YEDEINK 275

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Search completed: July 5, 2006, 19:24:27
Job time : 16.767 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 5, 2006, 19:20:41 ; Search time 8.25 Seconds
(without alignments)
104.964 Million cell updates/sec

Title: US-10-774-928A-2

Perfect score: 45

Sequence: 1 AQVEDIAQK 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Pirl2.*

3: Pirl3.*

4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	93.3	629	2	A29666 keratin, 65K type
2	42	93.3	629	2	S42629 keratin K3 - rabbit
3	41	91.1	524	2	A23518 keratin, 57K type
4	40	88.9	513	2	S08381 keratin, 58K type
5	39	86.7	461	2	A43782 keratin, type II -
6	39	86.7	502	2	A23547 keratin, type II c
7	38	84.4	384	2	I61769 keratin 6d, type I
8	38	84.4	534	2	I37942 keratin 4, type II
9	38	84.4	564	1	KRHUEA keratin 6a, type I
10	38	84.4	564	1	KRHUEB keratin 6b, type I
11	38	84.4	564	2	I61770 keratin 6e, type I
12	38	84.4	564	2	I61768 keratin 6c, type I
13	38	84.4	564	2	I61771 keratin 6f, type I
14	38	84.4	645	2	A44861 keratin, 67K type
15	37	82.2	330	2	A60093 cytokekeratin, type
16	37	82.2	483	2	A34720 keratin 8, type II
17	37	82.2	487	2	JT0407 keratin 8, type II
18	37	82.2	489	2	S05474 keratin 8, type II
19	37	82.2	490	2	JS0858 cytokekeratin EndoA
20	37	82.2	520	2	JS0291 intermediate filament
21	36	80.0	159	2	H83845 stage V sporulation
22	36	80.0	643	1	KRHU2 keratin 1, type II
23	35	77.8	174	2	S39790 male-enhanced anti
24	35	77.8	174	2	B34421 male-enhanced anti
25	35	77.8	185	2	A34421 male-enhanced anti
26	35	77.8	368	2	A28825 keratin, type I no
27	35	77.8	875	2	S70115 ZIP1 protein - yea
28	34	75.6	395	2	D97193 PLP-dependent amin
29	34	75.6	424	2	S14887 peripherin (clone

RESULT 1

A29666

keratin, 65K type II cytoskeletal - human

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 20-Apr-2001

C:Accession: A29666

R:Klinge, E.M.; Sylvestre, Y.R.; Freedberg, I.M.; Blumenberg, M.

J. Mol. Evol. 24, 319-329, 1987

A:Title: Evolution of keratin genes: different protein domains evolve by different pathways

A:Reference number: A29666, MUID:87254239; PMID:2439698

A:Accession: A29666

A:Molecule type: DNA

A:Residues: 1-629 <KLI>

A:Cross-references: UNIPARC:UPI0000161C35; GB:X05418; NID:G34040; PIDN:CAA28991.1; PID:G-

92; PIDN:CAA28994.1; PID:G1335193; PIDN:CAA28995.1; PID:G1335194; GB:X05421; NID:G34047;

A>Note: the authors translated the codon AAC for residue 63 as Asp and ACA for residue 29;

A>Note: the complete translation is not annotated in GenBank entries HSKR65A, HSKR65B,

s mistranslated as a Met initiator codon

C:Genetics:

A:Introns: 215/3; 289/2; 309/3; 341/3; 396/3; 438/3; 512/2; 525/1

C:Superfamily: cytoskeletal keratin

C:Keywords: Coiled coil

Query Match 93.3%; Score 42; DB 2; Length 629;

Best Local Similarity 88.9%; Pred. No. 0.96;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AQVEDIAQK 9

Db 376 AQVEDIAQK 384

RESULT 2

S42629

keratin K3 - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S42629

R:Wu, R.L.; Galvin, S.; Wu, S.K.; Xu, C.; Blumenberg, M.; Sun, T.T.

J. Cell Sci. 105, 303-316, 1993

A:Title: A 300 bp 5'-upstream sequence of a differentiation-dependent rabbit K3 keratin

A:Reference number: S42629; MUID:94013038; PMID:7691837

A:Accession: S42629

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-629 <WUR>

A:Cross-references: UNIPARC:UPI0000087A39; EMBL:X74371; NID:G433957; PID:

C:Genetics:

A:Introns: 200/3; 274/2; 294/3; 326/3; 381/3; 423/3; 497/2; 509/1

C:Superfamily: cytoskeletal keratin

Query Match 93.3%; Score 42; DB 2; Length 629;

Best Local Similarity 88.9%; Pred. No. 0.96; Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AQYEDIAQK 9
| | | | | | | |
Db 361 AQYEDIAQR 369

RESULT 3
A23518
keratin, 57K type II cytoskeletal - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
C:Accession: A23518
R:Knapp, B.; Rentrop, M.; Schweizer, J.; Winter, H.
Nucleic Acids Res. 14, 751-763, 1986
A:Title: Nonepidermal members of the keratin multigene family: cDNA sequences and in situ hybridization
A:Reference number: A93640; MUID:86120369; PMID:2418416
A:Accession: A23518
A:Molecule type: mRNA
A:Residues: 1-524 <KNA>
A:Cross-references: UNIPROT:P07744; UNIPARC:UPI000000298E2; GB:X03491; NID:G52784; PIDN:C00000
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil

Query Match 91.1%; Score 41; DB 2; Length 524;
Best Local Similarity 88.9%; Pred. No. 1.3; Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AQYEDIAQK 9
| | | | | | | |
Db 322 AQYEDIAQR 330

RESULT 4
S08381
keratin, 50K type II, cytoskeletal (clone pXENCK55(5/6)) - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
C:Accession: S08381
R:Fouquet, B.; Herrmann, H.; Franz, J.K.; Franke, W.W.
Development 104, 533-548, 1988
A:Title: Expression of intermediate filament proteins during development of Xenopus laevis
A:Reference number: S08381; MUID:90032362; PMID:2478354
A:Accession: S08381
A:Molecule type: mRNA
A:Residues: 1-513 <FOU>
A:Cross-references: UNIPROT:P16878; UNIPARC:UPI0000017151D; EMBL:X14427; NID:G64625; PIDN:C00000
C:Superfamily: cytoskeletal keratin

Query Match 88.9%; Score 40; DB 2; Length 513;
Best Local Similarity 88.9%; Pred. No. 2; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AQYEDIAQK 9
| | | | | | | |
Db 303 AQYEDIAQR 311

RESULT 5
A43782
keratin, type II - eastern newt (fragment)
C:Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C:Accession: A43782
R:Ferretti, P.; Brookes, J.P.; Brown, R.
Development 111, 497-507, 1991
A:Title: A new type II keratin restricted to normal and regenerating limbs and tails is expressed in the developing tail of the newt
A:Reference number: A43782; MUID:91372147; PMID:1716554
A:Accession: A43782
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <FER>

A; Cross-references: UNIPROT:O42435; UNIPARC:UPI00001774C4; GB:X57671
C; Superfamily: cytoskeletal keratin

Query Match 86.7%; Score 39; DB 2; Length 461;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 AQYEDIAQK 9
|||||:
DB 220 AQYEDVANK 228

RESULT 6
A23547
keratin, type II cytoskeletal - African clawed frog
C; Species: Xenopus laevis (African clawed frog)
C; Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
C; Accession: A23547
R; Franz, J.K.; Franke, W.W.
Proc. Natl. Acad. Sci. U.S.A. 83, 6475-6479, 1986
A; Title: Cloning of cDNA and amino acid sequence of a cyto keratin expressed in oocytes of
A; Reference number: A23547; MUID:86313601; PMID:2428034
A; Accession: A23547
A; Molecule type: mRNA
A; Residues: 1-502 <FRA>
A; Cross-references: UNIPROT:P08776; UNIPARC:UPI000012DB12; GB:M13811; NID:g214555; PIDN:1
C; Superfamily: cytoskeletal keratin
C; Keywords: coiled coil

Query Match 86.7%; Score 39; DB 2; Length 502;
Best Local Similarity 77.8%; Pred. No. 3.2;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 AQYEDIAQK 9
|||||:
DB 273 AQYEDVANK 281

RESULT 7
I61769
keratin 6d, type II - human (fragment)
C; Species: Homo sapiens (man)
C; Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C; Accession: I61769
R; Takahashi, K.; Couladini, R.D.; Coulombe, P.A.
J. Biol. Chem. 270, 18581-18592, 1995
A; Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
A; Reference number: A57398; MUID:95355491; PMID:7543104
A; Accession: I61769
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-384 <RES>
A; Cross-references: UNIPROT:P48667; UNIPARC:UPI000012DB17; GB:L42602; NID:g914823; GB:L42
28; GB:L42608; NID:g914829; GB:L42609; NID:g914830; GB:L42610; NID:g1488252; PIDN:AA86065
C; Genetics:

A; Gene: KRT6D
A; Introns: 72/2; 92/3; 124/3; 179/3; 221/3; 295/2; 307/1
C; Superfamily: cytoskeletal keratin
C; Keywords: coiled coil

Query Match 84.4%; Score 38; DB 2; Length 384;
Best Local Similarity 77.8%; Pred. No. 3.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQYEDIAQK 9
|||||:
DB 159 AQYEDIAQK 167

RESULT 8
I37942
keratin 4, type II, cytoskeletal - human
N; Alternate names: basic cyto keratin; cyto keratin 4

C;Species: Homo sapiens (man)
 C;Date: 12-Aug-1996 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
 C;Accession: I37942; S01068; S21884; A30186; S31662
 R;Wanner, R.; Forster, H.H.; Tilmans, I.; Mischke, D.
 J. Invest. Dermatol. 100, 735-741, 1993
 A;Title: Allelic variations of human keratins K4 and K5 provide polymorphic markers with
 A;Reference number: I37942; MUID:93267125; PMID:7684424
 A;Accession: I37942
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-127, 'I', 129-144 <WAN1>
 A;Cross-references: UNIPROT:P19013; UNIPARC:UPI000016AB8C; EMBL:X67683; NID:g34020; PIDN:
 R;Leube, R.E.; Bader, B.L.; Bosch, F.X.; Zimbelmann, R.; Achtsaetter, T.; Franke, W.W.
 J. Cell Biol. 106, 1249-1261, 1988
 A;Title: Molecular characterization and expression of the stratification-related cytokin
 A;Reference number: S01068; MUID:88198369; PMID:2452170
 A;Accession: S01068
 A;Molecule type: mRNA
 A;Residues: 'S', 128-534 <LEU>
 A;Cross-references: UNIPARC:UPI000016ABA3; EMBL:X07695; NID:g34072; PIDN:CAA30534.1; PID
 R;Wanner, R.; Tilmans, I.; Mischke, D.
 submitted to the EMBL Data Library, July 1991
 A;Reference number: S21884
 A;Accession: S21884
 A;Molecule type: DNA
 A;Residues: 411-534 <WAN2>
 A;Cross-references: UNIPARC:UPI000016ABA5; EMBL:X61028; NID:g34076; PIDN:CAA43362.1; PID
 A;Experimental source: allele K4a
 C;Genetics:
 A;Gene: GDB:KRT4; CYK4
 A;Cross-references: GDB:120697; OMIM:123940
 A;Map position: 12p11.2-12q11
 A;Introns: 463/2; 475/1
 C;Superfamily: cytoskeletal keratin
 C;Keywords: coiled coil; intermediate filament
 F;1-152/Domain: head #status predicted <HEA>
 F;153-464/Domain: helical rod #status predicted <ROD>
 F;465-534/Domain: tail #status predicted <TAI>

Query Match 84.4%; Score 38; DB 2; Length 534;
 Best Local Similarity 77.8%; Pred. No. 5.6;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQVEDIAQK 9
 |||||:
 Db 327 AQVEEIAQR 335

RESULT 9
 KRHUEA
 keratin 6a, type II - human
 N;Alternate names: 56-kDa type II keratin; keratin cytoskeletal
 C;Species: Homo sapiens (man)
 C;Date: 15-Nov-1984 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: A57398; A02944
 R;Takahashi, K.; Paladini, R.D.; Coulombe, P.A.
 J. Biol. Chem. 270, 18581-18592, 1995
 A;Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
 A;Reference number: A57398; MUID:95355491; PMID:7543104
 A;Accession: A57398
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-564 <TAK>
 A;Cross-references: UNIPROT:P02538; UNIPARC:UPI000013CD4C; GB:L42575; NID:g908769; GB:L4
 74; GB:L42581; NID:g908775; GB:L42582; NID:g908776; GB:L42583; NID:g908777; PIDN:AAC4176
 R;Hanukoglu, I.; Fuchs, E.
 Cell 33, 915-924, 1983
 A;Title: The cDNA sequence of a type II cytoskeletal keratin reveals constant and variab
 A;Reference number: A02944; MUID:83259278; PMID:6191871
 A;Accession: A02944
 A;Molecule type: mRNA
 A;Residues: 208-394, 'S', 396-564 <HAN>
 A;Cross-references: UNIPARC:UPI000016AB87; GB:J00269; NID:g34068; PIDN:CAA24760.1; PID:9

C;Comment: The cytoskeletal and microfibrillar keratins are classified into two types, ty
 atin IF protein subunit appears to be a heterotetramer of two type I and two type II prot
 C;Genetics:
 A;Gene: GDB:KRT6A
 A;Cross-references: GDB:128111; OMIM:148041
 A;Map position: 12q12-12q21
 A;Introns: 180/3; 252/2; 272/3; 304/3; 359/3; 401/3; 475/2; 487/1
 C;Superfamily: cytoskeletal keratin
 C;Keywords: coiled coil; intermediate filament
 F;2-163/Domain: head <HED>
 F;2-163/Domain: E1 and V1 subdomains
 F;127-163/Region: H1 subdomain
 F;162-476/Domain: rod <ROD>
 F;199-210/Region: linker 1
 F;211-311/Region: coil 1B
 F;312-328/Region: linker 12
 F;329-347/Region: coil 2A
 F;348-355/Region: linker 2
 F;356-476/Region: coil 2B
 F;414/Region: stutter
 F;477-564/Domain: tail <END>
 F;477-496/Region: H2 subdomain
 F;497-564/Region: V2 and E2 subdomains

Query Match 84.4%; Score 38; DB 1; Length 564;
 Best Local Similarity 77.8%; Pred. No. 6;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQVEDIAQK 9
 |||||:
 Db 339 AQVEEIAQR 347

RESULT 10
 KRHUEB
 keratin 6b, type II - human
 N;Alternate names: 56K type II keratin; keratin, cytoskeletal
 C;Species: Homo sapiens (man)
 C;Date: 04-Dec-1986 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: I61767; A02945
 R;Takahashi, K.; Paladini, R.D.; Coulombe, P.A.
 J. Biol. Chem. 270, 18581-18592, 1995
 A;Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
 A;Reference number: A57398; MUID:95355491; PMID:7543104
 A;Accession: I61767
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-564 <RES>
 A;Cross-references: UNIPROT:P04259; UNIPARC:UPI0000167B39; GB:L42584; NID:g908780; GB:L42
 85; GB:L42590; NID:g908786; GB:L42591; NID:g908787; GB:L42592; NID:g908788; PIDN:AAC41768
 R;Tyner, A.L.; Eichman, M.J.; Fuchs, E.
 Proc. Natl. Acad. Sci. U.S.A. 82, 4683-4687, 1985
 A;Title: The sequence of a type II keratin gene expressed in human skin: conservation of
 A;Reference number: A02945; MUID:85270392; PMID:2410904
 A;Accession: A02945
 A;Molecule type: DNA
 A;Residues: 2-88, 'AG', 91-115, 'PA', 118, 'LC', 122-158, 'IG', 161-254, 'V', 256-564 <TYN>
 A;Cross-references: UNIPARC:UPI0000173D58; GB:M11229; GB:L00205; NID:g186714; PIDN:AAA594
 A;Note: Initiator Met not shown
 C;Comment: There are two types of cytoskeletal and microfibrillar keratin, I (acidic) and
 bligate heteropolymers, composed of complexes formed by the aggregation of at least one t
 C;Genetics:
 A;Gene: GDB:KRT6B
 A;Cross-references: GDB:128113; OMIM:148042
 A;Map position: 12pter-12qter
 A;Introns: 180/3; 252/2; 272/3; 304/3; 359/3; 401/3; 475/2; 487/1
 C;Superfamily: cytoskeletal keratin
 C;Keywords: coiled coil; intermediate filament
 F;2-163/Domain: head <HED>
 F;128-163/Region: E1 and V1 subdomains
 F;164-476/Domain: rod <ROD>
 F;164-198/Region: coil 1A

F:199-210/Region: linker 1
F:211-311/Region: coil 1B
F:312-328/Region: linker 12
F:329-347/Region: coil 2A
F:348-355/Region: linker 2
F:356-476/Region: coil 2B
F:414/Region: stutter
F:477-564/Domain: tail <END>
F:477-496/Region: H2 subdomain
F:497-564/Region: V2 and E2 subdomains

Query Match 84.4%; Score 38; DB 1; Length 564;
Best Local Similarity 77.8%; Pred. No. 6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQYEDIAQK 9
|||||:
Db 339 AQYEBIAQR 347

RESULT 11
I61770
keratin 6e, type II - human
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: I61770
R:Takahashi, K.; Paladini, R.D.; Coulombe, P.A.
J. Biol. Chem. 270, 18581-18592, 1995
A:Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
A:Reference number: A57398; MUID:95355491; PMID:7543104
A:Accession: I61770
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-564 <RES>
A:Cross-references: UNIPROT:P48668; UNIPARC:UPI0000167E31; GB:L42611; NID:G908802; PIDN:
C:Genetics:
A:Gene: KRT6E
A:Note: this may not be a distinct gene
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil

Query Match 84.4%; Score 38; DB 2; Length 564;
Best Local Similarity 77.8%; Pred. No. 6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQYEDIAQK 9
|||||:
Db 339 AQYEBIAQR 347

RESULT 12
I61768
keratin 6c, type II - human
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: I61768
R:Takahashi, K.; Paladini, R.D.; Coulombe, P.A.
J. Biol. Chem. 270, 18581-18592, 1995
A:Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
A:Reference number: A57398; MUID:95355491; PMID:7543104
A:Accession: I61768
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-564 <RES>
A:Cross-references: UNIPROT:P48666; UNIPARC:UPI0000167EE0; GB:L42593; NID:G908791; GB:L4
96; GB:L42599; NID:G908797; GB:L42600; NID:G908798; GB:L42601; NID:G908799; PIDN:AAC4176
C:Genetics:
A:Gene: KRT6C
A:Introns: 180/3; 252/2; 272/3; 304/3; 359/3; 401/3; 475/2; 487/1
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil

Query Match 84.4%; Score 38; DB 2; Length 564;

Best Local Similarity 77.8%; Pred. No. 6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQYEDIAQK 9
|||||:
Db 339 AQYEBIAQR 347

RESULT 13
I61771
keratin 6f, type II - human
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: I61771
R:Takahashi, K.; Paladini, R.D.; Coulombe, P.A.
J. Biol. Chem. 270, 18581-18592, 1995
A:Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
A:Reference number: A57398; MUID:95355491; PMID:7543104
A:Accession: I61771
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-564 <RES>
A:Cross-references: UNIPROT:P48669; UNIPARC:UPI000013CD50; GB:L42612; NID:G908804; PIDN:
C:Genetics:
A:Gene: KRT6F
A:Note: this may not be a distinct gene
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil

Query Match 84.4%; Score 38; DB 2; Length 564;
Best Local Similarity 77.8%; Pred. No. 6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQYEDIAQK 9
|||||:
Db 339 AQYEBIAQR 347

RESULT 14
A44861
keratin, 67K type II epidermal - human
N:Alternate names: cytokeratin 2, CK 2; epidermal cytokeratin 2
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A44861
R:Collin, C.; Moll, R.; Kubicka, S.; Ouhayoun, J.P.; Franke, W.W.
Exp. Cell Res. 202, 132-141, 1992
A:Title: Characterization of human cytokeratin 2, an epidermal cytoskeletal protein synt
A:Reference number: A44861; MUID:92380238; PMID:I380918
A:Accession: A44861
A:Molecule type: mRNA
A:Residues: 1-645 <COL>
A:Cross-references: UNIPROT:P35908; UNIPARC:UPI000012DB03; GB:S43646
A:Experimental source: epidermis
A:Note: the authors translated the codon GGC for residue 146 as Cys
C:Note: sequence extracted from NCBI backbone (NCBIN:112351)
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament

Query Match 84.4%; Score 38; DB 2; Length 645;
Best Local Similarity 77.8%; Pred. No. 6.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQYEDIAQK 9
|||||:
Db 360 AQYEBIAQR 368

RESULT 15
A60093
cytokeratin, type II, early ectodermal - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993

C;Accession: A60093
R;Charlebois, T.S.; Spencer, D.H.; Tarkington, S.K.; Henry, J.J.; Grainger, R.M.
Development 108, 33-45, 1990
A;Title: Isolation of a chick cytokeratin cDNA clone indicative of regional specialization
A;Reference number: A60093; MUID:90276238; PMID:1693557
A;Accession: A60093
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-390 <CHA>
A;Cross-references: UNIPARC:UPI00001774C6
C;Superfamily: cytoskeletal keratin
C;Keywords: intermediate filament

Query Match 82.2%; Score 37; DB 2; Length 390;
Best Local Similarity 77.8%; Pred. No. 6.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDIAQK 9
Db 187 AQYEDIANR 195

Search completed: July 5, 2006, 19:25:11
Job time : 8.25 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 19:01:48 ; Search time 104.625 Seconds
(without alignments)
79.571 Million cell updates/sec

Title: US-10-774-928A-2

Perfect score: 45

Sequence: 1 AQVEDIAQK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	594	2	Q3UV17 MOUSE
2	42	93.3	278	2	Q9CV72 MOUSE
3	42	93.3	552	1	K2C6A_MOUSE
4	42	93.3	554	2	Q3UV11 MOUSE
5	42	93.3	561	1	K2C6B_MOUSE
6	42	93.3	581	2	Q6IFZ5 RAT
7	42	93.3	629	1	K2C3_HUMAN
8	42	93.3	629	1	K2C3_RABIT
9	41	91.1	525	1	K2C4_MOUSE
10	41	91.1	580	2	Q98UJ3 XENLA
11	41	91.1	619	2	Q6E1Y9 CANFA
12	41	91.1	633	2	Q6E1Z1 CANFA
13	40	88.9	496	2	Q42434 NOTVI
14	40	88.9	508	2	Q6NVR6 XENTR
15	40	88.9	511	2	Q90ZF7 RANCA
16	40	88.9	512	1	K2C5 XENLA
17	40	88.9	537	2	Q91219 ONCMY
18	39	86.7	459	2	Q7SYF7 ACIBE
19	39	86.7	461	2	Q42435 NOTVI
20	39	86.7	473	2	Q4RMX0 TETNG
21	39	86.7	487	2	Q7SYF6 ACIBE
22	39	86.7	502	1	K2C8 XENLA
23	39	86.7	507	2	Q7ZXU4 XENLA
24	39	86.7	538	2	Q90VH3 ONCMY
25	38	84.4	384	1	K2C6D_HUMAN
26	38	84.4	497	2	Q5K2N3 PROAT
27	38	84.4	534	1	K2C4_HUMAN
28	38	84.4	536	2	Q6PVZ4 CHICK
29	38	84.4	539	2	Q6NXH9 MOUSE
30	38	84.4	553	2	Q6IG03 RAT
31	38	84.4	563	1	K2C6A_HUMAN

32	38	84.4	563	1	K2C6B_HUMAN	P04259	homo sapien
33	38	84.4	563	1	K2C6C_HUMAN	P48666	homo sapien
34	38	84.4	563	1	K2C6E_HUMAN	P48668	homo sapien
35	38	84.4	564	2	Q2TAZ9_HUMAN	Q42a29	homo sapien
36	38	84.4	639	2	Q4VAQ2_HUMAN	Q4vaq2	homo sapien
37	38	84.4	645	1	K22E_HUMAN	P35908	homo sapien
38	38	84.4	653	2	Q9SLG9 CANFA	Q95lg9	canis famil
39	37	82.2	79	2	Q63280_RAT	Q63280	rattus norv
40	37	82.2	176	2	Q4J123 ICTPU	Q4j123	ictalurus p
41	37	82.2	279	2	Q7L4M3_HUMAN	Q7l4m3	homo sapien
42	37	82.2	305	2	Q4SY71_TETNG	Q4sy71	tetraodon n
43	37	82.2	346	2	Q4QV72_SPAU	Q4qv72	sparus aura
44	37	82.2	365	2	Q96910_HUMAN	Q96910	homo sapien
45	37	82.2	378	1	CAAL_BDEBA	Q6mkw4	bdellovibri

ALIGNMENTS

RESULT 1
Q3UV17_MOUSE PRELIMINARY; PRT; 594 AA.
AC Q3UV17;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 6.
DE Adult female vagina cDNA, RIKEN full-length enriched library,
GN Name=2310001L23Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Vagina;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Vagina;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crome M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., Di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Georgii-Heminger P., Gogerbas T.R., Gojovic T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jakt M., Kanincki A., Katoh M., Kawasaki Y., Kelso J., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.P., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakaguchi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G., Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Sheng Y., Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K., Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,

RA Yamamichi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlesed C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563 (2005).
 RN [3]
 RN NUCLEOTIDE SEQUENCE
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX PubMed16141073; DOI=10.1126/science.1112009;
 RG RIKEN genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566 (2005).
 RN [4]
 RN NUCLEOTIDE SEQUENCE
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Bacalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia K., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanaï A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konggaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Nunata K., Okido T., Pavan W.J., Perteau G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shinada K.,
 RA Suterano R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlesed C., Wang Y., Watanabe Y., Wells C.,
 RA Wu Ming L., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 RN [5]
 RN NUCLEOTIDE SEQUENCE
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischnmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN [6]
 RN NUCLEOTIDE SEQUENCE
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 RN [7]
 RN NUCLEOTIDE SEQUENCE
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaehiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771 (2000).
 RN [8]
 RN NUCLEOTIDE SEQUENCE
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
 RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
 RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -- SIMILARITY: Belongs to the intermediate filament family.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AK137676; BAE23456.1; -; mRNA.
 DR MGI; MGI:1924305; 2310001L23Rik.
 DR GO; GO:0005882; C:intermediate filament; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR001664; IF.
 DR InterPro; IPR003054; Keratin_II.
 DR Pfam; PF00038; Filament; I.
 DR PRINTS; PR01276; TYPE2KERATIN.
 DR PROSITE; PS00226; IF; 1.
 KW Coiled coil; Intermediate filament; Keratin.
 SQ SEQUENCE 594 AA; 62845 MW; 00998F2B496DF612 CRC64;
 Query Match 100.0%; Score 45; DB 2; Length 594;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AQYEDIAQK 9
 DB 343 AQYEDIAQK 351
 RESULT 2
 Q9CV72_MOUSE
 ID Q9CV72_MOUSE PRELIMINARY; PRT; 278 AA.
 AC Q9CV72;
 DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2001, sequence version 1.
 DT 07-FEB-2006, entry version 22.
 DE Adult male tongue cDNA, RIKEN full-length enriched library,
 DE clone-2310008N03 product:keratin complex 2, basic, gene 6b, full
 DE insert sequence. (fragment).
 GN Name=Krt2-6b;

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX PubMed=16141073; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilmink L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Banerji M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.K., Gojobori T., Green R.E.,
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Huminec L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.P., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam M., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlandini V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Tesdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Lida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashina T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
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 RG (Genome Network Core Team) and the FANTOM Consortium;
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 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Tesdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyszewski-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
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 RL Nature 420:563-573(2002).
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 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Iwama M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
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 RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsumi T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Ozawa K., Tanaka T., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ogawa K., Tanaka T., Matsuda S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;

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RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukuishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Horii F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Mateuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saïto H., Saïto R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sojabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi P., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; AK009241; BAB26162.1; -; mRNA.
DR HSSP; P08670; 1GK4.
DR Ensembl; ENSMUSG0000023041; Mus musculus.
DR MGI; MGI:1333768; Krt2-6b.
DR GO; GO:0046021; C:integral to membrane; RCA.
DR GO; GO:0005739; C:mitochondrion; IDA.
DR GO; GO:0045109; P:intermediate filament organization; IGI.
DR GO; GO:0031424; P:keratinization; IGI.
DR GO; GO:0002009; P:morphogenesis of an epithelium; IGI.
DR InterPro; IPR001664; IF.
DR InterPro; IPR003054; Keratin II.
DR PANTHER; PTHR18893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
FT NON_TER
FT SEQUENCE 278 AA; 30011 MW; BC641612D2959191 CRC64;
Query Match 93.3%; Score 42; DB 2; Length 278;
Best Local Similarity 88.9%; Pred. No. 4.5;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AQYEDIAQK 9
Db 52 AQYEDIAQR 60
RESULT 3
K2C6A_MOUSE
ID K2C6A_MOUSE STANDARD; PRT; 552 AA.
AC P50446; Q9Z332;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2005, sequence version 2.
DT 21-FEB-2006, entry version 42.
DE Keratin, type II cytoskeletal 6A (Cytokeratin-6A) (CK 6A) (K6a
DE keratin) (Keratin-6 alpha) (mk6-alpha).
GN Name=Krt6a; Synonyms=Ker2, Krt2-6, Krt2-6a, Krt6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Epidermis;
RX MEDLINE=85014838; PubMed=6207530;
RA Steinert P.M., Parry D.A.D., Racoosin E.L., Idler W.W., Steven A.C.,
RA Trus B.L., Roop D.R.;
RT "The complete cDNA and deduced amino acid sequence of a type II mouse
RT epidermal keratin of 60,000 Da: analysis of sequence differences
RT between type I and type II keratins.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5709-5713 (1984).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION.
RC STRAIN=129/Sv; TISSUE=Skin;

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RX Takahashi K., Yan B., Yamanishi K., Imamura S., Coulombe P.A.;
RT "The two functional keratin 6 genes of mouse are differentially
RL regulated and evolved independently from their human orthologs.";
RN Genomics 53:170-183 (1998).
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Jaw, and Limb;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP NUCLEOTIDE SEQUENCE OF 527-552.
RX PubMed=1713533;
RA Finch J., Andrews K., Krieg P., Furstenberger G., Slaga T.,
RA Ocsuysu A., Tanooka H., Bowden G.T.;
RT "Identification of a cloned sequence activated during multi-stage
RT carcinogenesis in mouse skin.";
RL Carcinogenesis 12:1519-1522 (1991).
CC -!- FUNCTION: There are two types of cytoskeletal and microfilbrillar
CC keratin: I (acidic; 40-55 kDa) [K9 to K20] and II (neutral to
CC basic; 56-70 kDa) [K1 to K8]. Both a basic and an acidic keratin
CC are required for filament assembly.
CC -!- SUBUNIT: Heterodimer of a type I and a type II keratin. KRT6
CC isomers associate with KRT16 and/or KRT17.
CC -!- TISSUE SPECIFICITY: Predominates in the adult trunk skin, tongue,
CC trachea/esophagus and eye. In adult skin, localization is
CC restricted to hair follicles, where it is localized predominantly
CC in the outer root sheath.
CC -!- INDUCTION: With the exception of specific body sites, keratin 6
CC expression is induced under conditions of epithelial
CC hyperproliferation such as wound healing, certain skin diseases,
CC cancer, and by treatment of the skin with the phorbol ester PMA.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
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CC -----
DR EMBL; K02108; AAA39395.1; -; mRNA.
DR EMBL; AB012033; BAA34178.1; -; Genomic_DNA.
DR EMBL; BC080820; AAB80820.1; -; mRNA.
DR F01; I59009; I59009.
DR HSSP; P08670; 1GK7.
DR IntAct; P50446; -.
DR Ensembl; ENSMUSG0000058354; Mus musculus.
DR MGI; MGI:1100845; Krt2-6a.
DR GO; GO:0005882; C:intermediate filament; ISS.
DR GO; GO:0005198; P:cytoskeletal molecule activity; ISS.
DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; ISS.
DR InterPro; IPR001664; IF.
DR InterPro; IPR003054; Keratin II.
DR PANTHER; PTHR18893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.

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KW Coiled coil; Intermediate filament; Keratin; Phosphorylation.
 FT INIT_MET 0 By similarity.
 FT CHAIN 1 552 Keratin, type II cytoskeletal 6A.
 FT /FTid=PRO_0000063736.
 FT REGION 1 150 Head.
 FT REGION 151 460 Rod.
 FT REGION 151 186 Coil 1A.
 FT REGION 187 205 Linker 1.
 FT REGION 206 297 Linker 1B.
 FT REGION 298 321 Linker 12.
 FT REGION 322 460 Coil 2.
 FT REGION 461 552 Tail.
 FT SITE 402 Stutter.
 FT MOD_RES 57 57 Phosphoserine (By similarity).
 FT CONFLICT 23 23 P -> L (in Ref. 1).
 FT CONFLICT 120 120 P -> L (in Ref. 1).
 FT CONFLICT 172 172 L -> M (in Ref. 1).
 FT CONFLICT 179 179 L -> M (in Ref. 1).
 FT CONFLICT 190 190 G -> D (in Ref. 1).
 FT CONFLICT 198 198 L -> M (in Ref. 1).
 FT CONFLICT 223 224 LD -> MN (in Ref. 1).
 FT CONFLICT 232 239 DTVEDYKS -> ELVEELRN (in Ref. 1).
 FT CONFLICT 250 250 A -> D (in Ref. 1).
 FT CONFLICT 311 311 D -> V (in Ref. 1).
 FT CONFLICT 317 317 D -> V (in Ref. 1).
 FT CONFLICT 329 331 YED -> FEV (in Ref. 1).
 FT CONFLICT 343 343 W -> L (in Ref. 1).
 FT CONFLICT 431 431 R -> M (in Ref. 1).
 FT CONFLICT 437 437 Q -> H (in Ref. 1).
 FT CONFLICT 497 497 L -> M (in Ref. 1).
 SQ SEQUENCE 552 AA; 59204 MW; DEB02A645EBA8DAF CRC64;

Query Match 93.3%; Score 42; DB 1; Length 552;
 Best Local Similarity 88.9%; Pred. No. 9.5;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AQVEDIAQK 9
 DB 327 AQVEDIAQK 335

RESULT 4

ID Q3UV11_MOUSE PRELIMINARY; PRT; 554 AA.
 AC Q3UV11;
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2005, sequence version 1.
 DE 07-FEB-2006, entry version 5.
 DE Adult female vagina cDNA, RIKEN full-length enriched library,
 DE clone:9930033J10 product:keratin complex 2, basic, gene 6b, full
 DE insert sequence.
 GN Name=Krt2-6b;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX PubMed=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44 (1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,

Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Huminicki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
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 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
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 RA Petrovsky N., Piazza S., Reed J., Reid J.P., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563 (2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566 (2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaio I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schraml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Gough J.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sakai D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of

60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Vagina; DOI=10.1038/35055500;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
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RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
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RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Vagina;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Vagina; DOI=10.1101/gr.152600;
RX MEDLINE=20530913; PubMed=11076961; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Vagina;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Horii F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Takagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
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CC -----
CC EMBL: AK137688; BAE23462.1; -; mRNA.
CC MGI: 1333768; Krt2-6b.
CC GO: 00016021; C: integral to membrane; RCA.
CC GO: 0005739; C: mitochondrion; IDA.
CC GO: 00045109; P: intermediate filament organization; IGI.
CC GO: 0031424; P: keratinization; IGI.
CC GO: 0002009; P: morphogenesis of an epithelium; IGI.
CC InterPro: IPR001664; IF.
CC InterPro: IPR003054; Keratin_II.

DR Pfam: PF00038; Filament; 1.
DR PRINTS: PR01276; TYPE2KERATIN.
DR PROSITE: PS00226; IF; 1.
KW Intermediate filament; Keratin.
SQ SEQUENCE 554 AA; 59526 MW; 440DE8AE398488AA CRC64;

Query Match 93.3%; Score 42; DB 2; Length 554;
Best Local Similarity 88.9%; Pred. No. 9.5;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AQYEDIAQK 9
Db 328 AQYEDIAQK 336
|||||||:
328 AQYEDIAQK 336

RESULT 5
K2C6B MOUSE STANDARD; PRT; 561 AA.
ID K2C6B MOUSE
AC Q92331;
DT 15-FEB-2005, integrated into UniProtKB/Swiss-Prot.
DT 15-FEB-2005, sequence version 2.
DT 07-FEB-2006, entry version 33.
DE Keratin, type II cytoskeletal 6B (Cytokeratin-6B) (CK 6B) (K6b
DE keratin) (Keratin-6 beta) (mk6-beta).
GN Name=Krt6b; Synonyms=K6-beta, Krt2-6b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Murioidea; Muridae; Murinae; Mus.
RX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION.
RC STRAIN=129/SV; TISSUE=Skin;
RX MEDLINE=95009332; PubMed=9790766; DOI=10.1006/geno.1998.5476;
RA Takahashi K., Yan B., Yamashita K., Imamura S., Coulombe P.A.;
RT "The two functional keratin 6 genes of mouse are differentially
RT regulated and evolved independently from their human orthologs.";
RL Genomics 53:170-183(1998).
CC -!- FUNCTION: There are two types of cytoskeletal and microfilillar
CC keratin: I (acidic; 40-55 kDa) [K9 to K20] and II (neutral to
CC basic; 56-70 kDa) [K1 to K8]. Both a basic and an acidic keratin
CC are required for filament assembly.
CC -!- SUBUNIT: Heterodimer of a type I and a type II keratin. KRT6
CC isomers associate with KRT16 and/or KRT17.
CC -!- TISSUE SPECIFICITY: Expressed in adult epithelia including the
CC tongue, esophagus/trachea, eye and skin. Localized preferentially
CC to the suprabasal layers of thickened epidermis in injured and
CC chemically treated skin.
CC -!- INDUCTION: By injury, and treatment of the skin with the phorbol
CC ester PMA.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----
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CC -----
CC EMBL: AB012042; BAA334179.1; -; Genomic DNA.
CC HSSP: P08670; 1GK7.
DR Ensembl: ENSMUSG00000023041; Mus musculus.
DR MGI: 1333768; Krt2-6b.
DR GO: 00016021; C: integral to membrane; TAS.
DR GO: 0005882; C: intermediate filament; ISS.
DR GO: 0005739; C: mitochondrion; IDA.
DR GO: 0005198; P: structural molecule activity; ISS.
DR GO: 0007010; P: cytoskeleton organization and biogenesis; ISS.
DR InterPro: IPR001664; IF.
DR InterPro: IPR003054; Keratin_II.
DR PANTHER: PTHR18993.SF5; Keratin_II; 1.
DR Pfam: PF00038; Filament; 1.
DR PRINTS: PR01276; TYPE2KERATIN.
DR PROSITE: PS00226; IF; 1.
KW Coiled coil; Intermediate filament; Keratin; Phosphorylation.
FT INIT MET 0 0 By similarity.
FT CHAIN 1 561 Keratin, type II cytoskeletal 6B.

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FT REGION 1 158 /FTID=PRO_0000063737.
FT REGION 159 468 Head.
FT REGION 159 468 Rod.
FT REGION 159 194 Coil 1A.
FT REGION 195 213 Linker 1.
FT REGION 214 305 Coil 1B.
FT REGION 306 329 Linker 12.
FT REGION 330 468 Coil 2.
FT REGION 469 561 Tail.
FT SITE 410 410 Stutter.
FT MOD RES 57 57 Phosphoserine (By similarity).
SQ SEQUENCE 561 AA; 60191 MW; 65B71CAB7F9564E1 CRC64;

Query Match 93.3%; Score 42; DB 1; Length 561;
Best Local Similarity 88.9%; Pred. No. 9.6;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQVEDIAQK 9
Db 335 AQVEDIAQR 343
|||||:

RESULT 6
Q6IFZ5_RAT PRELIMINARY; PRT; 581 AA.
AC Q6IFZ5;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Type II keratin Kb9.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE
RX MEDLINE=23257644; PubMed=15085952; DOI=10.1078/0171-9335-00354;
RA Hesse M., Zimek A., Weber K., Magin T.W.;
RT "Comprehensive analysis of keratin gene clusters in humans and rodents.";
RL Eur. J. Cell Biol. 83:19-26(2004).
CC -I- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
CC -I- SIMILARITY: Belongs to the intermediate filament family.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BK003994; DAA02235.1; -; mRNA.
DR Ensembl; ENSRNOG00000031785; Rattus norvegicus.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893:SFS; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
SQ SEQUENCE 581 AA; 61758 MW; 13B0F3D23BDF4E49 CRC64;

Query Match 93.3%; Score 42; DB 2; Length 581;
Best Local Similarity 88.9%; Pred. No. 10;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQVEDIAQK 9
Db 337 AQVEDIAQR 345
|||||:

RESULT 7
K2C3_HUMAN STANDARD; PRT; 629 AA.
ID K2C3_HUMAN
AC P12035; Q701L8;
DT 01-OCT-1989, integrated into UniProtKB/Swiss-Prot.
DT 08-NOV-2005, sequence version 2.
DT 07-FEB-2006, entry version 48.
DE Keratin, type II cytoskeletal 3 (Cytokeratin-3) (CK-3) (Keratin-3)
DE (K3) (65 kDa cyokeratin).
GN Name=KRT3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=87254239; PubMed=2439698;
RA Klinge E.M., Sylvestre Y.R., Freedberg I.M., Blumenberg M.;
RT "Evolution of keratin genes: different protein domains evolve by
RT different pathways.";
RL J. Mol. Evol. 24:319-329(1987).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 16-629.
RC TISSUE=Eye;
RX PubMed=15737194; DOI=10.1111/j.0022-202X.2004.23530.x;
RA Rogers M.A., Edler L., Winter H., Langbein L., Beckmann I.,
RA Schweizer J.;
RT "Characterization of new members of the human type II keratin gene
RT family and a general evaluation of the keratin gene domain on
RT chromosome 12q13.13.";
RL J. Invest. Dermatol. 124:536-544(2005).
RN [3]
RP VARIANT MCD LYS-509.
RX MEDLINE=97315826; PubMed=9171831;
RA Irvine A.D., Corden L.D., Swensson O., Swensson B., Moore J.E.,
RA Frazer D.G., Smith F.J.D., Knowlton R.G., Christophers E., Rochels R.,
RA Uitto J., McLean W.H.I.;
RT "Mutations in cornea-specific keratin K3 or K12 genes cause Meesmann's
RT corneal dystrophy.";
RL Nat. Genet. 16:184-187(1997).
CC -I- SUBUNIT: Heterotetramer of two type I and two type II keratins.
CC Keratin-3 associates with keratin-12.
CC -I- TISSUE SPECIFICITY: Cornea specific.
CC -I- DISEASE: Defects in KRT3 are a cause of Meesmann corneal dystrophy
CC (MCD) [MIM:122100]. MCD is an autosomal dominant disease that
CC causes fragility of the anterior corneal epithelium. Patients are
CC usually asymptomatic until adulthood when rupture of the corneal
CC microcysts may cause erosions, producing clinical symptoms such as
CC photophobia, contact lens intolerance and intermittent diminution
CC of visual acuity. Rarely, subepithelial scarring causes irregular
CC corneal astigmatism and permanent visual impairment. Histological
CC examination shows a disorganized and thickened epithelium with
CC widespread cytoplasmic vacuolation and numerous small, round,
CC debris-laden intraepithelial cysts.
CC -I- MISCELLANEOUS: There are two types of cytoskeletal and
CC microfibrillar keratin: I (acidic; 40-55 kDa) [K9 to K20] and II
CC (neutral to basic; 56-70 kDa) [K1 to K8].
CC -I- SIMILARITY: Belongs to the intermediate filament family.
CC -I- DATABASE: NAMB=Human Intermediate Filament Mutation Database;
CC WWW="http://www.interfil.org".
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; X05418; CAA28991.1; -; Genomic DNA.
DR EMBL; X05419; CAA28992.1; ALT_SEQ; Genomic DNA.
DR EMBL; X05420; CAA28993.1; ALT_SEQ; Genomic DNA.
DR EMBL; X05420; CAA28994.1; ALT_SEQ; Genomic DNA.
DR EMBL; X05420; CAA28995.1; ALT_SEQ; Genomic DNA.
DR EMBL; X05421; CAA28996.1; ALT_SEQ; Genomic DNA.
DR EMBL; X05421; CAA28996.1; ALT_SEQ; Genomic DNA.
DR EMBL; X05421; CAA28996.1; ALT_SEQ; Genomic DNA.
DR HSSP; P08670; 1GK7.
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DR Ensemble; ENSG00000186442; Homo sapiens.
DR HGNC; HGNC:6440; KRT3.
DR MIM; 122100; phenotype.
DR MIM; 148043; Gene.
DR LinkHub; P12035; -.
DR GO; GO:0005882; C:intermediate filament; NAS.
DR GO; GO:0005198; P:structural molecule activity; NAS.
DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; NAS.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR PANTHER; PTHR1893:SF5; Keratin_II.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Coiled coil; Disease mutation; Intermediate filament; Keratin;
KW Phosphorylation.
FT CHAIN 1 629 Keratin, type II cytoskeletal 3.
FT REGION 1 197 Head.
FT REGION 198 509 Rod.
FT REGION 198 233 Coiled coil 1A.
FT REGION 234 254 Linker 1.
FT REGION 255 346 Coiled coil 1B.
FT REGION 347 370 Linker 12.
FT REGION 371 509 Coiled coil 2.
FT REGION 510 629 Tail.
FT MOD_RES 56 56 Phosphoserine (By similarity).
FT VARIANT 509 509 E -> K (in MCD).
FT CONFLICT 63 63 /FTID=VAR_003868.
FT CONFLICT 162 162 N -> D (in Ref. 1).
FT CONFLICT 175 175 G -> A (in Ref. 1).
FT CONFLICT 175 175 I -> T (in Ref. 1).
FT CONFLICT 184 184 N -> K (in Ref. 1).
FT CONFLICT 187 187 I -> T (in Ref. 1).
FT CONFLICT 298 298 T -> Y (in Ref. 1).
FT CONFLICT 375 375 R -> G (in Ref. 1).
FT CONFLICT 409 409 D -> G (in Ref. 2).
FT CONFLICT 448 448 E -> Q (in Ref. 1).
FT CONFLICT 512 512 Missing (in Ref. 2).
FT CONFLICT 563 563 S -> I (in Ref. 1).
FT CONFLICT 581 581 S -> T (in Ref. 1).
SQ SEQUENCE 629 AA; 64504 MW; D15D10C11DA90AD0 CRC64;

Query Match 93.3%; Score 42; DB 1; Length 629;
Best Local Similarity 88.9%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AQYEDIAQK 9
Db 376 AQYEDIAQR 384

RESULT 8
ID K2C3 RABIT STANDARD; PRT; 629 AA.
AC Q29426;
DT 08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-MAR-2006, entry version 30.
DE Keratin, type II cytoskeletal 3 (Cytokeratin-3) (CK-3) (Keratin-3) (K3).
GN Name=KRT3;
OS Oryctolagus cuniculus (Rabbit);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OC NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=94013038; PubMed=7691837;
Wu R.L., Galvin S., Wu S.K., Xu C., Blumenberg M., Sun T.T.;

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RT "A 300 bp 5'-upstream sequence of a differentiation-dependent rabbit
RT K3 keratin gene can serve as a keratinocyte-specific promoter.";
RL J. Cell Sci. 105:303-316(1993).
CC -!- SUBUNIT: Heterotrimer of two type I and two type II keratins.
CC Keratin-3 associates with keratin-12.
CC -!- MISCELLANEOUS: There are two types of cytoskeletal and
CC microfibrillar keratin: I (acidic; 40-55 kDa) [K9 to K20] and II
CC (neutral to basic; 56-70 kDa) [K1 to K8].
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; S65740; AAB28323.1; -; Genomic DNA.
DR EMBL; X74371; CAA52409.1; -; Genomic DNA.
DR PIR; S42629; S42629.
DR HSSP; P08670; 10K7.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR InterPro; IPR03054; Keratin_II.
DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Coiled coil; Intermediate filament; Keratin; Phosphorylation.
FT CHAIN 1 629 Keratin, type II cytoskeletal 3.
FT REGION 1 182 Head (By similarity).
FT REGION 183 494 Rod (By similarity).
FT REGION 183 218 Coiled coil 1A (By similarity).
FT REGION 219 239 Linker 1 (By similarity).
FT REGION 240 331 Coiled coil 1B (By similarity).
FT REGION 332 355 Linker 12 (By similarity).
FT REGION 356 494 Coiled coil 2 (By similarity).
FT REGION 495 629 Tail (By similarity).
FT MOD_RES 62 62 Phosphoserine (By similarity).
SQ SEQUENCE 629 AA; 64341 MW; A4F456D366AC1A72 CRC64;

Query Match 93.3%; Score 42; DB 1; Length 629;
Best Local Similarity 88.9%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AQYEDIAQK 9
Db 361 AQYEDIAQR 369

RESULT 9
ID K2C4 MOUSE STANDARD; PRT; 525 AA.
AC P07744; O6P3F5;
DT 01-AUG-1988, integrated into UniProtKB/Swiss-Prot.
DT 22-NOV-2005, sequence version 2.
DT 07-MAR-2006, entry version 48.
DE Keratin, type II cytoskeletal 4 (Cytokeratin-4) (CK-4) (Keratin-4) (K4) [Cytoskeletal 57 kDa keratin].
GN Name=Krt4; Synonyms=Krt2-4;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA] AND TISSUE SPECIFICITY.
RX MEDLINE=86120369; PubMed=2418416;
RA Knapp B., Rentsch M., Schweizer J., Winter H.;
RT "Nonepidermal members of the keratin multigene family: cDNA sequences and in situ localization of the mRNAs.";
RL Nucleic Acids Res. 14:751-763(1986).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauser R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.P., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBUNIT: Heterotetramer of two type I and two type II keratins.
CC -!- Keratin-4 is generally associated with keratin-13.
CC -!- TISSUE SPECIFICITY: Expressed in the dorsal and ventral epithelium
of the tongue. Highest expression levels are detected in the
suprabasal layer with low levels detected in the basal cell layer.
CC Within the suprabasal layer expression is highest in the spinous
cells, decreases in the granular cells and is not detected in the
stratum corneum.
CC -!- MISCELLANEOUS: There are two types of cytoskeletal and
microfibrillar keratin, I (acidic; 40-55 kDa) [K9 to K20] and II
(neutral to basic; 56-70 kDa) [K1 to K8].
CC -!- SIMILARITY: Belongs to the intermediate filament family.
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CC -----
CC EMBL: X03491; CAA27207.1; -; mRNA.
CC EMBL: BC064008; AAH64008.1; ALT_INT; mRNA.
CC F1R: A23518; A23518.
CC HSSP: P08670; 1GK7.
CC Ensembl: ENSMUSG0000059668; Mus musculus.
CC MGI: MGI:96701; Krt2-4.
CC InterPro: IPR001664; IF.
CC InterPro: IPR002957; Keratin I.
CC InterPro: IPR003054; Keratin II.
CC Pfam: PF00038; Filament; 1.
CC PRINTS: PR01248; TYPE1KERATIN.
CC PRINTS: PR01276; TYPE2KERATIN.
CC PROSITE: PS00226; IF; 1.
CC Coiled coil; Intermediate filament; Keratin; Phosphorylation.
KW Coiled coil; Intermediate filament; Keratin, type II cytoskeletal 4.
CHAIN 1 525 /FTid=PRO_0000063723.
FT REGION 1 145 Head.
FT REGION 146 455 Rod.
FT REGION 146 181 Coil 1A.
FT REGION 182 200 Linker 1.
FT REGION 201 292 Coil 1B.
FT REGION 293 316 Linker 12.
FT REGION 317 455 Coil 2.
FT REGION 456 524 Tail.
FT COMPIAS 10 117 Gly-rich.
FT COMPIAS 473 510 Gly-rich.
FT SITE 397 397 Stutter.
FT MOD_RES 51 51 Phosphoserine (By similarity).
FT CONFLICT 13 13 R -> P (in Ref. 1).
FT CONFLICT 16 16 S -> T (in Ref. 1).
FT CONFLICT 79 79 G -> D (in Ref. 2; AAH64008).
FT CONFLICT 388 388 L -> P (in Ref. 1).
FT CONFLICT 476 480 ASIGG -> QHWR (in Ref. 1).
SQ SEQUENCE 525 AA; 56283 MW; 27A3A3DFE87DF90 CRC64;

Query Match 91.1%; Score 41; DB 1; Length 525;
Best Local Similarity 88.9%; Pred. No. 15;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AQVEDIAQK 9
Db 322 AQVEDIAK 330
RESULT 10
Q98UJ3 XENLA PRELIMINARY; PRT; 580 AA.
ID Q98UJ3 XENLA PRELIMINARY; PRT; 580 AA.
AC Q98UJ3;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Larval keratin XLK.
GN Name=xlk;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21240324; PubMed=11342212; DOI=10.1016/S0167-4781(00)00281-5;
RA Watanabe Y., Kobayashi H., Suzuki K., Korani K., Yoshizato K.;
RT "New epidermal keratin genes from Xenopus laevis: hormonal and
RT regional regulation of their expression during anuran skin
RT metamorphosis.";
RL Biochim. Biophys. Acta 1517:339-350(2001).
CC -!- SIMILARITY: Belongs to the intermediate filament family.
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: AB045599; BAB32829.1; -; mRNA.
CC HSSP: P08670; 1GK7.
CC GO: GO:0005882; C:intermediate filament; IEA.
CC GO: GO:0005198; F:structural molecule activity; IEA.
CC InterPro: IPR013326; ApoA/E_Apolp.
CC InterPro: IPR001664; IF.
CC InterPro: IPR002957; Keratin I.
CC InterPro: IPR003054; Keratin II.
CC PANTHER: PTHR18893; SFS; Keratin II; 1.
CC Pfam: PF00038; Filament; 1.
CC PRINTS: PR01248; TYPE1KERATIN.
CC PRINTS: PR01276; TYPE2KERATIN.
CC PROSITE: PS00226; IF; 1.
CC Intermediate filament; Keratin.
SQ SEQUENCE 580 AA; 59940 MW; 7284092F7B6BC1CB CRC64;
Query Match 91.1%; Score 41; DB 2; Length 580;
Best Local Similarity 88.9%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AQVEDIAQK 9
Db 338 AQVEDIAK 346
RESULT 11
Q6EII9 CANFA PRELIMINARY; PRT; 619 AA.
ID Q6EII9 CANFA PRELIMINARY; PRT; 619 AA.
AC Q6EII9;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Epithelial keratin 1.
GN Name=keri;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;

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RN NUCLEOTIDE SEQUENCE.
RX PubMed-15627753; DOI=10.1159/000081527;
RA Credille K.M., Guyon R., Andre C., Murphy K., Tucker K.,
RA Barnhart K.F., Dunstan R.W.;
RT "Comparative sequence analysis and radiation hybrid mapping of two
RT epidermal type II keratin genes in the dog: keratin 1 and keratin
RT 2e.";
RL Cytogenet. Genome Res. 108:328-332(2005).
CC -!- SIMILARITY: Belongs to the intermediate filament family.
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CC -----
DR EMBL; AY318945; AAQ83910.1; -; mRNA.
DR Ensembl; ENSCAFG0000007212; Canis familiaris.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
SQ SEQUENCE 619 AA; 63790 MW; E45A8B709AD0909F CRC64;

Query Match 91.1%; Score 41; DB 2; Length 619;
Best Local Similarity 88.9%; Pred. No. 17;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQYEDIAQK 9
Db 357 AQYEIAQK 365

RESULT 12
Q6E1Z1_CANFA PRELIMINARY; PRT; 633 AA.
AC Q6E1Z1;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Epithelial keratin 2e.
GN Name=K2e;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed-15627753; DOI=10.1159/000081527;
RA Credille K.M., Guyon R., Andre C., Murphy K., Tucker K.,
RA Barnhart K.F., Dunstan R.W.;
RT "Comparative sequence analysis and radiation hybrid mapping of two
RT epidermal type II keratin genes in the dog: keratin 1 and keratin
RT 2e.";
RL Cytogenet. Genome Res. 108:328-332(2005).
CC -!- SIMILARITY: Belongs to the intermediate filament family.
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CC -----
DR EMBL; AY318943; AAQ83908.1; -; mRNA.
DR Ensembl; ENSCAFG0000007223; Canis familiaris.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR InterPro; IPR003054; Keratin_II.

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DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
SQ SEQUENCE 633 AA; 64567 MW; 445D509166A23CB1 CRC64;

Query Match 91.1%; Score 41; DB 2; Length 633;
Best Local Similarity 88.9%; Pred. No. 18;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQYEDIAQK 9
Db 366 AQYEIAQK 374

RESULT 13
O42434_NOTVI PRELIMINARY; PRT; 496 AA.
AC O42434;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE Cytokeratin 8 (Fragment).
OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
OC Notophthalmus.
OX NCBI_TaxID=8316;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Limb blastema;
RX MEDLINE=98075904; PubMed=9415422;
RX DOI=10.1002/(SICI)1097-0177(199712)210:4<355::AID-AJAL>3.3.CO;2-K;
RA Corcoran J.P., Ferretti P.;
RT "Keratin 8 and 18 expression in mesenchymal progenitor cells of
RT regenerating limbs is associated with cell proliferation and
RT differentiation.";
RL Dev. Dyn. 210:355-370(1997).
CC -!- SIMILARITY: Belongs to the intermediate filament family.
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CC -----
DR EMBL; AJ001296; CAA04656.1; -; mRNA.
DR HSPF; P08670; IGK7.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
FT NON TER 1
SQ SEQUENCE 496 AA; 55152 MW; D327911FBB7A1CBA CRC64;

Query Match 88.9%; Score 40; DB 2; Length 496;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDIAQK 9
Db 261 AQYEDIAQK 269

RESULT 14
Q6NVR6_XENTR PRELIMINARY; PRT; 508 AA.
ID Q6NVR6_XENTR

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AC G6NVR6;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Keratin complex 2, basic, gene 5.
GN Name=krt2-5-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCBI_TaxID=8364;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zerbahn B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
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CC -----
CC EMBL; BC067939; AAH67939.1; -; mRNA.
CC Ensembl; ENSXETG0000020454; Xenopus tropicalis.
CC GO; GO:0005882; C:intermediate filament; IEA.
CC GO; GO:0005198; F:structural molecule activity; IEA.
CC InterPro; IPR001664; IF.
CC InterPro; IPR002957; Keratin I.
CC InterPro; IPR003054; Keratin II.
CC PANTHER; PTHR1893:SF5; Keratin_II; 1.
CC Pfam; PF00038; Filament; 1.
CC PRINTS; PR01248; TYPE1KERATIN.
CC PRINTS; PR01276; TYPE2KERATIN.
CC PROSITE; PS00226; IF; 1.
CC Intermediate filament; Keratin.
SQ SEQUENCE 508 AA; 55854 MW; B0FEC774C2F66476 CRC64;

Query Match 88.9%; Score 40; DB 2; Length 508;
Best Local Similarity 88.9%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQVEDIAQK 9
DB 277 AQVEDIANK 285
RESULT 15
ID Q90ZF7_RANCA PRELIMINARY; PRT; 511 AA.
AC Q90ZF7;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Keratin 8.
GN Name=rk8;
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;
OC Aquarana.
OX NCBI_TaxID=8400;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Suzuki K., Sato K., Katsu K., Hayashita H., Kristensen D.B.,
RA Yoshizato K.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
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CC -----
CC EMBL; AB056480; BAB63946.1; -; mRNA.
CC HSSP; P08670; IGK4
CC GO; GO:0005882; C:intermediate filament; IEA.
CC GO; GO:0005198; F:structural molecule activity; IEA.
CC InterPro; IPR001664; IF.
CC InterPro; IPR002957; Keratin I.
CC InterPro; IPR003054; Keratin II.
CC PANTHER; PTHR1893:SF5; Keratin_II; 1.
CC Pfam; PF00038; Filament; 1.
CC PRINTS; PR01248; TYPE1KERATIN.
CC PRINTS; PR01276; TYPE2KERATIN.
CC PROSITE; PS00226; IF; 1.
CC Intermediate filament; Keratin.
SQ SEQUENCE 511 AA; 56378 MW; 68366DD1EF8EAS3D CRC64;
Query Match 88.9%; Score 40; DB 2; Length 511;
Best Local Similarity 88.9%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQVEDIAQK 9
DB 277 AQVEDIANK 285

Search completed: July 5, 2006, 19:18:13
Job time : 104.625 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 18:44:12 ; Search time 83.0625 Seconds
(without alignments)
49.540 Million cell updates/sec

Title: US-10-774-928a-2

Perfect score: 45

Sequence: 1 AQVEDIAQK 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_8.*

1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*
10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	45	100.0	9	6	Aao26382 Psoriasis
2	45	100.0	9	9	Adv04407 Leishmani
3	45	100.0	644	9	Aeal15501 Human pol
4	42	93.3	420	8	Adp29879 Human sec
5	42	93.3	629	9	Aeal15502 Human pol
6	40	88.9	30	2	Aay14568 Partial a
7	38	84.4	82	4	Aam20776 Peptide #
8	38	84.4	82	4	Abba42330 Peptide #
9	38	84.4	82	4	Aam36136 Peptide #
10	38	84.4	82	4	Abb25821 Protein #
11	38	84.4	82	4	Aam76029 Human bon
12	38	84.4	82	4	Aam63216 Human bra
13	38	84.4	82	4	Abg57755 Human liv
14	38	84.4	82	5	Abg45427 Human pep
15	38	84.4	268	8	Adr98973 Lung spec
16	38	84.4	295	8	Adr98974 Lung spec
17	38	84.4	327	7	Adj98669 Human hea
18	38	84.4	521	5	Abb78802 Human NOV
19	38	84.4	534	5	Abp43881 57kd kera
20	38	84.4	534	7	Adf09537 Human ker
21	38	84.4	534	7	Aeal15503 Human pol
22	38	84.4	564	5	Abp65226 Hypoxia-r
23	38	84.4	564	8	Adj75686 Marker ge

24	38	84.4	564	8	ADN04584
25	38	84.4	564	8	ADN04384
26	38	84.4	564	8	ADN04382
27	38	84.4	564	8	ADO55108
28	38	84.4	564	8	ADQ18800
29	38	84.4	564	9	AEAl15493
30	38	84.4	564	9	AEAl15491
31	38	84.4	564	9	AEAl15492
32	38	84.4	564	9	AEAl15494
33	38	84.4	564	9	AEBl17592
34	38	84.4	564	9	AEBl17594
35	38	84.4	564	9	AEBl17594
36	38	84.4	585	9	AEBl17594
37	38	84.4	608	6	ADA54878
38	38	84.4	625	6	ABP98825
39	38	84.4	645	5	ABG77177
40	38	84.4	645	8	ADN04309
41	38	84.4	645	9	ADV85790
42	38	84.4	645	9	AEAl15500
43	37	82.2	9	6	ABR75646
44	37	82.2	9	7	ADN07174
45	37	82.2	125	4	ABG20747

ALIGNMENTS

RESULT 1

AAO26382

ID AAO26382 standard; peptide; 9 AA.

XX

AC AAO26382;

XX

DT 30-JAN-2003 (first entry)

XX

XX Psoriasis treating immunotherapeutic peptide, SEQ ID No 2.

DE

XX

XX

KW

KW

XX

OS

XX

XX

PN

XX

XX

PD

XX

PF

XX

PR

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XX

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XX

XX

XX

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XX

XX

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XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 45; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.le+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AQYEDIAQK 9
| | | | | | | |
Db 1 AQYEDIAQK 9

RESULT 2
ADV04407
ID ADV04407 standard; peptide; 9 AA.
XX
AC ADV04407;
XX
DT 24-FEB-2005 (first entry)
XX
DE Leishmania immunotherapeutic peptide SEQ ID NO:2.
XX
KW T-lymphocyte; immunogenicity; antigen; antipsoriatic; immunostimulant;
KW psoriasis.
XX
OS Leishmania sp.
XX
PN US2004241168-A1.
XX
PD 02-DEC-2004.
XX
PF 09-FEB-2004; 2004US-00774928.
XX
PR 16-MAR-2001; 2001US-00809003.
PR 17-OCT-2003; 2003US-00687892.
XX
PA (ODAL/) ODALY J A.
PI Odaly JA;
XX
DR WPI; 2005-011563/01.
XX
PT Inhibiting selectively T-cell rolling in human, by administering compound
PT interfering with cutaneous lymphocyte antigen-E selectin interaction and
PT leukocyte function associated antigen-1 interaction.
XX
PS Claim 9; SEQ ID NO 2; 21pp; English.
XX
CC The invention relates to a novel method for selectively inhibiting T-cell
CC rolling in a human host, comprising administering a compound that
CC selectively interferes with the cutaneous lymphocyte antigen (CLA)-E
CC selectin interaction and leukocyte function associated antigen (LFA)-
CC 1/intercellular adhesion molecule (ICAM) and very late antigen
CC (VLA)/vascular cell adhesion molecule (VCAM) interactions. The compound
CC includes an immunotherapeutic agent, which comprises a purified protein
CC extract that is isolated by diethylaminoethyl Sephadex chromatography of
CC a Nonidet P-40 insoluble particulate antigen fraction derived from
CC isolated killed cells of anastigotes from one or more species of the
CC Leishmania genus, where the particulate antigen fraction is solubilized
CC with 8M urea and 0.025 M Tris(hydroxymethyl)aminomethane pH 8.3 applied
CC to diethylaminoethyl Sephadex and is eluted with a solution comprising
CC 0.1 M sodium chloride, 8 M urea and 0.025 M
CC Tris(hydroxymethyl)aminomethane pH 8.3, and the purified protein extract
CC includes polypeptides having apparent molecular weights of 73, 80 and 82
CC kDa, after total reduction and alkylation. The species is L. amazonensis,
CC L. venezuelensis, L. brasiliensis and/or L. chagasi. A compound of the
CC invention has antipsoriatic and immunostimulant activity, and inhibits T-
CC cell rolling by interfering with CLA-E selectin interaction and LFA-
CC 1/ICAM and VLA/VCAM interactions. The method is useful for selectively
CC inhibiting T-cell rolling in a human host, and for treating psoriasis.
CC The present sequence represents an Leishmania peptide used in the
CC invention.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 45; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.le+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AQYEDIAQK 9
| | | | | | | |
Db 1 AQYEDIAQK 9

RESULT 3
AEA15501
ID AEA15501 standard; protein; 644 AA.
XX
AC AEA15501;
XX
DT 28-JUL-2005 (first entry)
XX
DE Human polypeptide #120.
XX
KW Diagnosis; prognosis; cancer; breast tumor; ovary tumor; stomach tumor;
KW colon tumor; esophagus tumor; bladder tumor; non-small-cell lung cancer;
KW cytostatic; neoplasm.
XX
OS Homo sapiens.
XX
PN WO2005047534-A2.
XX
PD 26-MAY-2005.
XX
PF 15-OCT-2004; 2004WO-EP011599.
XX
PR 28-OCT-2003; 2003EP-00024565.
XX
PA (FARB) BAYER HEALTHCARE AG.
XX
PI Wirtz R, Munnes M;
XX
DR WPI; 2005-372393/38.
DR N-PSDB; AEA15423.
XX
PT Predicting a response to cancer treatment by detecting at least 2
PT markers, which are genes or genomic nucleic acid sequences that are
PT located on one chromosomal region, which is altered in malignant
PT neoplasia.
XX
PS Claim 7; SEQ ID NO 463; 464pp; English.
XX
CC The invention relates to a method of predicting response to cancer
CC treatment comprising detection of at least 2 markers, where the markers
CC are genes and fragments or genomic nucleic acid sequences that are
CC located on one chromosomal region, which is altered in malignant
CC neoplasia. The invention also relates to a method for the prediction,
CC diagnosis or prognosis of malignant neoplasia, methods for detecting
CC deregulations in malignant neoplasia and breast cancer, a method of
CC determining the phenotype of a cell or tissue, a method for identifying
CC genomic regions which are altered on the chromosomal level and encode
CC genes that are linked by function and are differentially expressed in
CC malignant neoplasia and breast cancer, methods of screening for agents
CC which regulate the activity of a polypeptide or a polynucleotide and
CC antibodies that specifically bind to a full length or partial
CC polypeptide. The method is useful for predicting response to cancer
CC treatment. The methods and compositions are useful for predicting,
CC diagnosing, prognosing, preventing or treating malignant neoplasia
CC including breast cancer, ovarian cancer, gastric cancer, colon cancer,
CC esophageal cancer, mesenchymal cancer, bladder cancer or non-small-cell
CC lung cancer. This sequence represents a human polypeptide used in the
CC scope of the invention.
XX
SQ Sequence 644 AA;

Query Match 100.0%; Score 45; DB 9; Length 644;
Best Local Similarity 100.0%; Pred. No. 3.5;

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AQVEDIAQK 9
Db 356 AQVEDIAQK 364

RESULT 4
ADP29879
ID ADP29879 standard; protein; 420 AA.
XX
AC ADP29879;
XX
DT 01-DEC-2005 (revised)
DT 12-AUG-2004 (first entry)
XX
DE Human secreted protein SEQ ID #1877.
XX
KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW cancer; inflammatory; immune; human secreted protein.
XX
OS Homo sapiens.
XX
PN WO2004035732-A2.
XX
PD 29-APR-2004.
XX
PF 28-AUG-2003; 2003WO-US026780.
XX
PR 29-AUG-2002; 2002US-0406576P.
PR 29-AUG-2002; 2002US-0406579P.
PR 29-AUG-2002; 2002US-0406585P.
PR 29-AUG-2002; 2002US-0406588P.
PR 29-AUG-2002; 2002US-0406608P.
PR 29-AUG-2002; 2002US-0406609P.
PR 29-AUG-2002; 2002US-0406611P.
PR 29-AUG-2002; 2002US-0406612P.
PR 29-AUG-2002; 2002US-0406616P.
PR 29-AUG-2002; 2002US-0406616P.
PR 29-AUG-2002; 2002US-0406640P.
PR 29-AUG-2002; 2002US-0406642P.
PR 29-AUG-2002; 2002US-0406646P.
PR 29-AUG-2002; 2002US-0406653P.
PR 29-AUG-2002; 2002US-0406655P.
PR 29-AUG-2002; 2002US-0406666P.
PR 17-SEP-2002; 2002US-0410946P.
PR 17-SEP-2002; 2002US-0410947P.
PR 17-SEP-2002; 2002US-0410948P.
PR 17-SEP-2002; 2002US-0410949P.
PR 17-SEP-2002; 2002US-0410953P.
PR 17-SEP-2002; 2002US-0410957P.
PR 17-SEP-2002; 2002US-0410958P.
PR 17-SEP-2002; 2002US-0410959P.
PR 17-SEP-2002; 2002US-0410960P.
PR 17-SEP-2002; 2002US-0410961P.
PR 17-SEP-2002; 2002US-0410962P.
PR 17-SEP-2002; 2002US-0411019P.
PR 17-SEP-2002; 2002US-0411022P.
PR 17-SEP-2002; 2002US-0411023P.
PR 17-SEP-2002; 2002US-0411024P.
PR 17-SEP-2002; 2002US-0411032P.
PR 17-SEP-2002; 2002US-0411035P.
PR 17-SEP-2002; 2002US-0411037P.
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PR 17-SEP-2002; 2002US-0411045P.
PR 17-SEP-2002; 2002US-0411046P.
PR 17-SEP-2002; 2002US-0411048P.
PR 17-SEP-2002; 2002US-0411052P.
PR 17-SEP-2002; 2002US-0411055P.
PR 17-SEP-2002; 2002US-0411073P.
PR 17-SEP-2002; 2002US-0411082P.
PR 17-SEP-2002; 2002US-0411101P.
PR 17-SEP-2002; 2002US-0411111P.
PR 18-APR-2003; 2003US-0463700P.
PR 18-APR-2003; 2003US-0463708P.

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AQVEDIAQK 9
Db 356 AQVEDIAQK 364

RESULT 5
AEA15502
ID AEA15502 standard; protein; 629 AA.
XX
AC AEA15502;
XX
DT 28-JUL-2005 (first entry)
DE Human polypeptide #121.
XX
KW Diagnosis; prognosis; cancer; breast tumor; ovary tumor; stomach tumor;
```

KW colon tumor; esophagus tumor; bladder tumor; non-small-cell lung cancer;
 KW cytostatic; neoplasm.
 OS Homo sapiens.
 XX WO2005047534-A2.
 PN 26-MAY-2005.
 PD 15-OCT-2004; 2004WO-EP011599.
 XX 28-OCT-2003; 2003EP-00024565.
 PF (FARB) BAYER HEALTHCARE AG.
 XX Wirtz R, Munnes M;
 PI WPI; 2005-372393/38.
 DR N-PSDB; AEA15424.
 XX Predicting a response to cancer treatment by detecting at least 2
 PT markers, which are genes or genomic nucleic acid sequences that are
 PT located on one chromosomal region, which is altered in malignant
 PT neoplasia.
 PS Claim 7; SEQ ID NO 464; 464pp; English.
 XX The invention relates to a method of predicting response to cancer
 CC treatment comprising detection of at least 2 markers, where the markers
 CC are genes and fragments or genomic nucleic acid sequences that are
 CC located on one chromosomal region, which is altered in malignant
 CC neoplasia. The invention also relates to a method for the prediction,
 CC diagnosis or prognosis of malignant neoplasia, methods for detecting
 CC deregulations in malignant neoplasia and breast cancer, a method of
 CC determining the phenotype of a cell or tissue, a method for identifying
 CC genomic regions which are altered on the chromosomal level and encode
 CC genes that are linked by function and are differentially expressed in
 CC malignant neoplasia and breast cancer, methods of screening for agents
 CC which regulate the activity of a polypeptide or a polynucleotide and
 CC antibodies that specifically bind to a full length or partial
 CC polypeptide. The method is useful for predicting response to cancer
 CC treatment. The methods and compositions are useful for predicting,
 CC diagnosing, prognosing, preventing or treating malignant neoplasia
 CC including breast cancer, ovarian cancer, gastric cancer, colon cancer,
 CC esophageal cancer, mesenchymal cancer, bladder cancer or non-small-cell
 CC lung cancer. This sequence represents a human polypeptide used in the
 CC scope of the invention.
 XX SQ Sequence 629 AA;
 Query Match 93.3%; Score 42; DB 9; Length 629;
 Best Local Similarity 88.9%; Pred. No. 14; Mismatches 0; Gaps 0;
 Matches 8; Conservative 1; Indels 0; Indels 0; Gaps 0;
 QY 1 AQYEDIAQK 9
 Db 376 AQYEDIAQR 384
 RESULT 6
 ID AAY14568 standard; peptide; 30 AA.
 XX AAY14568;
 AC AAY14568;
 XX 14-SEP-1999 (first entry)
 DT Partial amino acid sequence of D-sequence binding protein.
 DE D-sequence; binding protein; phosphorylation; adeno-associated virus;
 KW AAV; transgene; expression; DNA synthesis; cancer; EMSA; detection;
 KW competitive electrophoretic mobility shift assay.
 XX

OS Synthetic.
 XX WO9911652-A1.
 XX 11-MAR-1999.
 PD 01-SEP-1998; 98WO-US018194.
 PF 02-SEP-1997; 97US-0056052P.
 PR (ADRE-) ADVANCED RES & TECHNOLOGY INST.
 XX Srivastava A, Qing K, Wang X, Ponnazhagan S, Bajpai A;
 PI WPI; 1999-394757/33.
 DR New isolated D sequence binding protein.
 XX Disclosure; Page 23; 163pp; English.
 XX The invention relates to an isolated and purified D sequence binding
 CC protein (D-BP) having a molecular weight of about 53 kD. This peptide
 CC represents a partial amino acid sequence of the complete D-BP. The D-BP
 CC is phosphorylated at tyrosine residues and blocks AAV-mediated transgene
 CC expression in infected cells by inhibiting the leading strand viral DNA
 CC synthesis. Inhibiting the function of D-BP in host cells can increase
 CC expression of selected nucleic acids from an AAV, particularly for
 CC increasing therapeutic nucleic acids for treating a disease such as
 CC cancer
 XX SQ Sequence 30 AA;
 Query Match 88.9%; Score 40; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1-2; Mismatches 0; Gaps 0;
 Matches 8; Conservative 0; Indels 0; Indels 0; Gaps 0;
 QY 1 AQYEDIAQ 8
 Db 17 AQYEDIAQ 24
 RESULT 7
 ID AAM20776 standard; protein; 82 AA.
 XX AAM20776;
 AC AAM20776;
 XX 12-OCT-2001 (first entry)
 DT Peptide #7210 encoded by probe for measuring cervical gene expression.
 DE Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer.
 XX Homo sapiens.
 OS WO200157278-A2.
 XX 09-AUG-2001.
 PD 30-JAN-2001; 2001WO-US000670.
 PF 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 PI

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XX DR WPI; 2001-488901/53.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human cervical epithelial cells.
XX PS Claim 27; SEQ ID NO 25602; 487pp; English.
XX CC The present invention relates to human single exon nucleic acid probes
XX CC (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded
XX CC by one such probe. The SENPs are derived from human Hela cells. The SENPs
XX CC can be used to produce a single exon microarray, which can be used for
XX CC measuring human gene expression in a sample derived from human cervical
XX CC epithelial cells. By measuring gene expression, the probes are therefore
XX CC useful in grading and/or staging of diseases of the cervix, notably
XX CC cervical cancer. Note: The sequence data for this patent did not form
XX CC part of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 82 AA;

Query Match      84.4%; Score 38; DB 4; Length 82;
Best Local Similarity 77.8%; Pred. No. 9.3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQVEDIAQK 9
Db      |||||:
      35 AQVEEIAQR 43

RESULT 8
ABB42330
ID ABB42330 standard; peptide; 82 AA.
XX AC ABB42330;
XX DT 04-FEB-2002 (first entry)
XX DE Peptide #9836 encoded by human foetal liver single exon probe.
XX DE Human; foetal liver; gene expression; single exon nucleic acid probe.
XX KW Homo sapiens.
XX OS Homo sapiens.
XX PN WO200157277-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US0000669.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX WPI; 2001-488901/53.
XX XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX XX gene expression in human foetal liver.
XX PS Claim 27; SEQ ID NO 34965; 639pp + Sequence Listing; English.
XX CC The invention relates to a single exon nucleic acid probe for measuring
XX CC human gene expression in a sample derived from human foetal liver. The
XX CC single exon nucleic acid probes may be used for predicting, measuring and
XX CC displaying gene expression in samples derived from human foetal liver. The
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CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 82 AA;

Query Match      84.4%; Score 38; DB 4; Length 82;
Best Local Similarity 77.8%; Pred. No. 9.3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQVEDIAQK 9
Db      |||||:
      35 AQVEEIAQR 43

RESULT 9
AAM36136
ID AAM36136 standard; protein; 82 AA.
XX AC AAM36136;
XX DT 17-OCT-2001 (first entry)
XX DE Peptide #10173 encoded by probe for measuring placental gene expression.
XX DE Probe; microarray; human; placenta; antenatal diagnosis;
XX KW genetic disorder.
XX OS Homo sapiens.
XX PN WO200157272-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US0000663.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX WPI; 2001-488901/53.
XX XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX XX gene expression in human placenta.
XX PS Claim 27; SEQ ID NO 36405; 654pp; English.
XX CC The present invention relates to single exon nucleic acid probes (SENP:
XX CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
XX CC such probe. The probes are useful for producing a microarray for
XX CC predicting, measuring and displaying gene expression in samples derived
XX CC from human placenta. The probes are useful for antenatal diagnosis of
XX CC human genetic disorders
XX SQ Sequence 82 AA;

Query Match      84.4%; Score 38; DB 4; Length 82;
Best Local Similarity 77.8%; Pred. No. 9.3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQVEDIAQK 9
Db      |||||:
      35 AQVEEIAQR 43
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RESULT 10
ABB25821
ID   ABB25821 standard; protein; 82 AA.
AC   ABB25821;
XX
XX
DT   23-JAN-2002 (first entry)
XX
DE   Protein #7820 encoded by probe for measuring heart cell gene expression.
XX
KW   Human; gene expression; heart; microarray; vascular system;
KW   cardiovascular disease; hypertension; cardiac arrhythmia;
KW   congenital heart disease.
XX
OS   Homo sapiens.
XX
PN   WO200157274-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000666.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR   WPI; 2001-488990/53.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   hearts.
XX
PS   Claim 15; SEQ ID NO 27591; 530pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes for
CC   measuring human gene expression in a sample derived from human heart (see
CC   ABA21535-ABA41303). The present sequence is a protein encoded by one such
CC   probe. The probes may be used for predicting, measuring and displaying
CC   gene expression in samples derived from the human heart via microarrays.
CC   By measuring gene expression, the probes are useful for predicting,
CC   diagnosing, grading, staging, monitoring and prognosing diseases of the
CC   human heart and vascular system e.g. cardiovascular disease,
CC   hypertension, cardiac arrhythmias and congenital heart disease. Note: The
CC   sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 82 AA;

Query Match      84.4%; Score 38; DB 4; Length 82;
Best Local Similarity 77.8%; Pred. No. 9.3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy   1 AQYEDIAQK 9
Db   |||||:
     35 AQYEEIAQR 43

RESULT 11
AAM76029
ID   AAM76029 standard; protein; 82 AA.
AC   AAM76029;
XX
XX
DT   06-NOV-2001 (first entry)
XX
DE   Human brain expressed single exon probe encoded protein SEQ ID NO: 35321.
XX
KW   Human; brain expressed exon; gene expression analysis; probe; microarray;
KW   Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
OS   Homo sapiens.
XX
PN   WO200157275-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000667.
XX
PR   04-FEB-2000; 2000US-0180312P.

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XX
DE   Human bone marrow expressed probe encoded protein SEQ ID NO: 36335.
XX
KW   Human; bone marrow expressed exon; gene expression analysis; probe;
KW   microarray; cancer; leukaemia; lymphoma; myeloma.
XX
OS   Homo sapiens.
XX
PN   WO200157276-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000668.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR   WPI; 2001-488990/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for analyzing
PT   gene expression in human bone marrow.
XX
PS   Example 4; SEQ ID NO 36335; 658pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   bone marrow. They can be used to measure gene expression in bone marrow
CC   samples, which may enable the improved diagnosis and treatment of cancers
CC   such as lymphoma, leukaemia and myeloma. The present sequence is a
CC   protein encoded by one of the probes of the invention
XX
SQ   Sequence 82 AA;

Query Match      84.4%; Score 38; DB 4; Length 82;
Best Local Similarity 77.8%; Pred. No. 9.3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy   1 AQYEDIAQK 9
Db   |||||:
     35 AQYEEIAQR 43

RESULT 12
AAM63216
ID   AAM63216 standard; protein; 82 AA.
XX
AC   AAM63216;
XX
DT   05-NOV-2001 (first entry)
XX
DE   Human brain expressed single exon probe encoded protein SEQ ID NO: 35321.
XX
KW   Human; brain expressed exon; gene expression analysis; probe; microarray;
KW   Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
OS   Homo sapiens.
XX
PN   WO200157275-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000667.
XX
PR   04-FEB-2000; 2000US-0180312P.

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PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX Example 4; SEQ ID NO 35321; 650pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is a protein encoded by one of
XX the probes of the invention
XX
XX SQ Sequence 82 AA;
    Query Match 84.4%; Score 38; DB 4; Length 82;
    Best Local Similarity 77.8%; Pred. No. 9.3;
    Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
    QY 1 AQYEDIAQK 9
    Db 35 AQYEEIAQR 43
    RESULT 13
    ID ABG57755 standard; peptide; 82 AA.
    AC ABG57755;
    DT 25-FEB-2003 (first entry)
    DE Human liver peptide, SEQ ID No 36403.
    KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
    KW hypercholesterolaemia; coronary heart disease.
    XX Homo sapiens.
    OS
    XX
    PN WO200157273-A2.
    XX
    PD 09-AUG-2001.
    XX
    PF 30-JAN-2001; 2001WO-US000664.
    XX
    PR 04-FEB-2000; 2000US-0180312P.
    PR 26-MAY-2000; 2000US-0207456P.
    PR 30-JUN-2000; 2000US-00608408.
    PR 03-AUG-2000; 2000US-00632366.
    PR 21-SEP-2000; 2000US-0234687P.
    PR 27-SEP-2000; 2000US-0236359P.
    PR 04-OCT-2000; 2000GB-00024263.
    XX (MOLE-) MOLECULAR DYNAMICS INC.
    PA Penn SG, Hanzel DK, Chen W, Rank DR;
    XX WPI; 2001-488898/53.
    XX Human genome-derived single exon nucleic acid probes useful for analyzing
    PT
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PT gene expression in human adult liver.
XX Claim 27; SEQ ID NO 36403; 658pp; English.
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX measuring human gene expression in a sample derived from human adult
XX liver, comprising one of 13109 defined nucleotide sequences given in the
XX specification (or complements/ fragments). The probe hybridises at high
XX stringency to a nucleic acid molecule expressed in the human adult liver.
XX (I) may be used for predicting, measuring and displaying gene expression
XX in samples derived from human adult liver. The genes identified may be
XX involved in genetic liver diseases such as cirrhosis,
XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX associated with coronary heart disease. ABG47348-ABG59930 represent human
XX liver single exon encoded peptides of the invention. Note: The sequence
XX information for this patent does not appear in the printed specification
XX but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 82 AA;
    Query Match 84.4%; Score 38; DB 4; Length 82;
    Best Local Similarity 77.8%; Pred. No. 9.3;
    Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
    QY 1 AQYEDIAQK 9
    Db 35 AQYEEIAQR 43
    RESULT 14
    ID ABG45427 standard; peptide; 82 AA.
    AC ABG45427;
    DT 19-AUG-2002 (first entry)
    DE Human peptide encoded by genome-derived single exon probe SEQ ID 35092.
    KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
    KW chronic obstructive pulmonary disease; interstitial lung disease;
    KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
    KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
    KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
    KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
    KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
    KW primary ciliary dyskinesia; pulmonary hypertension;
    KW hyaline membrane disease.
    XX Homo sapiens.
    OS
    XX
    PN WO200186003-A2.
    XX
    PD 15-NOV-2001.
    XX
    PF 30-JAN-2001; 2001WO-US000665.
    XX
    PR 04-FEB-2000; 2000US-0180312P.
    PR 26-MAY-2000; 2000US-0207456P.
    PR 30-JUN-2000; 2000US-00608408.
    PR 03-AUG-2000; 2000US-00632366.
    PR 21-SEP-2000; 2000US-0234687P.
    PR 27-SEP-2000; 2000US-0236359P.
    PR 04-OCT-2000; 2000GB-00024263.
    XX (MOLE-) MOLECULAR DYNAMICS INC.
    PA Penn SG, Hanzel DK, Chen W, Rank DR;
    XX WPI; 2002-114183/15.
    XX Spatially-addressable set of single exon nucleic acid probes, used to
    PT
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PT measure gene expression in human lung samples.
PS Claim 27; SEQ ID NO 35092; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of probes
XX ; the novel set of probes which hybridize at high stringency to a nucleic
XX acid expressed in the human lung; measuring gene expression in a sample
XX derived from human lung, comprising (a) contacting the array with a
XX collection of detectably labeled nucleic acids derived from human lung
XX mRNA, and (b) measuring the label detectably bound to each probe of the
XX array; identifying exons in a eukaryotic genome, comprising (a)
XX algorithmically predicting at least one exon from genomic sequences of
XX the eukaryote; and (b) detecting specific hybridisation of detectably
XX labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
XX having a fragment identical to the predicted exon, the probe is included
XX in the above mentioned microarray; assigning exons to a single gene,
XX comprising (a) identifying exons from genomic sequence by the method
XX above and (b) measuring the expression of each of the exons in several
XX tissues and/or cell types using hybridisation to a single exon
XX microarrays having a probe with the exon, where a common pattern of
XX expression of the exons in the tissues and/or cell types indicates that
XX the exons should be assigned to a single gene; a peptide comprising one
XX of 12011 sequences, mentioned in the specification, or encoded by the
XX probes/open reading frames (ORF). The probes are used for gene expression
XX analysis, and for identifying exons in a gene, particularly using human
XX lung derived mRNA and for the study of lung diseases such as asthma, lung
XX cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
XX disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
XX tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
XX Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
XX histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
XX Karageney syndrome, fibrocystic pulmonary dysplasia, primary ciliary
XX dyskinesia, pulmonary hypertension and hyaline membrane disease. The
XX present sequence is a peptide/protein encoded by a single exon probe of
XX the invention. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIFO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 82 AA;
Query Match 84.4%; Score 38; DB 5; Length 82;
Best Local Similarity 77.8%; Pred. No. 9.3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 AQYEDIAQK 9
Db 35 AQYEEIAQR 43
|||.|.|.|.|
|.|.|.|.|
RESULT 15
ADR98973
ID ADR98973 standard; protein; 268 AA.
XX
XX ADR98973;
XX
XX 18-NOV-2004 (first entry)
XX
XX Lung specific gene splice variant encoded protein #145.
DE
XX
XX cytostatic; gene therapy; vaccine; lung; diagnosis; cancer;
KW non-cancerous lung disease; lung tissue; antagonist; gene therapy;
KW transgenic animal; splice variant.
XX
XX Homo sapiens.
OS
XX
XX WO2004074430-A2.
PN
XX 02-SEP-2004.
XX
XX

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XX
PF 08-DEC-2003; 2003WO-US038896.
XX
XX 06-DEC-2002; 2002US-0431307P.
PR 06-DEC-2002; 2002US-0431510P.
PR 06-DEC-2002; 2002US-0431516P.
XX
PA (DIAD-) DIADEXUS INC.
XX
XX Macina RA, Turner LR, Sun Y, Liu S;
XX
XX WPI; 2004-635553/61.
DR N-PSDB; ADR98818.
XX
XX New isolated human lung specific nucleic acid molecule, useful for
XX identifying, diagnosing, monitoring, staging, imaging and treating lung
XX cancer and non-cancerous diseases of the lung.
XX
XX Claim 1; SEQ ID NO 258; 542pp; English.
XX
XX The invention relates to a new isolated lung specific nucleic acid
XX molecule (I) comprising any of 113 fully defined nucleotide sequences
XX given in the specification, their encoded protein sequences, sequences
XX selectively hybridizing to the nucleotide sequences or a sequence having
XX at least 60% identity to the nucleotide sequences. The methods and
XX compositions of the present invention are useful for identifying,
XX diagnosing, monitoring, staging, imaging and treating lung cancer and non
XX -cancerous diseases of the lung. They are also used for identifying lung
XX tissue, monitoring and identifying and/or designing antagonists of the
XX polypeptide of the invention, gene therapy, production of transgenic
XX animals and production of engineered lung tissue for treatment and
XX research. Lung specific genes (LSGs) were identified by a systematic
XX analysis of gene expression data in the LIFESEQ Gold database using the
XX data mining software package candidate lead automatic search program
XX (CLASP). Genes were grouped into gene bins where each bin is a cluster of
XX sequences grouped together where they share a common contig.
XX Differentially expressed tissue-specific genes were selected based on the
XX percentage level in the targeted tissue versus all the other tissues. The
XX expression levels for each gene in libraries of normal tissues or non-
XX tumour tissues from cancer patients were compared with the expression
XX levels in tissue libraries associated with tumour or disease. This
XX sequence represents a protein of the invention.
XX
SQ Sequence 268 AA;
Query Match 84.4%; Score 38; DB 8; Length 268;
Best Local Similarity 77.8%; Pred. No. 34;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 AQYEDIAQK 9
Db 43 AQYEEIAQR 51
|||.|.|.|.|
|.|.|.|.|
Search completed: July 5, 2006, 19:08:49
Job time : 84.0625 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 20:52:16 ; Search time 47.625 Seconds
(without alignments)
87.537 Million cell updates/sec

Title: US-10-774-928A-2

Perfect score: 45

Sequence: 1 AQVEDIAQK 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	5	US-10-774-928-2
2	41	91.1	524	3	US-09-976-782-88
3	38	84.4	82	3	US-09-864-761-41119
4	38	84.4	327	4	US-10-408-765A-1475
5	38	84.4	521	3	US-09-976-782-10
6	38	84.4	534	3	US-09-976-782-86
7	38	84.4	534	3	US-09-976-782-87
8	38	84.4	534	4	US-10-231-913-86
9	38	84.4	534	4	US-10-231-913-87
10	38	84.4	534	5	US-10-367-057-38
11	38	84.4	564	4	US-10-170-385-421
12	38	84.4	564	5	US-10-723-860-1619
13	38	84.4	564	4	US-10-756-149-5130
14	38	84.4	564	5	US-10-631-467-938
15	38	84.4	564	6	US-11-037-713-27
16	38	84.4	585	5	US-10-821-234-875
17	38	84.4	608	4	US-10-094-749-2446
18	38	84.4	645	3	US-09-919-172-41
19	38	84.4	645	5	US-10-752-986-41
20	37	82.2	9	4	US-10-285-394-33
21	37	82.2	125	5	US-10-450-763-51106
22	37	82.2	181	3	US-09-864-761-35721
23	37	82.2	222	4	US-10-231-913-263
24	37	82.2	267	5	US-10-450-763-38184
25	37	82.2	273	5	US-10-450-763-56735
26	37	82.2	275	5	US-10-450-763-45641
27	37	82.2	279	6	US-11-013-684-21

28 37 82.2 310 6 US-11-156-300-71 Sequence 71, Appl
29 37 82.2 311 6 US-11-156-300-70 Sequence 70, Appl
30 37 82.2 312 3 US-09-976-782-32 Sequence 32, Appl
31 37 82.2 312 4 US-10-080-334-167 Sequence 167, Appl
32 37 82.2 312 4 US-10-080-334-188 Sequence 188, Appl
33 37 82.2 312 4 US-10-080-334-270 Sequence 270, Appl
34 37 82.2 312 4 US-10-231-913-260 Sequence 260, Appl
35 37 82.2 315 4 US-10-231-913-259 Sequence 259, Appl
36 37 82.2 318 4 US-10-231-913-261 Sequence 261, Appl
37 82.2 398 5 US-10-883-020-5 Sequence 5, Appl
38 37 82.2 422 3 US-09-779-307-18 Sequence 18, Appl
39 37 82.2 424 5 US-10-450-763-49620 Sequence 49620, A
40 37 82.2 428 3 US-09-779-307-21 Sequence 21, Appl
41 37 82.2 430 3 US-09-779-307-19 Sequence 19, Appl
42 37 82.2 482 3 US-09-779-307-17 Sequence 17, Appl
43 37 82.2 482 4 US-10-080-334-187 Sequence 187, Appl
44 37 82.2 482 5 US-10-883-020-1 Sequence 1, Appl
45 37 82.2 483 3 US-09-919-497-79 Sequence 79, Appl

ALIGNMENTS

RESULT 1

US-10-774-928-2
; Sequence 2, Application US/10774928
; Publication No. US20040241168A1
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; FILE OF INVENTION: Psoriasis
; FILE REFERENCE: 302178
; CURRENT APPLICATION NUMBER: US/10/774,928
; CURRENT FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Leishmania
US-10-774-928-2

Query Match 100.0%; Score 45; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQVEDIAQK 9
Db 1 AQVEDIAQK 9

RESULT 2

US-09-976-782-88
; Sequence 88, Application US/09976782
; Publication No. US20030190715A1
; GENERAL INFORMATION:
; APPLICANT: Grosse et al
; TITLE OF INVENTION: No. US20030190715A1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-157
; CURRENT APPLICATION NUMBER: US/09/976,782
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,113
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,662
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,732
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,625
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,703
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/241,190
; PRIOR FILING DATE: 2000-10-16

; PRIOR APPLICATION NUMBER: 60/240,637
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,669
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/262,455
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/240,648
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 88
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-976-782-88

Query Match 91.1%; Score 41; DB 3; Length 524;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AQYEDIAQK 9
Db 322 AQYEDIAQK 330
|||||:|

RESULT 3

US-09-864-761-41119
; Sequence 41119, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 41119
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC024196.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.6
; OTHER INFORMATION: EST HUMAN HIT: BE272256.1, EVALUE 5.00e-17
; OTHER INFORMATION: SWISSPROT HIT: P35908, EVALUE 2.00e-24
US-09-864-761-41119

Query Match 84.4%; Score 38; DB 3; Length 82;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AQYEDIAQK 9
Db 35 AQYEDIAQK 43
|||||:

RESULT 4

US-10-408-765A-1475
; Sequence 1475, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1475
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1475

Query Match 84.4%; Score 38; DB 4; Length 327;
Best Local Similarity 77.8%; Pred. No. 51;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AQYEDIAQK 9
Db 120 AQYEDIAQK 128
|||||:

RESULT 5

US-09-976-782-10
; Sequence 10, Application US/09976782
; Publication No. US20030190715A1
; GENERAL INFORMATION:
; APPLICANT: Grosse et al
; TITLE OF INVENTION: No. US20030190715A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-157

; CURRENT APPLICATION NUMBER: US/09/976,782
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,113
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,662
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,732
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,625
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,703
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/241,190
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,637
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,669
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/262,455
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/240,648
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-976-782-10

Query Match 84.4%; Score 38; DB 3; Length 521;
Best Local Similarity 77.8%; Pred. No. 83;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQVEDIAQK 9
Db 314 AQVEEIAQR 322

RESULT 6

US-09-976-782-86
; Sequence 86, Application US/09976782
; Publication No. US20030190715A1
; GENERAL INFORMATION:
; APPLICANT: Grosse et al

; TITLE OF INVENTION: No. US20030190715A1e1 Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-157
; CURRENT APPLICATION NUMBER: US/09/976,782
; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,113
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,662
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,732
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,625
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,703
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/241,190
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,637
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,669
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/262,455
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/240,648
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 534

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-976-782-86

Query Match 84.4%; Score 38; DB 3; Length 534;
Best Local Similarity 77.8%; Pred. No. 85;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQVEDIAQK 9
Db 327 AQVEEIAQR 335

RESULT 7

US-09-976-782-87
; Sequence 87, Application US/09976782
; Publication No. US20030190715A1
; GENERAL INFORMATION:
; APPLICANT: Grosse et al

; TITLE OF INVENTION: No. US20030190715A1e1 Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-157
; CURRENT APPLICATION NUMBER: US/09/976,782
; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,113
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,662
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,732
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,625
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,703
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/241,190
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,637
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,669
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/262,455
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/240,648
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-976-782-87

Query Match 84.4%; Score 38; DB 3; Length 534;
Best Local Similarity 77.8%; Pred. No. 85;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQVEDIAQK 9
Db 327 AQVEEIAQR 335

RESULT 8

US-10-231-913-86
; Sequence 86, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.

; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.

```
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schalomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Coleman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-913-86

Query Match      84.4%; Score 38; DB 4; Length 534;
Best Local Similarity 77.8%; Pred. No. 85;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 AQYEDIAQK 9
Db      327 AQYEEIAQR 335

RESULT 9
US-10-231-913-87
; Sequence 87, Application US/10231913
; Publication No. US2004000576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schalomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A.
```

```
; APPLICANT: Boldog, Ference L.
; APPLICANT: Coleman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-913-87

Query Match      84.4%; Score 38; DB 4; Length 534;
Best Local Similarity 77.8%; Pred. No. 85;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 AQYEDIAQK 9
Db      327 AQYEEIAQR 335

RESULT 10
US-10-367-057-38
; Sequence 38, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; FILE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 38
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-38

Query Match      84.4%; Score 38; DB 5; Length 534;
Best Local Similarity 77.8%; Pred. No. 85;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 AQYEDIAQK 9
Db      327 AQYEEIAQR 335
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Db 327 AQYEETIAQR 335

RESULT 11
US-10-170-385-421
; Sequence 421, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 421
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-421

Query Match 84.4%; Score 38; DB 4; Length 564;
Best Local Similarity 77.8%; Pred. No. 90;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQVEDIAQK 9
|||||:
Db 339 AQYEETIAQR 347

RESULT 12
US-10-723-860-1619
; Sequence 1619, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882_0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1619
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-1619

Query Match 84.4%; Score 38; DB 5; Length 564;
Best Local Similarity 77.8%; Pred. No. 90;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQVEDIAQK 9
|||||:
Db 339 AQYEETIAQR 347

RESULT 13

US-10-756-149-5130
; Sequence 5130, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5130
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-5130

Query Match 84.4%; Score 38; DB 5; Length 564;
Best Local Similarity 77.8%; Pred. No. 90;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQVEDIAQK 9
|||||:
Db 339 AQYEETIAQR 347

RESULT 14

US-10-631-467-938
; Sequence 938, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive p
; TITLE OF INVENTION: disease
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 938
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-938

Query Match 84.4%; Score 38; DB 5; Length 564;
Best Local Similarity 77.8%; Pred. No. 90;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQVEDIAQK 9
|||||:
Db 339 AQYEETIAQR 347

RESULT 15

US-11-037-713-27
; Sequence 27, Application US/11037713
; Publication No. US20050221398A1
; GENERAL INFORMATION:
; APPLICANT: JACQUEMIER, JOCELYNE
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: DEBONO, STEPHANE
; APPLICANT: TAGETT, REBECCA

```

; TITLE OF INVENTION: PROTEIN EXPRESSION PROFILING AND BREAST CANCER
; TITLE OF INVENTION: PROGNOSIS
; FILE REFERENCE: 1016-R-04 (B)
; CURRENT APPLICATION NUMBER: US/11/037,713
; CURRENT FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: 60/537,412
; PRIOR FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 27
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-713-27

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Query Match      84.4%; Score 38; DB 6; Length 564;
Best Local Similarity 77.8%; Pred. No. 90;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY      1 AQYEDIAQK 9
Db      339 AQYEEIAQR 347

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Search completed: July 5, 2006, 20:57:18
Job time : 47.625 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 5, 2006, 20:53:13 ; Search time 4.125 Seconds
(without alignments)
58.543 Million cell updates/sec

Title: US-10-774-928A-2

Perfect score: 45

Sequence: 1 AQVEDIAQK 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 112942

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New.*

- 1: /EMC_Celerra_SID33/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 2: /EMC_Celerra_SID33/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC_Celerra_SID33/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC_Celerra_SID33/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC_Celerra_SID33/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 6: /EMC_Celerra_SID33/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Celerra_SID33/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SID33/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	37	82.2	483	7	US-11-251-208-284
2	35	77.8	655	6	US-10-449-902-51488
3	35	77.8	656	6	US-10-449-902-53558
4	33	73.3	915	6	US-10-449-902-45529
5	32	71.1	430	7	US-11-105-233-181
6	32	71.1	450	7	US-11-293-697-4090
7	32	71.1	514	7	US-11-251-208-284
8	31	68.9	175	6	US-10-953-349-4732
9	31	68.9	195	6	US-10-953-349-4731
10	31	68.9	195	6	US-10-566-644-36
11	31	68.9	195	7	US-11-251-208-345
12	31	68.9	196	6	US-10-566-644-8
13	31	68.9	196	6	US-10-566-644-16
14	31	68.9	196	7	US-11-251-208-304
15	31	68.9	196	7	US-11-251-208-407
16	31	68.9	197	6	US-10-566-644-66
17	31	68.9	197	6	US-10-566-644-294
18	31	68.9	565	6	US-10-471-571A-1676
19	31	68.9	3113	6	US-10-505-928-325
20	30	66.7	103	6	US-10-953-349-26513
21	30	66.7	175	6	US-10-953-349-1173
22	30	66.7	196	6	US-10-953-349-1172
23	30	66.7	196	6	US-10-566-644-136
24	30	66.7	197	6	US-10-566-644-20
25	30	66.7	197	6	US-10-566-644-22

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26 30 66.7 197 7 US-11-251-208-417 Sequence 417, App
27 30 66.7 197 7 US-11-251-208-431 Sequence 431, App
28 30 66.7 198 6 US-10-566-644-62 Sequence 62, Appl
29 30 66.7 220 6 US-10-449-902-32059 Sequence 32059, A
30 30 66.7 220 6 US-10-449-902-47373 Sequence 47373, A
31 30 66.7 220 6 US-10-449-902-56490 Sequence 56490, A
32 30 66.7 275 6 US-10-449-902-48344 Sequence 48344, A
33 30 66.7 282 6 US-10-953-349-21448 Sequence 21448, A
34 30 66.7 329 6 US-10-471-571A-4880 Sequence 4880, Ap
35 30 66.7 394 6 US-10-449-902-35309 Sequence 35309, A
36 30 66.7 490 7 US-11-293-697-4335 Sequence 4335, Ap
37 29 64.4 130 6 US-10-953-349-525 Sequence 525, App
38 29 64.4 143 6 US-10-449-902-53316 Sequence 53316, A
39 29 64.4 290 6 US-10-449-902-54864 Sequence 54864, A
40 29 64.4 469 6 US-10-505-928-457 Sequence 457, App
41 29 64.4 550 6 US-10-449-902-29669 Sequence 29669, A
42 29 64.4 574 6 US-10-449-902-52042 Sequence 52042, A
43 29 64.4 591 6 US-10-449-902-53151 Sequence 53151, A
44 29 64.4 601 7 US-11-293-697-3847 Sequence 3847, Ap
45 29 64.4 603 6 US-10-471-571A-3718 Sequence 3718, Ap

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ALIGNMENTS

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RESULT 1
US-11-105-233-180
; Sequence 180, Application US/11105233
; Publication No. US20060134653A1
; GENERAL INFORMATION:
; APPLICANT: Thiagalingam et al
; TITLE OF INVENTION: Differential Expression of Genes in MSI
; FILE OF INVENTION: Tumors
; FILE REFERENCE: 1657/2001
; CURRENT APPLICATION NUMBER: US/11/105,233
; CURRENT FILING DATE: 2005-04-13
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 180
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-233-180

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Query Match      82.2%; Score 37; DB 7; Length 483;
Best Local Similarity 77.8%; Pred. No. 4.3;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 AQVEDIAQK 9
Db 265 AQVEDIANR 273

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RESULT 2

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US-10-449-902-51488
; Sequence 51488, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51488

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; LENGTH: 655
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-51488

Query Match      77.8%; Score 35; DB 6; Length 655;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 AQYEDIAQK 9
Db 171 AQNEDVAQK 179

RESULT 3
US-10-449-902-53558
; Sequence 53558, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53558
; LENGTH: 656
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-53558

Query Match      77.8%; Score 35; DB 6; Length 656;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 AQYEDIAQK 9
Db 172 AQNEDVAQK 180

RESULT 4
US-10-449-902-45529
; Sequence 45529, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45529
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-45529

Query Match      73.3%; Score 33; DB 6; Length 915;
Best Local Similarity 66.7%; Pred. No. 55;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDIAQK 9
Db 898 SQYEDIYQR 906

RESULT 5
US-11-105-233-181
; Sequence 181, Application US/11105233
; Publication No. US20060134653A1
; GENERAL INFORMATION:
; APPLICANT: Thiagalingam et al
; TITLE OF INVENTION: Differential Expression of Genes in MSI
; FILE REFERENCE: 1657/2001
; CURRENT APPLICATION NUMBER: US/11/105,233
; CURRENT FILING DATE: 2005-04-13
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 181
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-233-181

Query Match      71.1%; Score 32; DB 7; Length 430;
Best Local Similarity 55.6%; Pred. No. 40;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQYEDIAQK 9
Db 254 AQYDELARK 262

RESULT 6
US-11-293-697-4090
; Sequence 4090, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4090
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4090

Query Match      71.1%; Score 32; DB 7; Length 450;
Best Local Similarity 77.8%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AQYEDIAQK 9
Db 259 AQYETIAAK 267

RESULT 7
US-11-251-208-284
; Sequence 284, Application US/11251208
; Publication No. US20060137043A1
; GENERAL INFORMATION:
; APPLICANT: Puzio, Piotr
; APPLICANT: Chardonnens, Agnes
```


; APPLICANT: McKersie, Bryan
; APPLICANT: Chen, Ruoying
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING PROTEINS ASSOCIATED WITH ABIOTIC
; TITLE OF INVENTION: STRESS RESPONSE AND PLANT CELLS AND PLANTS WITH INCREASED
; TITLE OF INVENTION: TOLERANCE TO ENVIRONMENTAL STRESS
; FILE REFERENCE: 13311-00015-US
; CURRENT APPLICATION NUMBER: US/11/251,208
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: PCT/US2004/011888
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: EP 03008080.8
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: EP 03009728.1
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: EP 03016672.2
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: EP 03022225.1
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 345
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Brassica napus
US-11-251-208-345

Query Match 68.9%; Score 31; DB 7; Length 195;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDIAQK 9
| | | | | : |
Db 91 ASYENIAKK 99

RESULT 12
US-10-566-644-8
; Sequence 8, Application US/10566644
; Publication No. US20060137042A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Puzio, Piotr
; APPLICANT: Blau, Astrid
; APPLICANT: Looser, Ralf
; APPLICANT: Wendel, Birgit
; APPLICANT: Kamlage, Beate
; APPLICANT: Chardonnens, Agnes
; APPLICANT: Shirley, Amber
; APPLICANT: Wang, Xi-Qing
; APPLICANT: Sarría-Millan, Rodrigo
; APPLICANT: McKersie, Bryan
; APPLICANT: Chen, Ruoying
; TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF FINE CHEMICALS
; FILE REFERENCE: 12810-00197-US
; CURRENT APPLICATION NUMBER: US/10/566,644
; CURRENT FILING DATE: 2006-01-31
; PRIOR APPLICATION NUMBER: EP 03016672.2
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/US2004/11887
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 400
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Brassica napus
US-10-566-644-8

Query Match 68.9%; Score 31; DB 6; Length 196;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDIAQK 9

Db 91 ASYENIAKK 99
| | | | | : |
RESULT 13
US-10-566-644-16
; Sequence 16, Application US/10566644
; Publication No. US20060137042A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Puzio, Piotr
; APPLICANT: Blau, Astrid
; APPLICANT: Looser, Ralf
; APPLICANT: Wendel, Birgit
; APPLICANT: Kamlage, Beate
; APPLICANT: Chardonnens, Agnes
; APPLICANT: Shirley, Amber
; APPLICANT: Wang, Xi-Qing
; APPLICANT: Sarría-Millan, Rodrigo
; APPLICANT: McKersie, Bryan
; APPLICANT: Chen, Ruoying
; TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF FINE CHEMICALS
; FILE REFERENCE: 12810-00197-US
; CURRENT APPLICATION NUMBER: US/10/566,644
; CURRENT FILING DATE: 2006-01-31
; PRIOR APPLICATION NUMBER: EP 03016672.2
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/US2004/11887
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 400
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Glycine max
US-10-566-644-16

Query Match 68.9%; Score 31; DB 6; Length 196;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDIAQK 9
| | | | | : |
Db 91 ASYENIAKK 99

RESULT 14
US-11-251-208-304
; Sequence 304, Application US/11251208
; Publication No. US20060137043A1
; GENERAL INFORMATION:
; APPLICANT: Puzio, Piotr
; APPLICANT: Chardonnens, Agnes
; APPLICANT: Shirley, Amber
; APPLICANT: Wang, Xi-Qing
; APPLICANT: Sarría-Millan, Rodrigo
; APPLICANT: McKersie, Bryan
; APPLICANT: Chen, Ruoying
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING PROTEINS ASSOCIATED WITH ABIOTIC
; TITLE OF INVENTION: STRESS RESPONSE AND PLANT CELLS AND PLANTS WITH INCREASED
; TITLE OF INVENTION: TOLERANCE TO ENVIRONMENTAL STRESS
; FILE REFERENCE: 13311-00015-US
; CURRENT APPLICATION NUMBER: US/11/251,208
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: PCT/US2004/011888
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: EP 03008080.8
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: EP 03009728.1
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: EP 03016672.2
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: EP 03022225.1

; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 304
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Brassica napus
US-11-251-208-304

Query Match 68.9%; Score 31; DB 7; Length 196;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 AQYEDIAQK 9
Db 91 ASYENIAKK 99

RESULT 15
US-11-251-208-407
; Sequence 407, Application US/11251208
; Publication No. US20060137043A1
; GENERAL INFORMATION:
; APPLICANT: Puzio, Piotr
; APPLICANT: Chardonens, Agnes
; APPLICANT: Shirley, Amber
; APPLICANT: Wang, Xi-Qing
; APPLICANT: Sarria-Millan, Rodrigo
; APPLICANT: Mckersie, Bryan
; APPLICANT: Chen, Ruyong
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING PROTEINS ASSOCIATED WITH ABIOTIC
; TITLE OF INVENTION: STRESS RESPONSE AND PLANT CELLS AND PLANTS WITH INCREASED
; TITLE OF INVENTION: TOLERANCE TO ENVIRONMENTAL STRESS
; FILE REFERENCE: 13311-00015-US
; CURRENT APPLICATION NUMBER: US/11/251,208
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: PCT/US2004/011888
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: EP 03008080.8
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: EP 03009728.1
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: EP 03016672.2
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: EP 03022225.1
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 407
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Glycine max
US-11-251-208-407

Query Match 68.9%; Score 31; DB 7; Length 196;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 AQYEDIAQK 9
Db 91 ASYENIAKK 99

Search completed: July 5, 2006, 20:57:47
Job time : 5.125 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 19:24:38 ; Search time 15.9375 Seconds
(without alignments)
49.429 Million cell updates/sec

Title: US-10-774-928A-2

Perfect score: 45

Sequence: 1 AQVEDIAQK 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SID33/ptodata/2/iaa/5_COMB.pep.*
- 2: /EMC_Celerra_SID33/ptodata/2/iaa/6_COMB.pep.*
- 3: /EMC_Celerra_SID33/ptodata/2/iaa/7_COMB.pep.*
- 4: /EMC_Celerra_SID33/ptodata/2/iaa/H_COMB.pep.*
- 5: /EMC_Celerra_SID33/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /EMC_Celerra_SID33/ptodata/2/iaa/RE_COMB.pep.*
- 7: /EMC_Celerra_SID33/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	2	US-09-809-003A-2
2	45	100.0	637	2	US-09-949-016-8152
3	38	84.4	384	2	US-09-949-016-11034
4	38	84.4	564	2	US-09-949-016-6628
5	38	84.4	569	2	US-09-949-016-11035
6	38	84.4	569	2	US-09-949-016-11036
7	38	84.4	608	2	US-10-094-749-2446
8	38	84.4	645	2	US-09-919-172-41
9	37	82.2	482	2	US-09-538-092-858
10	37	82.2	483	2	US-09-919-497-79
11	37	82.2	502	2	US-09-949-016-11033
12	37	82.2	551	1	US-09-067-351-2
13	37	82.2	551	2	US-09-360-490-2
14	36	80.0	233	2	US-10-163-214-10
15	36	80.0	443	2	US-09-949-016-10582
16	36	80.0	643	2	US-09-538-092-844
17	36	80.0	914	2	US-10-163-214-12
18	35	77.8	8	2	US-09-809-003A-10
19	35	77.8	9	2	US-09-809-003A-4
20	35	77.8	315	2	US-09-543-681A-6875
21	34	75.6	398	2	US-10-104-047-3388
22	34	75.6	564	2	US-09-252-991A-24049
23	33	73.3	110	2	US-09-205-258-811
24	33	73.3	110	2	US-10-004-860-811
25	33	73.3	283	2	US-09-252-991A-21171
26	33	73.3	411	2	US-09-205-258-815

27	33	73.3	411	2	US-10-004-860-815	Sequence 815, App
28	33	73.3	471	2	US-09-949-016-10880	Sequence 10880, A
29	33	73.3	493	2	US-09-949-016-6203	Sequence 6203, Ap
30	33	73.3	528	2	US-09-949-016-9678	Sequence 9678, Ap
31	33	73.3	566	2	US-09-328-352-4809	Sequence 4809, Ap
32	33	73.3	567	2	US-10-104-047-3772	Sequence 3772, Ap
33	33	73.3	591	2	US-09-543-681A-5171	Sequence 5171, Ap
34	33	73.3	596	2	US-09-489-039A-9470	Sequence 9470, Ap
35	33	73.3	730	2	US-09-949-016-11573	Sequence 11573, A
36	33	73.3	915	2	US-10-163-214-6	Sequence 6, Appli
37	32	71.1	114	2	US-09-902-540-13061	Sequence 13061, A
38	32	71.1	232	2	US-09-919-497-78	Sequence 78, Appl
39	32	71.1	315	2	US-09-248-796A-14850	Sequence 14850, A
40	32	71.1	430	2	US-09-919-039-105	Sequence 105, App
41	32	71.1	447	2	US-09-949-016-11032	Sequence 11032, A
42	32	71.1	469	2	US-09-538-092-948	Sequence 948, App
43	32	71.1	496	2	US-09-949-016-11133	Sequence 11133, A
44	32	71.1	514	2	US-09-538-092-495	Sequence 495, App
45	32	71.1	613	2	US-09-328-352-5116	Sequence 5116, Ap

ALIGNMENTS

RESULT 1

US-09-809-003A-2
; Sequence 2, Application US/09809003A
; Patent No. 6673351
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission of Psoriasis
; FILE REFERENCE: 302178
; CURRENT APPLICATION NUMBER: US/09/809,003A
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Leishmania
US-09-809-003A-2

Query Match 100.0%; Score 45; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQVEDIAQK 9
Db 1 AQVEDIAQK 9

RESULT 2

US-09-949-016-8152
; Sequence 8152, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8152
; LENGTH: 637

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; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8152

Query Match      100.0%; Score 45; DB 2; Length 637;
Best Local Similarity 100.0%; Pred. No. 0.61; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 AQYEDIAQK 9
Db 356 AQYEDIAQK 364

RESULT 3
US-09-949-016-11034
; Sequence 11034, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11034
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11034

Query Match      84.4%; Score 38; DB 2; Length 384;
Best Local Similarity 77.8%; Pred. No. 9.3; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 0;

Qy 1 AQYEDIAQK 9
Db 362 AQYEEIAQR 370

RESULT 4
US-09-949-016-6628
; Sequence 6628, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6628
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6628

Query Match      84.4%; Score 38; DB 2; Length 564;
Best Local Similarity 77.8%; Pred. No. 14; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 0;

Qy 1 AQYEDIAQK 9
Db 339 AQYEEIAQR 347

RESULT 5
US-09-949-016-11035
; Sequence 11035, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11035
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11035

Query Match      84.4%; Score 38; DB 2; Length 569;
Best Local Similarity 77.8%; Pred. No. 14; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 0;

Qy 1 AQYEDIAQK 9
Db 344 AQYEEIAQR 352

RESULT 6
US-09-949-016-11036
; Sequence 11036, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11036
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11036

Query Match      84.4%; Score 38; DB 2; Length 569;
Best Local Similarity 77.8%; Pred. No. 14; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 0;

Qy 1 AQYEDIAQK 9
Db 344 AQYEEIAQR 352

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Db 344 AQYEIAQR 352

RESULT 7
US-10-094-749-2446
; Sequence 2446, Application US/10094749
; Patent No. 6979557
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KELLICH
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2446
; LENGTH: 608
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2446

Query Match 84.4%; Score 38; DB 2; Length 608;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQYEDIAQK 9
Db 401 AQYEIAQR 409

RESULT 8
US-09-919-172-41
; Sequence 41, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 41
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 1798379CD1

US-09-919-172-41
Query Match 84.4%; Score 38; DB 2; Length 645;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQYEDIAQK 9
Db 360 AQYEIAQR 368

RESULT 9
US-09-538-092-858
; Sequence 858, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurPatSeqFormatter Version 0.9
; SEQ ID NO 858
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P05787
US-09-538-092-858

Query Match 82.2%; Score 37; DB 2; Length 482;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDIAQK 9
Db 264 AQYEDIAQR 272

RESULT 10
US-09-919-497-79
; Sequence 79, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: US-09-919-497-79

US-09-919-497-79
Query Match 82.2%; Score 37; DB 2; Length 483;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDIAQK 9
Db 264 AQYEDIAQR 272
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Db      265 AQYEDIANR 273

RESULT 11
US-09-949-016-11033
; Sequence 11033, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11033
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11033

Query Match      82.2%; Score 37; DB 2; Length 502;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AQYEDIAQK 9
Db      284 AQYEDIANR 292

RESULT 12
US-09-067-351-2
; Sequence 2, Application US/09067351
; Patent No. 5994081
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN KERATINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/360,490
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/067,351
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0511 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 551 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KERANOT02
; CLONE: 2029060
US-09-360-490-2

Query Match      82.2%; Score 37; DB 2; Length 551;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AQYEDIAQK 9
Db      325 AQYEDIANR 333

RESULT 13
US-09-360-490-2
; Sequence 2, Application US/09360490
; Patent No. 6221843
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN KERATINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/360,490
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/067,351
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0511 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 551 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KERANOT02
; CLONE: 2029060
US-09-360-490-2

Query Match      82.2%; Score 37; DB 2; Length 551;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AQYEDIAQK 9
Db      325 AQYEDIANR 333
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RESULT 14
US-10-163-214-10
; Sequence 10, Application US/10163214
; Patent No. 6849781
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Broglie, Karen B.
; APPLICANT: Butler, Karlene H.
; APPLICANT: Thorpe, Catherine J.
; TITLE OF INVENTION: Starch Synthase Isoform V
; FILE REFERENCE: BB1520 US NA
; CURRENT APPLICATION NUMBER: US/10/163,214
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/297,099
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 10
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-163-214-10

Query Match 80.0%; Score 36; DB 2; Length 293;
Best Local Similarity 77.8%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDIAQK 9
Db 276 SQYEDIYQK 284

RESULT 15
US-09-949-016-10582
; Sequence 10582, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10582
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10582

Query Match 80.0%; Score 36; DB 2; Length 443;
Best Local Similarity 77.8%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDIAQK 9
Db 225 AQYEDIAQK 233

Search completed: July 5, 2006, 19:26:42
Job time : 15.9375 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 19:20:41 ; Search time 14.6667 Seconds
(without alignments)
104.964 Million cell updates/sec

Title: US-10-774-928A-3

Perfect score: 87

Sequence: 1 EIFTYHNLEGGQEDF 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:**

1: Pirl:**

2: Pirl:**

3: Pirl:**

4: Pirl:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	622	2 I37984	keratin 9, type I,
2	46	52.9	483	2 A55033	keratin 12 - mouse
3	45.5	52.3	400	1 KRHU9	keratin 19, type I
4	45	51.7	399	2 A25470	cytokeatin 19 - b
5	45	51.7	419	2 A25438	keratin, type I cy
6	45	51.7	450	2 I50484	vimentin beta - go
7	45	51.7	3678	2 S28316	dystrophin - mouse
8	44.5	51.1	423	2 I59463	keratin, type I, c
9	44.5	51.1	430	2 S05481	keratin 18, type I
10	44	50.6	105	2 S55691	keratin type I (cl
11	44	50.6	368	2 A28925	keratin, type I no
12	44	50.6	728	2 A54603	transcription fact
13	44	50.6	834	2 A97178	probable perase
14	43	49.4	135	2 PNO494	NAD ADP-ribosyltra
15	43	49.4	304	2 I50721	synenin - chicken
16	43	49.4	526	1 KRBOVI	keratin, 54K type
17	43	49.4	561	2 A31994	keratin 10, type I
18	43	49.4	569	1 KRMSE1	keratin, 59K type
19	43	49.4	570	2 S07330	keratin, epidermal
20	43	49.4	593	1 KRHU0	keratin 10, type I
21	43	49.4	911	2 JC6016	chitin synthase (E
22	43	49.4	916	2 JC2315	chitin synthase (E
23	43	49.4	1011	1 JH0581	NAD ADP-ribosyltra
24	43	49.4	1028	2 I51173	myosin I beta - bu
25	42	48.3	209	2 T17294	hypothetical prote
26	42	48.3	222	2 G86168	hypothetical prote
27	42	48.3	327	2 S04511	keratin 3, type I,
28	42	48.3	411	2 S45318	keratin 12 - rabbi
29	42	48.3	429	2 A25145	keratin, 47K type

30 42 48.3 436 1 A70409
31 42 48.3 486 1 KRXL
32 42 48.3 566 2 S42257
33 42 48.3 566 2 T20390
34 42 48.3 3263 2 E82410
35 41.5 47.7 520 2 JS0291
36 41 47.1 175 2 C97138
37 41 47.1 256 2 A95887
38 41 47.1 257 2 I38025
39 41 47.1 264 2 H64086
40 41 47.1 335 2 G96607
41 41 47.1 346 2 S34165
42 41 47.1 394 2 B82931
43 41 47.1 401 2 E70646
44 41 47.1 403 2 JQ0028
45 41 47.1 480 2 A56694

ALIGNMENTS

RESULT 1

I37984

keratin 9, type I, cytoskeletal - human

N;Alternate names: cytokeatin 9; scatter protein 60K chain, placental

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text change 09-Jul-2004

C;Accession: I37984; S40307; S77921; S41161; B35494; I37943

R;Reis, A.; Hennies, H.C.; Langbein, L.; Digweed, M.; Mischke, D.; Drechsler, M.; Schroe

Nature Genet. 6, 174-179, 1994

A;Title: Keratin 9 gene mutations in epidermolytic palmoplantar keratoderma (EPPK).

A;Reference number: I37984; MUID:94214498; PMID:7512862

A;Accession: I37984

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-622 <RES>

A;Cross-references: UNIPROT:P35527; UNIPARC:UPI000012DAE1; EMBL:X75015; NID:g453154; PIDN

R;Langbein, L.; Heid, H.W.; Moll, I.; Franke, W.W.

Differentiation 55, 57-71, 1993

A;Title: Molecular characterization of the body site-specific human epidermal cytokeatin

A;Reference number: I37943; MUID:94131202; PMID:7507869

A;Accession: S40307

A;Molecule type: mRNA

A;Residues: 1-622 <LAN>

A;Cross-references: UNIPARC:UPI000012DAE1; EMBL:Z29074; NID:g435475; PIDN:CAA82315.1; PI

A;Accession: S77921

A;Molecule type: protein

A;Residues: 29-53;62-104;167-188;199-233;241-249;295-362;374-430;450-480;579-604 <LAF>

A;Cross-references: UNIPARC:UPI00001774A9; UNIPARC:UPI00001774AB; UNIPARC:UPI00001774AC;

4B0; UNIPARC:UPI00001774B1

R;Langbein, L.

submitted to the EMBL Data Library, December 1993

A;Reference number: S41161

A;Accession: S41161

A;Molecule type: mRNA

A;Residues: 1-11,'SB',13-622 <LAW>

A;Cross-references: UNIPARC:UPI000016ABA2; EMBL:Z29074; NID:g435475; PIDN:CAA82315.1; PI

R;Rosen, E.M.; Meromsky, L.; Romero, R.; Setter, E.; Goldberg, I.

Biochem. Biophys. Res. Commun. 168, 1082-1088, 1990

A;Title: Human placenta contains an epithelial scatter protein.

A;Reference number: A35494; MUID:90267446; PMID:2140676

A;Accession: B35494

A;Molecule type: protein

A;Residues: 'X',450-465 <ROS>

A;Cross-references: UNIPARC:UPI00001774E2

C;Genetics:

A;Gene: GDB:KRT9; EPPK

A;Cross-references: GDB:303970; OMIM:144200

A;Map position: 17q12-17q21

A;Introns: 213/3; 241/2; 293/3; 347/3; 389/3; 464/2

A;Note: Defects in this gene may cause epidermolytic palmoplantar keratoderma

C;Superfamily: cytoskeletal keratin

C;Keywords: coiled coil; intermediate filament

F:1-153/Domain: head #status predicted <HEA>
 F:154-459/Domain: helical rod #status predicted <ROD>
 F:460-622/Domain: tail #status predicted <TAI>

Query Match 100.0%; Score 87; DB 2; Length 622;
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIETHNLLGGQEDF 16
 |||||
 DB 449 EIETHNLLGGQEDF 464

RESULT 2
 AS5033
 keratin 12 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 18-Nov-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: A55033
 R:Lin, C.Y.; Zhu, G.; Converse, R.; Kao, C.W.C.; Nakamura, H.; Tseng, S.C.G.; Mui, M.M.; J. Biol. Chem. 269, 24627-24636, 1994
 A:Title: Characterization and chromosomal localization of the cornea-specific murine keratin 12
 A:Reference number: A55033; MUID:95014223; PMID:7523376
 A:Accession: A55033
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-483 <LIU>
 A:Cross-references: UNIPROT:Q64291; UNIPARC:UPI00002996F; GB:U08095; NID:G565659; PIDN: A:Cross-references: UNIPROT:Q64291; UNIPARC:UPI00002996F; GB:U08095; NID:G565659; PIDN: A:Note: authors translated the codon ATC for residue 225 as Thr, and GCG for residue 388
 C:Superfamily: cytoskeletal keratin

Query Match 52.9%; Score 46; DB 2; Length 483;
 Best Local Similarity 64.3%; Pred. No. 8.2;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIETHNLLGGQEE 14
 |||||
 DB 418 EIETHNLLGGQSD 431

RESULT 3
 KRH09
 keratin 19, type I, cytoskeletal - human
 N:Alternate names: cytokeratin 19
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1991 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
 C:Accession: A31370; A61556; A60779; S00658; S60152
 R:Eckert, R.L.
 Proc. Natl. Acad. Sci. U.S.A. 85, 1114-1118, 1988
 A:Title: Sequence of the human 40-kDa keratin reveals an unusual structure with very high content of proline
 A:Reference number: A31370; MUID:88124966; PMID:2448790
 A:Accession: A31370
 A:Molecule type: mRNA
 A:Residues: 1-400 <ECK>
 A:Cross-references: UNIPROT:Q96A53; UNIPARC:UPI0000071F08; GB:J03607; NID:G184658; PIDN: R:Bader, B.L.; Jahn, L.; Franke, W.W.
 Eur. J. Cell Biol. 47, 306-319, 1988
 A:Title: Low level expression of cytokeratins 8, 18 and 19 in vascular smooth muscle cells containing the cytokeratin 19 gene.
 A:Reference number: A61556; MUID:89210901; PMID:2468493
 A:Accession: A61556
 A:Molecule type: mRNA
 A:Residues: 1-400 <BAD>
 A:Cross-references: UNIPARC:UPI0000071F08
 R:Stasiak, P.C.; Purkis, P.E.; Leigh, I.M.; Lane, E.B.
 J. Invest. Dermatol. 92, 707-716, 1989
 A:Title: Keratin 19: predicted amino acid sequence and broad tissue distribution suggest a role in cell-cell interactions
 A:Reference number: A60779; MUID:89235250; PMID:2469734
 A:Accession: A60779
 A:Molecule type: mRNA
 A:Residues: 1-349, 'A', 351-400 <STA>
 A:Cross-references: UNIPARC:UPI000012DAE; EMBL:Y00503; NID:G34038; PIDN:CAA68556.1; PID R:Stasiak, P.C.; Lane, E.B.

Nucleic Acids Res. 15, 10058, 1987
 A:Title: Sequence of cDNA coding for human keratin 19.
 A:Reference number: S00658; MUID:88096504; PMID:2447559
 A:Accession: S00658
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-75, 'H', 78-341, 'Y', 343-349, 'A', 351-400 <ST2>
 A:Cross-references: UNIPARC:UPI0000173D4D; EMBL:Y00503
 A:Note: this sequence has been revised
 R:Peterson, G.; Song, D.; Huegle-Doerr, B.; Oldenburg, I.; Bautz, E.K.F.
 Mol. Gen. Genet. 249, 425-431, 1995
 A:Title: Mapping of linear epitopes recognized by monoclonal antibodies with gene-fragment
 A:Reference number: S60151; MUID:96133682; PMID:8552047
 A:Accession: S60152
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 331-349, 'A', 351-380 <PET>
 A:Cross-references: UNIPARC:UPI0000173D4E
 C:Comment: Keratin 19 is the smallest human keratin, as the non-alpha-helical tail preser

C:Genetics: GDB:KRT19
 A:Gene: GDB:KRT19
 A:Cross-references: GDB:120131; OMIM:148020
 A:Map position: 17q21-17q23
 C:Superfamily: cytoskeletal keratin
 C:Keywords: coiled coil; intermediate filament
 F:1-73/Domain: head <HEA>
 F:74-386/Domain: helical rod #status predicted <ROD>
 F:387-399/Domain: tail <TAI>

Query Match 52.3%; Score 45.5; DB 1; Length 400;
 Best Local Similarity 73.3%; Pred. No. 8;
 Matches 11; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 EIETHNLLGGQED 15
 |||||
 DB 376 EIATYRSLLG-QED 389

RESULT 4
 A25470
 cytokeratin 19 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 09-Jul-2004
 C:Accession: A25470
 R:Bader, B.L.; Magin, T.M.; Hatzfeld, M.; Franke, W.W.
 EMBO J. 5, 1865-1875, 1986
 A:Title: Amino acid sequence and gene organization of cytokeratin no. 19, an exceptional
 A:Reference number: A25470; MUID:87004553; PMID:2428612
 A:Accession: A25470
 A:Molecule type: DNA
 A:Residues: 1-399 <BAD>
 A:Cross-references: UNIPROT:P08728; UNIPARC:UPI000012DAED; GB:X04152; NID:G469; PIDN:CAA: A:Superfamily: cytoskeletal keratin
 C:Keywords: coiled coil

Query Match 51.7%; Score 45; DB 2; Length 399;
 Best Local Similarity 81.8%; Pred. No. 9.7;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIETHNLLLEG 11
 |||||
 DB 375 EIATYRNLLLEG 385

RESULT 5
 A25438
 keratin, type I cytoskeletal protein, B2 - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
 C:Accession: A25438
 R:Myatani, S.; Winkles, J.A.; Sargent, T.D.; Dawid, I.B.
 J. Cell Biol. 103, 1957-1965, 1986
 A:Title: Stage-specific keratins in Xenopus laevis embryos and tadpoles: the XK81 gene fi

A;Reference number: A25438; MUID:87057649; PMID:2430981

A;Accession: A25438

A;Molecule type: mRNA

A;Residues: 1-419 <MY>

A;Cross-references: UNIPROT:P05781; UNIPARC:UPI000012DADF; GB:M18155; GB:X05865; NID:g21

C;Superfamily: cytoskeletal keratin

C;Keywords: coiled coil

Query Match 51.7%; Score 45; DB 2; Length 419;

Best Local Similarity 81.8%; Pred. No. 10;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIEYHNLLGG 11

Db 382 EIEYRNLLGG 392

RESULT 6

I50484

vinentin beta - goldfish

C;Species: Carassius auratus (goldfish)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C;Accession: I50484

R;Glasgow, E.; Druger, R.K.; Fuchs, C.; Levine, E.M.; Giordano, S.; Schechter, N.

J. Neurochem. 63, 470-481, 1994

A;Title: Cloning of multiple forms of goldfish vinentin: differential expression in CNS.

A;Reference number: I50482; MUID:94308773; PMID:8035174

A;Accession: I50484

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-450 <GLA>

A;Cross-references: UNIPROT:P48673; UNIPARC:UPI000013881F; GB:L23841; NID:g388285; PIDN:

C;Superfamily: cytoskeletal keratin

Query Match 51.7%; Score 45; DB 2; Length 450;

Best Local Similarity 81.8%; Pred. No. 11;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIEYHNLLGG 11

Db 382 EIEYRNLLGG 392

RESULT 7

S28916

dystrophin - mouse

N;Alternate names: duchenne muscular dystrophy protein

C;Species: Mus musculus (house mouse)

C;Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C;Accession: S28916; B27162; S10922; C43837; B40134

R;Bies, R.D.; Phelps, S.F.; Cortez, M.D.; Roberts, R.; Caskey, C.T.; Chamberlain, J.S.

Nucleic Acids Res. 20, 1725-1731, 1992

A;Title: Human and murine dystrophin mRNA transcripts are differentially expressed during

A;Reference number: S28916; MUID:92253376; PMID:1579466

A;Accession: S28916

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA

A;Residues: 1-3678 <BIE>

A;Cross-references: UNIPROT:P11531; UNIPARC:UPI00000279E7; EMBL:M68859

A;Note: The nucleotide sequence was submitted to the EMBL Data Library, October 1991

R;Koenig, M.; Hoffman, E.P.; Bertelson, C.J.; Monaco, A.P.; Feener, C.; Kunkel, L.M.

Cell 50, 509-517, 1987

A;Title: Complete cloning of the Duchenne muscular dystrophy (DMD) cDNA and preliminary

A;Reference number: A90897; MUID:87273512; PMID:3607877

A;Accession: B27162

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-201 <KOE>

A;Cross-references: UNIPARC:UPI0000177686

R;Nudel, U.; Zuk, D.; Einat, P.; Zeelon, E.; Levy, Z.; Neuman, S.; Yaffe, D.

Nature 337, 76-78, 1989

A;Title: Duchenne muscular dystrophy gene product is not identical in muscle and brain.

A;Reference number: S06461; MUID:8902658; PMID:2909892

A;Accession: S10922

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-106 <NUD>

A;Cross-references: UNIPARC:UPI0000177687; EMBL:X14183

R;Rapaport, D.; Lederfein, D.; den Dunnen, J.T.; Grootsholten, P.M.; Van Ommen, G.J.; F

Differentiation 49, 187-193, 1992

A;Title: Characterization and cell type distribution of a novel, major transcript of the

A;Reference number: A43837; MUID:92316332; PMID:1377655

A;Accession: C43837

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 'MREHLKG', 3069-3181 <RAP>

A;Cross-references: UNIPARC:UPI0000177688

A;Note: sequence extracted from NCBI backbone

R;Hoffman, E.P.; Monaco, A.P.; Feener, C.C.; Kunkel, L.M.

Science 238, 347-350, 1987

A;Title: Conservation of the Duchenne muscular dystrophy gene in mice and humans.

A;Reference number: A40134; MUID:88018015; PMID:3659917

A;Accession: B40134

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 300-676, 'F', 678-1390 <HOF>

A;Cross-references: UNIPARC:UPI0000177689; GB:M18025

C;Genetics: 11/1

A;Note: The list of introns may be incomplete

C;Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystroph

F;14-233/Domain: alpha-actinin actin-binding domain homology <ACT>

F;340-449/Domain: spectrin/dystrophin repeat homology <SP1>

F;450-558/Domain: spectrin/dystrophin repeat homology <SP2>

F;2797-2924/Domain: spectrin/dystrophin repeat homology <SP3>

F;3048-3085/Domain: WW repeat homology <WW1>

Query Match 51.7%; Score 45; DB 2; Length 3678;

Best Local Similarity 61.1%; Pred. No. 1.3e+02;

Matches 11; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 1 EIEETDTHVHLLGGQEE 14

Db 2737 EIEETDTHVHLLGGQEE 2754

RESULT 8

I59463

keratin, type I, cytoskeletal - mouse

N;Alternate names: endo B cyokeratin; keratin D

C;Species: Mus musculus (house mouse)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004

C;Accession: I59463; A25621; A28428; J0406

R;Alonso, A.; Weber, T.; Jorcano, J.L.

Roux's Arch. Dev. Biol. 196, 16-21, 1987

A;Title: Cloning and characterization of keratin D, a murine endodermal cytoskeletal prot

A;Reference number: I59463

A;Accession: I59463

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-423 <RES>

A;Cross-references: UNIPROT:P05784; UNIPARC:UPI000016CE78; GB:M36376; NID:g198587; PIDN:

R;Singer, P.A.; Trevor, K.; Oshima, R.G.

J. Biol. Chem. 261, 538-547, 1986

A;Title: Molecular cloning and characterization of the endo B cyokeratin expressed in p

A;Reference number: A25621; MUID:86085876; PMID:2416755

A;Accession: A25621

A;Molecule type: mRNA

A;Residues: 1-243, 'D', 245-252, 'A', 254-423 <SIN>

A;Cross-references: UNIPARC:UPI000016A33; GB:M1686; NID:g198620; PIDN:AAA39390.1; PID:

R;Oshima, R.G.; Trevor, K.; Shevinsky, L.H.; Ryder, O.A.; Cecena, G.

Genes Dev. 2, 505-516, 1988

A;Title: Identification of the gene coding for the endo B murine cyokeratin and its met

A;Reference number: A28428; MUID:88255838; PMID:2454868

A;Accession: A28428

```

A:Molecule type: DNA
A:Residues: 1-132 <OSH>
A:Cross-references: UNIPARC:UPI000011E072; GB:Y00217; NID:G50842; PIDN:CAA68365.1; PID:G
R:ichinoe, Y.; Morita, T.; Zhang, F.; Srimahasongscram, S.; Tondella, M.L.C.; Matsumoto,
Gene 70, 85-95, 1998
A:Title: Nucleotide sequence and structure of the mouse cytoke keratin endoB gene.
A:Reference number: JT0406; MUID:89196920; PMID:2467843
A:Accession: JT0406
A:Molecule type: DNA
A:Residues: 1-133, 'F', 135-243, 'D', 245-252, 'A', 254-423 <ICH>
A:Cross-references: UNIPARC:UPI000016CD33; GB:M22832; NID:G340757; PIDN:AAA37552.1; PID:
C:Genetics:
A:Gene: endoB; KERD
A:Introns: 132/3; 160/2; 212/3; 267/3; 309/3; 384/2
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament

Query Match 51.1%; Score 44.5; DB 2; Length 423;
Best Local Similarity 68.8%; Pred. No. 13;
Matches 11; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 EIETHNLLGGQEDF 16
||| ||| ||| ||| |||
DB 369 EIATYRRLLEDG-EDF 383

RESULT 9
S05481
keratin 18, type I, cytoskeletal - human
N:Alternate names: cytoke keratin 18
C:Species: Homo sapiens (man)
C:Date: 07-Sep-1990 #sequence revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S05481; S05482; S06889
R:Oshima, R.G.; Millan, J.L.; Cecena, G.
Differentiation 33, 61-68, 1986
A:Title: Comparison of mouse and human keratin 18: a component of intermediate filaments
A:Reference number: S05481; MUID:87134778; PMID:2434380
A:Accession: S05481
A:Molecule type: mRNA
A:Residues: 1-430 <OSH>
A:Cross-references: UNIPROT:P05783; UNIPARC:UPI000004284B; EMBL:X12881; NID:G34036; PIDN:
R:Romano, V.; Hatzfeld, M.; Magin, T.M.; Zimbelmann, R.; Franke, W.W.; Maier, G.; Ponst
Differentiation 30, 244-253, 1986
A:Title: Cytoke keratin expression in simple epithelia. I. Identification of mRNA coding fo
A:Reference number: S05482; MUID:86193258; PMID:2422083
A:Accession: S05482
A:Molecule type: mRNA
A:Residues: 199-201, 'Q', 203-245, 'S', 247-308, 'R', 310-311, 'R', 313-430 <ROM>
A:Cross-references: UNIPARC:UPI000016AB98; EMBL:X12876; NID:G34034; PIDN:CAA31369.1; PID
A:Note: part of this sequence was confirmed by protein sequencing
R:Leube, R.E.; Bosch, F.X.; Romano, V.; Zimbelmann, R.; Hoefler, H.; Franke, W.W.
Differentiation 33, 69-85, 1986
A:Title: Cytoke keratin expression in simple epithelia.
A:Reference number: S06888; MUID:87134779; PMID:2434381
A:Accession: S06888
A:Molecule type: mRNA
A:Residues: 7-430 <LEU>
A:Cross-references: UNIPARC:UPI000016A768; EMBL:X12883; NID:G30310; PIDN:CAA31377.1; PID
C:Genetics:
A:Gene: GDB:KRT18
A:Cross-references: GDB:120127; OMIM:148070
A:Map position: 17p12-17p11
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament
F:2/430/Product: keratin 18, type I, cytoskeletal #status predicted <MAT>

Query Match 51.1%; Score 44.5; DB 2; Length 430;
Best Local Similarity 68.8%; Pred. No. 13;
Matches 11; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 EIETHNLLGGQEDF 16
||| ||| ||| ||| |||
DB 376 EIATYRRLLEDG-EDF 390

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RESULT 10

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S55691
keratin type I (clone Jn7-4) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 28-Oct-1995 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C:Accession: S55691
R:Adati, N.; Ito, T.; Koga, C.; Kito, K.; Sakaki, Y.; Shiokawa, K.
Biochim. Biophys. Acta 1262, 43-51, 1995
A:Title: Differential display analysis of gene expression in developing embryos of Xenop
A:Reference number: S55691; MUID:95290493; PMID:7772598
A:Accession: S55691
A:Molecule type: mRNA
A:Residues: 1-105 <ADA>
A:Cross-references: UNIPROT:Q91404; UNIPARC:UPI00000FC2C7; EMBL:S78089; NID:G9992222; PIDN:
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament

```

```

Query Match 50.6%; Score 44; DB 2; Length 105;
Best Local Similarity 60.0%; Pred. No. 3;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```

```
QY 1 EIETHNLLGGQED 15
||| ||| ||| ||| |||

```

```
DB 51 EIQTYRRLLEDGSPD 65
```

RESULT 11

```

A28825
keratin, type I nonepidermal - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: A28825
R:Laflamme, S.E.; Jamrich, M.; Richter, K.; Sargent, T.D.; Dawid, I.B.
Genes Dev. 2, 853-862, 1988
A:Title: Xenopus endo B is a keratin preferentially expressed in the embryonic notochord.
A:Reference number: A28825; MUID:89092007; PMID:2463213
A:Accession: A28825
A:Molecule type: mRNA
A:Residues: 1-368 <LAF>
A:Cross-references: UNIPROT:P08802; UNIPARC:UPI000012DAEC; GB:Y00230; NID:G64863; PIDN:CF
C:Genetics:
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil

```

```

Query Match 50.6%; Score 44; DB 2; Length 368;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```

```
QY 1 EIETHNLLGGQED 15
||| ||| ||| ||| |||

```

```
DB 314 EIQTYRRLLEDGSPD 328
```

RESULT 12

```

A54603
transcription factor CTCF - chicken
N:Alternate names: finger protein CTCF
C:Species: Gallus gallus (chicken)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: A54603; S35919
R:Klenova, E.M.; Nicolas, R.H.; Paterson, H.F.; Carne, A.F.; Heath, C.M.; Goodwin, G.H.;
Mol. Cell. Biol. 13, 7612-7624, 1993
A:Title: CTCF, a conserved nuclear factor required for optimal transcriptional activity
A:Reference number: A54603; MUID:94067122; PMID:8246978
A:Accession: A54603
A:Molecule type: mRNA
A:Residues: 1-728 <KLG>
A:Cross-references: UNIPROT:C08705; UNIPARC:UPI0000128608; EMBL:Z22605; NID:G396093; PIDN:
C:Comment: This transcription factor with eleven zinc finger motifs binds specifically to
C:Comment: The detection of multiple isoforms by Western blotting and of multiple mRNA sp

```


C;Keywords: alternative splicing; DNA binding; nucleus; transcription factor

Query Match 50.6%; Score 44; DB 2; Length 728;
Best Local Similarity 60.0%; Pred. No. 29;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIETHNLLGGQED 15
Db 21 ERKYORRGGQED 35

RESULT 13

A97178
Probable permealase [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: A97178
R;Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: A97178
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-834 <KUR>
A;Cross-references: UNIPROT:Q97GM0; UNIPARC:UPI000000CA47D; GB:AE001437; PIDN:AAK80212.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2255

Query Match 50.6%; Score 44; DB 2; Length 834;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 YHNLGGQEDF 16
Db 47 YRNLKGSYEDF 58

RESULT 14

PN0494
NAD ADP-ribosyltransferase (EC 2.4.2.30) - cherry salmon (fragment)
N;Alternate names: poly ADP-ribose polymerase
C;Species: Oncorhynchus masou (cherry salmon)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-2004
C;Accession: PN0494
R;Ozawa, Y.; Uchida, K.; Uchida, M.; Ami, Y.; Kushida, S.; Okada, N.; Miwa, M.
Biochem. Biophys. Res. Commun. 193, 119-125, 1993
A;Title: Isolation of cDNAs encoding the catalytic domain of poly(ADP-ribose)polymerase
A;Reference number: PN0494; MUID:93277538; PMID:8503897
A;Accession: PN0494
A;Molecule type: mRNA
A;Residues: 1-135 <OZA>
A;Cross-references: UNIPROT:Q08824; UNIPARC:UPI00001320E4
C;Comment: This zinc-finger protein plays a role in DNA repair, cell growth, and differe
C;Superfamily: poly(ADP-ribose) polymerase
C;Keywords: DNA binding; glycosyltransferase; hexosyltransferase; NAD; nucleus; pentosyl

Query Match 49.4%; Score 43; DB 2; Length 135;
Best Local Similarity 53.3%; Pred. No. 6;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIETHNLLGGQED 15
Db 12 DIEVAYSLKGAED 26

RESULT 15

IS0721
synemin - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 31-Dec-2004

C;Accession: IS0721
R;Becker, B.; Bellin, R.M.; Sernett, S.W.; Huiatt, T.W.; Robson, R.M.
Biochem. Biophys. Res. Commun. 213, 796-802, 1995
A;Title: Synemin contains the rod domain of intermediate filaments.
A;Reference number: IS0721; MUID:95382823; PMID:7654240
A;Accession: IS0721
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-304 <BEC>
A;Cross-references: UNIPROT:Q90662; UNIPARC:UPI00001774FF; EMBL:U28143; NID:g1052880; PI

Query Match 49.4%; Score 43; DB 2; Length 304;
Best Local Similarity 81.8%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIETHNLLLEG 11
Db 289 EIETVRALLEG 299

Search completed: July 5, 2006, 19:25:12
Job time : 15.6667 secs

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GenCore version 5.1.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 19:01:48 ; Search time 186 Seconds
(without alignments)
79.571 Million cell updates/sec

Title: US-10-774-928A-3
Perfect score: 87
Sequence: 1 E1ETHVNLEGGQEDP 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	623	1 K1C9 HUMAN	P35527 homo sapien
2	70	80.5	618	2 Q8CIS9 RAT	Q8CIS9 rattus norv
3	70	80.5	743	2 Q6RHW0 MOUSE	Q6RHW0 mus musculu
4	70	80.5	786	2 O18740 CANFA	O18740 canis famil
5	53	60.9	384	2 Q6DBU4 BRARE	Q6DBU4 brachydanio
6	51	58.6	431	2 Q566F9 XENLA	Q566F9 xenopus lae
7	51	58.6	431	2 Q6GLQ7 XENLA	Q6GLQ7 xenopus lae
8	51	58.6	628	2 Q6FW44 CANGA	Q6FW44 candida gla
9	50	57.5	439	2 Q9BLX8 CIOIN	Q9BLX8 ciona intes
10	49	56.3	760	2 Q65KY8 BACLD	Q65KY8 bacillus li
11	48	55.2	453	1 K1C15 SHEEP	O77727 ovis aries
12	47	54.0	829	2 Q54DN9 DICDI	Q54DN9 dictyosteli
13	47	54.0	932	2 Q8IIF1 PLAF7	Q8IIF1 plasmodium
14	46	52.9	170	2 Q9S954 MESCR	Q9S954 mesembryant
15	46	52.9	447	1 K1C15 RAT	Q6IFV3 rattus norv
16	46	52.9	483	1 K1C12 MOUSE	Q64291 mus musculu
17	46	52.9	487	2 Q8GUB5 MESCR	Q8GUB5 mesembryant
18	46	52.9	524	2 Q8AWB2 LAMFL	Q8AWB2 lactobacill
19	46	52.9	525	2 Q5RDU9 LACAC	Q5RDU9 trypanosoma
20	46	52.9	1009	2 Q4DVU3 TRYCR	Q4DVU3 plasmodium
21	46	52.9	1081	2 Q8IIV9 PLAF7	Q8IIV9 plasmodium
22	46	52.9	1172	2 Q65KN1 BACLD	Q65KN1 bacillus li
23	45.5	52.3	400	1 K1C19 HUMAN	P08727 homo sapien
24	45.5	52.3	400	1 K1C19 PONPY	Q5R859 pongo pygma
25	45	51.7	131	2 Q33LM1 METHU	Q33LM1 methanospir
26	45	51.7	221	2 Q3TBO1 MOUSE	Q3TBO1 mus musculu
27	45	51.7	360	2 Q3UF47 MOUSE	Q3UF47 mus musculu
28	45	51.7	386	2 Q4HM53 CAMLA	Q4HM53 campylobact
29	45	51.7	399	1 K1C19 BOVIN	P08728 bos taurus
30	45	51.7	419	1 K1C4 XENLA	P05781 xenopus lae
31	45	51.7	438	2 Q5PR28 BRARE	Q5PR28 brachydanio

32	45	51.7	450	1 VIMB CARAU	P48673 carassius a
33	45	51.7	452	1 K1C15 MOUSE	Q61414 mus musculu
34	45	51.7	452	2 Q6IMF1 RAT	Q6IMF1 rattus norv
35	45	51.7	454	2 Q4QR57 XENLA	Q4QR57 xenopus lae
36	45	51.7	456	2 Q6IFW5 RAT	Q6IFW5 rattus norv
37	45	51.7	469	2 Q7ZV83 XENLA	Q7ZV83 xenopus lae
38	45	51.7	488	2 Q5M8X9 XENTR	Q5M8X9 xenopus tro
39	45	51.7	491	2 Q8AV12 XENLA	Q8AV12 xenopus lae
40	45	51.7	567	2 Q5MIV0 AEDAL	Q5MIV0 aedes albop
41	45	51.7	582	2 Q3NXA5 9GAMM	Q3NXA5 shewanella
42	45	51.7	587	2 Q3P3X2 9GAMM	Q3P3X2 shewanella
43	45	51.7	605	2 Q4UG78 THEAN	Q4UG78 theileria a
44	45	51.7	633	2 Q4N919 THEPA	Q4N919 theileria p
45	45	51.7	683	2 Q4RQR9 TETNG	Q4RQR9 tetraodon n

ALIGNMENTS

RESULT 1
K1C9 HUMAN
ID K1C9 HUMAN STANDARD; PRT; 623 AA.
AC P35527; O00109; Q14665;
DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
DT 08-NOV-2005, sequence version 2.
DT 07-FEB-2006, entry version 50.
DE Keratin, type I cytoskeletal 9 (Cytokeratin-9) (CK-9) (Keratin-9)
DE (K9).
GN Name=KRT9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND PARTIAL PROTEIN SEQUENCE.
RC TISSUE=Foot sole tissue;
RX MEDLINE=94131202; PubMed=7507869;
RA Langbein L., Heid H.W., Moll I., Franke W.W.;
RT "Molecular characterization of the body site-specific human epidermal
cytokeratin 9: cDNA cloning, amino acid sequence, and tissue
specificity of gene expression."
RT Differentiation 55:57-72(1993).
RL [2]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS EPPK LYS-161; GLN-163
AND TRP-163.
RX MEDLINE=94214498; PubMed=7512862;
RA Reis A., Hennies H.-C., Langbein L., Digweed M., Mischke D.,
Dreschler M., Schroek E., Royer-Pokora B., Franke W.W., Sperling K.,
Kuester W.;
RT "Keratin 9 gene mutations in epidermolytic palmoplantar keratoderma
(EPPK)."
RL Nat. Genet. 6:174-179(1994).
RN [3]
RP PROTEIN SEQUENCE OF 14-29, AND MASS SPECTROMETRY.
RC TISSUE=Cervix carcinoma;
RA Bienvenut W.V.;
RN Unpublished observations (AUG-2005).
RN [4]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 147-372, AND VARIANT EPPK GLN-163.
RX MEDLINE=96228052; PubMed=8647270; DOI=10.1016/0014-5793(96)00393-6;
RA Kobayashi S., Tanaka T., Matsuyoshi N., Imamura S.;
RT "Keratin 9 point mutation in the pedigree of epidermolytic hereditary
palmoplantar keratoderma perturbs keratin intermediate filament
network formation."
RL FEBS Lett. 386:149-155(1996).
RN [5]
RP PROTEIN SEQUENCE OF 450-466.
RX MEDLINE=90267446; PubMed=2140676;
RA Rosen E.M., Meromsky L., Romero R., Setter E., Goldberg I.;
RT "Human placenta contains an epithelial scatter protein."
RL Biochem. Biophys. Res. Commun. 168:1082-1088(1990).
RN [6]


```

OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley;
RA MEDLINE=20525596; PubMed=11071770; DOI=10.1006/dbio.2000.9911;
RX Mochida K., Rivkin E., Gil M., Kierszenbaum A.L.;
RT "Keratin 9 is a component of the perinuclear ring of the manchette of
   rat spermatozoa."
RL Dev. Biol. 227:510-519(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley;
RA Mochida K., Rivkin E., Gil M., Kierszenbaum A.L.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY128946; AA05455.1; -; mRNA.
DR HSSP; P08670; IGK7.
DR Ensembl; ENSRNOG0000014370; Rattus norvegicus.
DR RGD; 628785; Krt1-9.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PROSITE; PS00226; IF; 1.
DR Intermediate filament.
KW Intermediate filament.
SQ SEQUENCE 618 AA; 63009 MW; B0140A0E34E2A28F CRC64;

Query Match      80.5%; Score 70; DB 2; Length 618;
Best Local Similarity 81.2%; Pred. No. 0.014;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 EIETHNLLGGQEDF 16
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DB 435 EIETRYKLGGQQDF 450

RESULT 3
ID Q6RHW0_MOUSE PRELIMINARY; PRT; 743 AA.
AC Q6RHW0;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Cytokeratin 9.
GN Name=Krt1-9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SVJ;
RA Rivkin E., Tres L., Eddy M., Kierszenbaum A.L.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; AY497550; AAB89518.1; -; mRNA.
DR Ensembl; ENSMUSG0000051617; Mus musculus.
DR MGI; MGI:96696; Krt1-9.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR Pfam; PF00038; Filament; 1.

us-10-774-928a-3.rup
```

```

DR PRINTS; PR01248; TYPE1KERATIN.
KW Keratin.
SQ SEQUENCE 743 AA; 72516 MW; 76405B82F1C750B0 CRC64;

Query Match      80.5%; Score 70; DB 2; Length 743;
Best Local Similarity 81.2%; Pred. No. 0.018;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 EIETHNLLGGQEDF 16
   ||||| |||||:|
DB 428 EIETRYLGGQQDF 443

RESULT 4
ID O18740_CANFA PRELIMINARY; PRT; 786 AA.
AC O18740;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Keratin.
GN Name=KRT9;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lacharme P., Hitté C., Jouquand S., Priat C., Galibert F.;
RT "Identification and analysis of the dog keratin 9 (KRT9) gene."
RL Anim. Genet. 9:173-178(1998).
CC -----
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CC -----
DR EMBL; AF000949; AAC26971.1; -; Genomic_DNA.
DR HSSP; P08670; IGK7.
DR Ensembl; ENSCAFG0000015952; Canis familiaris.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002952; Eggshell.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01228; EGGSHLL.
DR PRINTS; PR01248; TYPE1KERATIN.
SQ SEQUENCE 786 AA; 76354 MW; 272AB5425DD09535 CRC64;

Query Match      80.5%; Score 70; DB 2; Length 786;
Best Local Similarity 81.2%; Pred. No. 0.019;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 EIETHNLLGGQEDF 16
   ||||| |||||:|
DB 434 EIKTRSLGGQEDF 449

RESULT 5
ID Q6DBU4_BRARE PRELIMINARY; PRT; 384 AA.
AC Q6DBU4;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Zgc:92380.
GN ORFNames=zgc:92380;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
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RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RA Director MGC Project;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----
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CC -----
DR EMBL; BC078359; AAH78359.1; -; mRNA.
DR Ensembl; ENSDARG0000041339; Danio rerio.
DR ZFIN; ZDB-GENE-040801-221; zgc:92380.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR Pfam; PF00038; Filament; I.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PROSITE; PS00226; IF; UNKNOWN_1.
KW Intermediate filament.
SQ SEQUENCE 384 AA; 43462 MW; 2DC3396DAR256657 CRC64;

Query Match 60.9%; Score 53; DB 2; Length 384;
Best Local Similarity 66.7%; Pred. No. 5.7;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIETVHNLLEGGQED 15
DB 354 EIDTVHRLLEGGVDD 368

RESULT 6
ID Q566F9_XENLA PRELIMINARY; PRT; 431 AA.
AC Q566F9_
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DE 07-FEB-2006, entry version 4.
DE MGC84388 protein.
GN Name=MGC84388;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,

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RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Klein S., Gerhard D.S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC093567; AAH93567.1; -; mRNA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR Pfam; PF00038; Filament; I.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PROSITE; PS00226; IF; UNKNOWN_1.
SQ SEQUENCE 431 AA; 47704 MW; 13BE6E9019731326 CRC64;

Query Match 58.6%; Score 51; DB 2; Length 431;
Best Local Similarity 76.9%; Pred. No. 14;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIETVHNLLEGGQ 13
DB 381 EISTYHKLLEGGQ 393

RESULT 7
ID Q6GLQ7_XENLA PRELIMINARY; PRT; 431 AA.
AC Q6GLQ7_
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DE 07-FEB-2006, entry version 15.
DE MGC84388 protein.
GN Name=MGC84388;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Atschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalon D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Richards S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting R.W., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S., Krzyzinski M.I., Skalska U., Smallus D.E.,
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT cDNA sequences";
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2].
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/gvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3].
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the intermediate filament family.
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 CC -----
 DR EMBL; BC074402; AAH74402.1; -; mRNA.
 DR GO; GO:0005882; C:intermediate filament; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR001664; IF.
 DR InterPro; IPR002957; Keratin_I.
 DR Pfam; PF00038; Filament; 1.
 DR PRINTS; PR01248; TYPEKERATIN.
 DR PROSITE; PS00226; IF; UNKNOWN_1.
 DR Intermediate filament.
 KW SEQUENCE 431 AA; 47723 MW; 0032E596D1B243C8 CRC64;
 QY Query Match 58.6%; Score 51; DB 2; Length 431;
 Db Best Local Similarity 76.9%; Pred. No. 14;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EIETHNLLGGQ 13
 Db 381 EISTYHKLLEGGQ 393
 RESULT 8
 Q6FW44_CANGA PRELIMINARY; PRT; 528 AA.
 AC Q6FW44;
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE Candida glabrata strain CBS138 chromosome D complete sequence.
 GN OrderedLocusNames=CAGL0D03080g;
 OS Candida glabrata (yeast) (Torulopsis glabrata).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5478;
 RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 2001 / CBS 138;
 RX PubMed=15229592; DOI=10.1038/nature02579;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
 RA Boismare A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.-L.;
 RT "Genome evolution in yeasts";
 RL Nature 430:35-44(2004).
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 CC -----
 DR EMBL; CR380950; CAG58461.1; -; Genomic_DNA.
 KW Complete proteome.
 SQ SEQUENCE 628 AA; 73024 MW; 5B61FC1B3D9AB450 CRC64;
 QY Query Match 58.6%; Score 51; DB 2; Length 628;
 Db Best Local Similarity 60.0%; Pred. No. 22;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IETYNLLGGQEDF 16
 Db 436 IELYNLLOGLKDY 450
 RESULT 9
 Q9BLX8_CIOIN PRELIMINARY; PRT; 439 AA.
 AC Q9BLX8;
 DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2001, sequence version 1.
 DT 07-FEB-2006, entry version 19.
 DE Intermediate filament protein IF-C.
 GN Name=if-c;
 OS Ciona intestinalis.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 OC Phlebobranchia; Cionidae; Ciona.
 OX NCBI_TaxID=7719;
 RN [1].
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole animal;
 RX MEDLINE=22061815; PubMed=12067066;
 RA Wang J., Karabinos A., Zimek A., Meyer M., Riemer D., Hudson C.,
 RA Lemaire P., Weber K.;
 RT "Cytoplasmic intermediate filament protein expression in tunicate
 RT development; a specific marker for the test cells";
 RL Eur. J. Cell Biol. 81:302-311(2002).
 CC -!- SIMILARITY: Belongs to the intermediate filament family.
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 CC -----
 DR EMBL; AJ298331; CAC24552.1; -; mRNA.
 DR HSSP; P08670; 1GK7.
 DR Ensembl; ENSCING0000008941; Ciona intestinalis.
 DR GO; GO:0005882; C:intermediate filament; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR001664; IF.
 DR InterPro; IPR002957; Keratin_I.
 DR Pfam; PF00038; Filament; 1.
 DR PRINTS; PR01248; TYPEKERATIN.
 DR PROSITE; PS00226; IF; UNKNOWN_1.

KW Intermediate filament.
SQ SEQUENCE 439 AA; 49875 MW; 22F60922B6D2E9D1 CRC64;

Query Match 57.5%; Score 50; DB 2; Length 439;
Best Local Similarity 68.8%; Pred. No. 21;
Matches 11; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 EIETHNLLGGQEDF 16
DB 385 ELSTYHKLLEG--EEF 398

RESULT 10
Q65KY8_BACLD PRELIMINARY; PRT; 760 AA.
AC Q65KY8_Q62WDS;
DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE YesS (Probable transcriptional regulator).
GN Name=YesS; OrderedLocustNames=BL03790, BLi01372;
OS Bacillus licheniformis (strain DSM 13 / ATCC 14580).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=279010;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed15383718; DOI=10.1159/000079829;
RA Veith B., Herrberg C., Steckel S., Feesche J., Maurer K.H.,
RA Ehrenreich P., Baumer S., Henne A., Liesegang H., Merkl R.,
RA Ehrenreich A., Gottschalk G.;
RT "The complete genome sequence of Bacillus licheniformis DSM13, an
RT organism with great industrial potential";
RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed15461803; DOI=10.1186/gb-2004-5-10-r77;
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretzky E.J.,
RA Tang M., Lopez de Leon A., Xiang H., Gusti V., Clausen I.G.,
RA Olsen P.B., Rasmussen M.D., Andersen J.T., Joergensen P.L.,
RA Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N.,
RA Erlich S.D., Berka R.M.;
RT "Complete genome sequence of the industrial bacterium Bacillus
RT licheniformis and comparisons with closely related Bacillus species.";
RL Genome Biol. 5:RESEARCH077.12(2004).
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DR EMBL; AE017333; AAU40276.1; -; Genomic DNA.
DR EMBL; CP000002; AAU22923.1; -; Genomic DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR000005; HTHArac.
DR Pfam; PF00165; HTH_Arac; 2.
DR SMART; SM00342; HTH_ARAC; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
KW Complete proteome; DNA-binding; Transcription;
KW Transcription regulation.
SQ SEQUENCE 760 AA; 87513 MW; 4E8D8B27EAC7BDA CRC64;

Query Match 56.3%; Score 49; DB 2; Length 760;
Best Local Similarity 66.7%; Pred. No. 58;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EIETHNLLGGQ 13
DB 147 LKAYHSLLEGGQ 158

RESULT 11

K1C15_SHEEP
ID K1C15_SHEEP STANDARD; PRT; 453 AA.
AC O77727;
DT 06-DEC-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1998, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Keratin, type I cytoskeletal 15 (Cytokeratin-15) (CK-15) (Keratin-15) (K15).
DE (K15).
GN Name=KRT15; (Sheep).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND TISSUE SPECIFICITY.
RC TISSUE=Spine;
RX MEDLINE=99026083; PubMed=9806795; DOI=10.1006/excr.1998.4217;
RA Whitbread L.A., Powell B.C.;
RT "Expression of the intermediate filament keratin gene, K15, in the
RT basal cell layers of epithelia and the hair follicle";
RL Exp. Cell Res. 244:448-459(1998).
CC -!- SUBUNIT: Heterotetramer of two type I and two type II keratins.
CC -!- TISSUE SPECIFICITY: Expressed in the basal cell layers of several
CC stratified epithelia including oesophagus, tongue, stomach,
CC epidermis and hair follicle. In the hair follicle, expression is
CC detected mainly in the basal layer of the outer root sheath (ORS),
CC except just above the follicle bulb where it occurs throughout
CC its' thickness. Low expression levels are seen in the single layer
CC of ORS cells around the base of the follicle which increases in
CC the palisade-like cells of the bulb. Also expressed in the basal
CC cells of the sebaceous glands, and expression in the epidermis
CC occurs in a punctate pattern.
CC -!- MISCELLANEOUS: There are two types of cytoskeletal and
CC microfibrillar keratin, I (acidic; 40-55 kDa) [K9 to K20] and II
CC (neutral to basic 56-70 kDa) [K1 to K8].
CC -!- SIMILARITY: Belongs to the intermediate filament family.

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DR EMBL; AJ006277; CA006944.1; -; Genomic DNA.
DR HSSP; P08670; 1GK7.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Coiled coil; Intermediate filament; Keratin.
FT CHAIN 1 453
FT REGION 1 102
FT REGION 103 411
FT REGION 103 138
FT REGION 139 157
FT REGION 158 249
FT REGION 250 269
FT REGION 270 411
FT REGION 412 453
FT COMPBIAS 14 101
FT COMPBIAS 426 431
FT COMPLETION 453 AA; 48770 MW; E90D5239DA45015A CRC64;
SQ SEQUENCE 453 AA; 48770 MW; E90D5239DA45015A CRC64;

Query Match 55.2%; Score 48; DB 1; Length 453;
Best Local Similarity 81.8%; Pred. No. 47;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIETHNLLLEG 11
DB 400 EIATYHSLLEG 410

RESULT 12


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Q54DN9_DICDI PRELIMINARY; PRT; 829 AA.
AC Q54DN9;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Hypothetical protein.
GN ORFNames=DDR0184228;
DE ORFNames=DDR0184228;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX PubMed=15875012; DOI=10.1038/nature03481;
RA Eichinger L., Fachebat J.A., Gloeckner G., Rajandream M.A.,
RA Sugang R., Berriman M., Song J., Olsen R., Konfortov B.A., Rivero P.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero P.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.M.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D.M., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,
RA Buchrieser C., Wardrop A., Felder M., Thangavelu M., Johnson D.,
RA Knights A., Loughsagh H., Mungall K.L., Oliver K., Price C.,
RA Quail M.A., Urushihara H., Hernandez J., Rabinowitsch E., Steffen D.,
RA Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,
RA Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,
RA Tanaka Y., Shaulsky G., Schleicher M., Weinstock G.M., Rosenthal A.,
RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzer M.,
RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
RA Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 435:43-57(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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EMBL: AAFI01000265; EAL61410.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW ATP-binding; Helicase; Hydrolase; Hypothetical protein.
SQ SEQUENCE 829 AA; 96165 MW; 4f17DC01E0C34F1E CRC64;

Query Match 54.0%; Score 47; DB 2; Length 829;
Best Local Similarity 64.3%; Pred. No. 1.4e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 ETVHNLLEGGQEDF 16
DB 663 EIVEDLLEGGQEDF 676

RESULT 13
ID Q8ILF1_PLAF7 PRELIMINARY; PRT; 992 AA.
AC Q8ILF1;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.

Q54DN9_MESCR PRELIMINARY; PRT; 170 AA.
AC Q54DN9;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Vacuolar H(+)-ATPase subunit B (Fragment).
OS Mesembryanthemum crystallinum (Common ice plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Caryophyllales; Alzooceae; Mesembryanthemum.
OX NCBI_TaxID=3544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96351503; PubMed=8587987; DOI=10.1104/pp.110.1.259;
RA Low R., Rockel B., Kirsch M., Katakczak R., Hertenstein S.,
RA Martinoia E., Luttge U., Rausch T.;
RT "Early salt stress effects on the differential expression of vacuolar
RT H(+)-ATPase genes in roots and leaves of Mesembryanthemum
RT crystallinum";
RL Plant Physiol. 110:259-265(1996).
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CC GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.
CC GO; GO:0005524; F:ATP binding; IEA.
CC GO; GO:0046933; F:hydrogen-transporting ATP synthase activity; IEA.
CC GO; GO:0046961; F:hydrogen-transporting ATPase activity; IEA.
CC GO; GO:0016787; F:hydrolase activity; IEA.
CC GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.
CC InterPro; IPR000194; ATPase_a/bcentre.

QY 2 IETYNLLEGGQEDF 16
DB 142 LDTYENLYEGILEDF 156

Query Match 54.0%; Score 47; DB 2; Length 992;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IETYNLLEGGQEDF 16
DB 142 LDTYENLYEGILEDF 156

RESULT 14
Q54DN9_MESCR PRELIMINARY; PRT; 170 AA.
AC Q54DN9;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Vacuolar H(+)-ATPase subunit B (Fragment).
OS Mesembryanthemum crystallinum (Common ice plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Caryophyllales; Alzooceae; Mesembryanthemum.
OX NCBI_TaxID=3544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96351503; PubMed=8587987; DOI=10.1104/pp.110.1.259;
RA Low R., Rockel B., Kirsch M., Katakczak R., Hertenstein S.,
RA Martinoia E., Luttge U., Rausch T.;
RT "Early salt stress effects on the differential expression of vacuolar
RT H(+)-ATPase genes in roots and leaves of Mesembryanthemum
RT crystallinum";
RL Plant Physiol. 110:259-265(1996).
CC -----
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-----
CC GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.
CC GO; GO:0005524; F:ATP binding; IEA.
CC GO; GO:0046933; F:hydrogen-transporting ATP synthase activity; IEA.
CC GO; GO:0046961; F:hydrogen-transporting ATPase activity; IEA.
CC GO; GO:0016787; F:hydrolase activity; IEA.
CC GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.
CC InterPro; IPR000194; ATPase_a/bcentre.
```

DR Pfam; PF00006; ATP-synt_ab; 1.
KW Hydrolase.
FT NON_TER 1 170
FT NON_TER 170 170
SQ SEQUENCE 170 AA; 19062 MW; 91AC0A63526E4BA2 CRC64;

Query Match 52.9%; Score 46; DB 2; Length 170;
Best Local Similarity 57.1%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 0; Gaps 0;

QY 2 IETVHNLEGGQED 15
Db :|||:||||:
52 LKTEENLMGGQED 65

RESULT 15
KIC15_RAT ID KIC15_RAT STANDARD; PRT; 447 AA.
AC Q6IFV3;
DT 06-DEC-2005, integrated into UniProtKB/Swiss-Prot.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Keratin, type I cytoskeletal 15 (Cytokeratin-15) (CK-15) (Keratin-15)
DE (K15) (Type I keratin K15).
GN Name=Krt15; Synonyms=K15;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Brown Norway;
RX PubMed=15057822; DOI=10.1038/nature02426;
RA Gibbs R.A., Weinstock G.M., Metzker M.L., Muzny D.M., Sodergren E.J.,
RA Scherer S., Scott G., Steffen D., Worley K.C., Burch P.E., Okwuonu G.,
RA Hines S., Lewis L., Deramo C., Delgado O., Dugan-Rocha S., Miner G.,
RA Morgan M., Hawes A., Gill R., Holt R.A., Adams M.D., Amanatides P.G.,
RA Baden-Rillson H., Barnstead M., Chin S., Evans C.A., Ferrieria S.,
RA Foster C., Glodok A., Gu Z., Jennings D., Kraft C.L., Nguyen T.,
RA Pfannkuch C.M., Sitter C., Sutton G.G., Venter J.C., Woodage T.,
RA Smith D., Lee H.M., Gustafson E., Cahill P., Kana A.,
RA Doucette-Stamm L., Weinstock K., Fichtel K., Weiss R.B., Dunn D.M.,
RA Green E.D., Blakesley R.W., Bouffard G.G., De Jong P.J., Osoegawa K.,
RA Zhu B., Marra M., Schein J., Bosdet I., Fjell C., Jones S.,
RA Krzywinski M., Mathewson C., Siddiqui A., Wye N., McPherson J.,
RA Zhao S., Fraser C.M., Shetty J., Shateman S., Geer K., Chen Y.,
RA Abramson S., Nierman W.C., Havlak P.H., Chen R., Durbin K.J., Egan A.,
RA Ren Y., Song X.Z., Li B., Liu Y., Qin X., Cawley S., Cooney A.J.,
RA D'Souza L.M., Martin K., Wu J.Q., Gonzalez-Garay M.L., Jackson A.R.,
RA Kalafus K.J., McLeod M.P., Milosavljevic A., Virk D., Volkov A.,
RA Wheeler D.A., Zhang Z., Bailey J.A., Eichler E.E., Tuzov E.,
RA Birney E., Mongin E., Ureta-Vidal A., Woodward C., Zdobnov E.,
RA Bork P., Suyama M., Torrents D., Alexandersson M., Trask B.J.,
RA Young J.M., Huang H., Wang H., Xing H., Daniels S., Gietzen D.,
RA Schmid J., Stevens K., Vitt U., Wingrove J., Camara F., Mar Alba M.,
RA April J.F., Guigo R., Smit A., Dubchak I., Rubin E.M., Couronne O.,
RA Poliakov A., Hubner N., Ganten D., Goesele C., Hummel O., Kreitler T.,
RA Lee Y.A., Monti J., Schulz H., Zindahl H., Himmelbauer H., Lehrach H.,
RA Jacob H.J., Bromberg S., Gullings-Handley J., Jensen-Seaman M.I.,
RA Wittek A.E., Lazar J., Pasko D., Tonellato P.J., Twigger S.,
RA Ponting C.P., Duarte J.M., Rice S., Goodstadt L., Beaton S.A.,
RA Ames R.D., Winter E.E., Webber C., Brandt P., Nyakatura G.,
RA Aderoti M., Chiaromonte F., Elmitaki L., Eswara P., Hardison R.C.,
RA Hou M., Kolbe D., Makova K., Miller W., Nekrutenko A., Riemer C.,
RA Schwartz S., Taylor J., Yang S., Zhang Y., Lindpaintner K.,
RA Andrews T.D., Caccamo M., Clamp M., Clarke L., Curwen V., Durbin R.,
RA Eyras E., Searle S.M., Cooper G.M., Batzoglu S., Brudno M., Sidow A.,
RA Stone E.A., Payseur B.A., Bourque G., Lopez-Otin C., Puente X.S.,
RA Chakrabarti K., Chatterji S., Dewey C., Pachter L., Bray N., Yap V.B.,
RA Caspi A., Tesler G., Pezner P.A., Haussler D., Roskin K.M.,
RA Baertsch R., Clawson H., Furey T.S., Hinrichs A.S., Karolchik D.,
RA Kent W.J., Rosenbloom K.R., Trumbower H., Weirauch M., Cooper D.N.,

RA Stenson P.D., Ma B., Brent M., Arumugam M., Shteynberg D.,
RA Copley R.R., Taylor M.S., Rietman H., Mudunuri U., Peterson J.,
RA Guyer M., Felsenfeld A., Old S., Mockrin S., Collins F.,
RT "Genome sequence of the Brown Norway rat yields insights into
RT mammalian evolution.";
RL Nature 428:493-521(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Prostate;
RG NIH - Mammalian Gene Collection (MGC) project;
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP IDENTIFICATION.
RC STRAIN=Brown Norway;
RX MEDLINE=23257644; PubMed=15085952; DOI=10.1078/0171-9335-00354;
RA Hesse M., Zimek A., Weber K., Magin T.M.;
RT "Comprehensive analysis of keratin gene clusters in humans and
RT rodents.";
RL Eur. J. Cell Biol. 83:19-26(2004).
CC -!- SUBUNIT: Heterotetramer of two type I and two type II keratins.
CC -!- MISCELLANEOUS: There are two types of cytoskeletal and
CC microfibrillar keratin, I (acidic; 40-55kDa) [K9 to K20] and II
CC (neutral to basic 56-70kDa) [K1 to K8].
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AABR03073341; -; NOT_ANNOTATED_CDS; Genomic_DNA.
CC EMBL; BC101868; AAO1869.1; -; mRNA.
CC EMBL; BK004045; DAA0479.1; -; mRNA.
CC Ensembl; ENSRNOG0000014099; Rattus norvegicus.
CC RGD; 1303044; K15.
CC InterPro; IPR001664; IF.
CC InterPro; IPR002957; Keratin_I.
CC Pfam; PF00038; Filament; 1.
CC PRINTS; PR01248; TYPE1KERATIN.
CC PROSITE; PS00226; IF; 1.
KW Coiled coil; Intermediate filament; Keratin.
FT CHAIN 1 447 Keratin, type I cytoskeletal 15.
FT /FTID=PRO_0000063659.
FT REGION 1 93 Head.
FT REGION 94 402 Rod.
FT REGION 94 129 Coil 1A.
FT REGION 130 148 Linker 1.
FT REGION 149 240 Coil 1B.
FT REGION 241 260 Linker 12.
FT REGION 261 402 Coil 2.
FT REGION 403 447 Tail.
FT COMPIAS 13 92 Gly-rich.
SQ SEQUENCE 447 AA; 48870 MW; CD16F2D55F193671 CRC64;

Query Match 52.9%; Score 46; DB 1; Length 447;
Best Local Similarity 81.8%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EITVHNLEGG 11
Db :|||:||||:
391 EISTVRLNLEGG 401

Search completed: July 5, 2006, 19:18:15
Job time : 188 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 18:44:12 ; Search time 147.667 Seconds
(without alignments)
49.540 Million cell updates/sec

Title: US-10-774-928a-3

Perfect score: 87

Sequence: 1 EIEYHNLLGGQEDF 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*
10: Geneseq2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	87	100.0	16	AAO26383	Aao26383 Psoriasis
2	87	100.0	16	ADV04408	Adv04408 Leishmani
3	87	100.0	622	ADS88365	Ads88365 Human pro
4	87	100.0	622	AEA15476	Aea15476 Human pol
5	87	100.0	622	AEb13340	Aeb13340 Mutant ke
6	75	86.2	600	ADF55631	Adf55631 Protein (
7	53	60.9	152	ABRS8600	Abrs8600 Human can
8	52.5	60.3	96	AAAM21022	Aam21022 Peptide #
9	52.5	60.3	96	ABBA43190	Abba43190 Peptide #
10	52.5	60.3	96	AAAM7030	Aam7030 Peptide #
11	52.5	60.3	96	AAAM76923	Aam76923 Human bon
12	52.5	60.3	96	ABG58585	Abg58585 Human liv
13	52.5	60.3	96	ABGA6033	Abga6033 Human pep
14	52.5	60.3	148	ABO59061	Abos9061 Human gen
15	52.5	60.3	385	ABG27716	Abg27716 Novel hum
16	52.5	60.3	417	AAE33677	Aae33677 Human str
17	47	54.0	433	ABMB1838	Abmb1838 Tumour-as
18	47	54.0	757	ABG06703	Abg06703 Novel hum
19	47	54.0	887	ABG23684	Abg23684 Novel hum
20	47	54.0	1113	ABG06702	Abg06702 Novel hum
21	46	52.9	209	ABG16549	Abg16549 Novel hum
22	46	52.9	209	ABG16692	Abg16692 Novel hum
23	46	52.9	387	AEA20209	Aea20209 Novel hum

24	46	52.9	483	7	ADF30445	Adf30445 Mouse ang
25	46	52.9	525	9	AEC57486	Aec57486 L. acidop
26	46	52.9	529	9	AEC57318	Aec57318 L. acidop
27	45.5	52.3	32	6	ABR63670	Abr63670 Human bre
28	45.5	52.3	56	8	ADP56620	Adp56620 Human bre
29	45.5	52.3	85	6	ABP76029	Abp76029 Human GEN
30	45.5	52.3	85	6	ABP76183	Abp76183 Human GEN
31	45.5	52.3	100	9	ADZ88838	Adz88838 Breast sp
32	45.5	52.3	165	4	AAG75797	Aag75797 Human col
33	45.5	52.3	194	8	ADP56616	Adp56616 Human bre
34	45.5	52.3	256	4	AAAB71659	Aab71659 Human col
35	45.5	52.3	263	8	ADP56625	Adp56625 Human bre
36	45.5	52.3	400	6	ABP55382	Abp55382 Human col
37	45.5	52.3	400	7	ADI62966	Adi62966 Human apo
38	45.5	52.3	400	7	ADI62989	Adi62989 Human apo
39	45.5	52.3	400	7	ADI62972	Adi62972 Human apo
40	45.5	52.3	400	7	ADI63032	Adi63032 Human apo
41	45.5	52.3	400	7	ADI63033	Adi63033 Human apo
42	45.5	52.3	400	7	ADI62990	Adi62990 Human apo
43	45.5	52.3	400	7	ADI63057	Adi63057 Human apo
44	45.5	52.3	400	7	ADI63010	Adi63010 Human apo
45	45.5	52.3	400	8	ADK70458	Adk70458 Respirato

ALIGNMENTS

RESULT 1
AAO26383
ID AAO26383 standard; peptide; 16 AA.
XX
AC AAO26383;
XX
DT 30-JAN-2003 (first entry)
XX
DE Psoriasis treating immunotherapeutic peptide, SEQ ID No 3.
XX
KW Antipsoriatic; immunostimulant; gene therapy; pharmaceutical composition;
KW vaccine; immunogenic variant; immunotherapeutic agent; psoriasis;
KW gene therapy.
XX
OS Leishmania sp.
XX
PN WO200274239-A2.
XX
PD 26-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006496.
XX
PR 16-MAR-2001; 2001US-00809003.
XX
(AKIV-) AKIVA LLC.
XX
O'daly JA;
XX
DR WPI; 2003-018763/01.
XX
PT New polypeptide and immunogenic variants comprising amino acid sequences
PT of particulate antigens, useful for the treatment and clinical remission
PT of psoriasis.
XX
PS Claim 1; Page 43; 56pp; English.
XX
CC The invention relates to a polypeptide comprising an isolated amino acid
CC sequence or immunogenic variants selected from any of 14 fully defined
CC sequences of 7-16 amino acids, given in the specification. The
CC immunotherapeutic agents and a pharmaceutical compositions comprising
CC polynucleotides and vectors of the invention are useful for the treatment
CC and clinical remission of psoriasis. The isolated nucleic acids are
CC useful as probes. The sequences of the invention can be used in the
CC treatment of disorders by gene therapy. This sequence represents one of
CC the 14 immunotherapeutic peptides of the invention
XX

```
SQ      Sequence 16 AA;
Query Match      100.0%; Score 87; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EIEYHNLLGGQEDF 16
      |||||
DB      1 EIEYHNLLGGQEDF 16
      |||||

RESULT 2
ADV04408
ID      ADV04408 standard; peptide; 16 AA.
XX
AC      ADV04408;
XX
DT      24-FEB-2005 (first entry)
XX
DE      Leishmania immunotherapeutic peptide SEQ ID NO:3.
XX
KW      T-lymphocyte; immunogenicity; antigen; antipsoriatic; immunostimulant;
KW      psoriasis.
XX
OS      Leishmania sp.
XX
PN      US2004241168-A1.
XX
PD      02-DEC-2004.
XX
PF      09-FEB-2004; 2004US-00774928.
XX
PR      16-MAR-2001; 2001US-00809003.
PR      17-OCT-2003; 2003US-00687892.
XX
PA      (ODAL/) ODALY J A.
PI      Odaly JA;
XX
WPI;    2005-011563/01.
XX
Inhibiting selectively T-cell rolling in human, by administering compound
interfering with cutaneous lymphocyte antigen-E selectin interaction and
leukocyte function associated antigen-1 interaction.
XX
Claim 9; SEQ ID NO 3; 21pp; English.
XX
The invention relates to a novel method for selectively inhibiting T-cell
rolling in a human host, comprising administering a compound that
selectively interferes with the cutaneous lymphocyte antigen (CLA)-E
selectin interaction and leukocyte function associated antigen (LFA)-
1/intercellular adhesion molecule (ICAM) and very late antigen
(VLA)/vascular cell adhesion molecule (VCAM) interactions. The compound
includes an immunotherapeutic agent, which comprises a purified protein
extract that is isolated by diethylaminoethyl Sephadex chromatography of
a Nonidet P-40 insoluble particulate antigen fraction derived from
isolated killed cells of amastigotes from one or more species of the
Leishmania genus, where the particulate antigen fraction is solubilized
with 8M urea and 0.025 M Tris(hydroxymethyl)aminomethane pH 8.3 applied
to diethylaminoethyl Sephadex and is eluted with a solution comprising
0.1 M sodium chloride, 8 M urea and 0.025 M
Tris(hydroxymethyl)aminomethane pH 8.3, and the purified protein extract
includes polypeptides having apparent molecular weights of 73, 80 and 82
kDa, after total reduction and alkylation. The species is L. amazonensis,
L. venezuelensis, L. brasiliensis and/or L. chagasi. A compound of the
invention has antipsoriatic and immunostimulant activity, and inhibits T-
cell rolling by interfering with CLA-E selectin interaction and LFA-
1/ICAM and VLA/VCAM interactions. The method is useful for selectively
inhibiting T-cell rolling in a human host, and for treating psoriasis.
XX
The present sequence represents an Leishmania peptide used in the
invention.
XX      Sequence 16 AA;
SQ      Sequence 622 AA;
Query Match      100.0%; Score 87; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EIEYHNLLGGQEDF 16
      |||||
DB      1 EIEYHNLLGGQEDF 16
      |||||

RESULT 3
ADS88365
ID      ADS88365 standard; protein; 622 AA.
XX
AC      ADS88365;
XX
DT      18-NOV-2004 (first entry)
XX
DE      Human protein of a TNF-alpha signalling pathway protein complex Seq 220.
XX
KW      protein complex; tumour necrosis factor-alpha signalling pathway;
KW      TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
KW      inflammatory bowel disease; infectious disease; septic shock;
KW      bacterial infection; neurological disease; stroke-induced inflammation;
KW      neurodegenerative disease; cancer; antiinflammatory; antiarthritic;
KW      antirheumatic; cytostatic; antibacterial; gene therapy; human.
XX
OS      Homo sapiens.
XX
PN      WO2004035783-A2.
XX
PD      29-APR-2004.
XX
PF      24-SEP-2003; 2003WO-EP050655.
PR      26-SEP-2002; 2002EP-00021809.
PR      10-FEB-2003; 2003EP-00100274.
XX
PA      (CELL-) CELLZONE AG.
XX
PI      Bouwmeester T, Huhse B, Bauch A, Ruffner H, Bauer A, Kuester B;
PI      Superti-Furga G, Kruse U;
XX
WPI;    2004-348460/32.
XX
New protein complex comprising at least one first and second protein of
the Tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful for
diagnosing or treating inflammation, neurological diseases, infectious
diseases or cancer.
XX
Example; SEQ ID NO 220; 1980pp; English.
XX
This invention relates to novel protein complexes of the tumour necrosis
factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to
methods for preparing these complexes comprising at least two component
proteins, as well as screening methods to identify modulators of the
pathway, which include antibodies, agonists and antagonists thereof. The
present invention describes a protein complex and kit that are useful for
diagnosing, prognosing or treating chronic inflammatory diseases such as
rheumatoid arthritis and inflammatory bowel disease; infectious diseases
such as septic shock and bacterial infections; neurodegenerative diseases
such as stroke-induced inflammation in neurons; neurodegenerative diseases
and cancer. Accordingly, these complexes can be used for the development of
pharmaceutical compositions that exhibit antiinflammatory, antiarthritic,
antirheumatic, cytostatic and antibacterial activities and can be used
for gene therapy purposes. In particular, the invention further provides
siRNA-oligonucleotides useful for inhibiting protein expression for in
vitro or cell culture assays. This polypeptide is a human protein that
can be used in combination with other proteins provided in the
specification to form novel complexes of the TNF-alpha signalling pathway
of the invention.
XX      Sequence 622 AA;
SQ
```

```
Query Match      100.0%; Score 87; DB 8; Length 622;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIETHNLLGGQEDF 16
    |||||
Db 449 EIETHNLLGGQEDF 464

RESULT 4
AEA15476
ID AEA15476 standard; protein; 622 AA.
XX
AC AEA15476;
XX
DT 28-JUL-2005 (first entry)
XX
DE Human polypeptide #95.
XX
KW Diagnosis; prognosis; cancer; breast tumor; ovary tumor; stomach tumor;
KW colon tumor; esophagus tumor; bladder tumor; non-small-cell lung cancer;
KW cytostatic; neoplasm.
XX
OS Homo sapiens.
XX
PN WO2005047534-A2.
XX
PD 26-MAY-2005.
XX
PF 15-OCT-2004; 2004WO-EP011599.
XX
PR 28-OCT-2003; 2003EP-00024565.
XX
PA (FARB ) BAYER HEALTHCARE AG.
XX
PI Wirtz R, Munnes M;
XX
WPI; 2005-372393/38.
DR N-PSDB; AEA15398.
XX
PT Predicting a response to cancer treatment by detecting at least 2
PT markers, which are genes or genomic nucleic acid sequences that are
PT located on one chromosomal region, which is altered in malignant
PT neoplasia.
XX
PS Claim 7; SEQ ID NO 438; 464pp; English.
XX
CC The invention relates to a method of predicting response to cancer
CC treatment comprising detection of at least 2 markers, where the markers
CC are genes and fragments or genomic nucleic acid sequences that are
CC located on one chromosomal region, which is altered in malignant
CC neoplasia. The invention also relates to a method for the prediction,
CC diagnosis or prognosis of malignant neoplasia, methods for detecting
CC deregulations in malignant neoplasia and breast cancer, a method of
CC determining the phenotype of a cell or tissue, a method for identifying
CC genomic regions which are altered on the chromosomal level and encode
CC genes that are linked by function and are differentially expressed in
CC malignant neoplasia and breast cancer, methods of screening for agents
CC which regulate the activity of a polypeptide or a polynucleotide and
CC antibodies that specifically bind to a full length or partial
CC polypeptide. The method is useful for predicting response to cancer
CC treatment. The methods and compositions are useful for predicting,
CC diagnosing, prognosing, preventing or treating malignant neoplasia
CC including breast cancer, ovarian cancer, gastric cancer, colon cancer,
CC esophageal cancer, mesenchymal cancer, bladder cancer or non-small-cell
CC lung cancer. This sequence represents a human polypeptide used in the
CC scope of the invention.
XX
SQ Sequence 622 AA;

Query Match      100.0%; Score 87; DB 9; Length 622;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIETHNLLGGQEDF 16
    |||||
Db 449 EIETHNLLGGQEDF 464

RESULT 5
AEB13340
ID AEB13340 standard; protein; 622 AA.
XX
AC AEB13340;
XX
DT 08-SEP-2005 (first entry)
XX
DE Mutant keratin-9 SEQ ID NO 5.
XX
KW antigen; tumor-associated antigen; diagnostic; therapeutic; tumor marker;
KW squamous cell carcinoma;
KW autoantibody-mediated identification of antigens; AMIDA; cytostatic;
KW neoplasm; cancer; skin tumor; ear, nose, throat disease; mutant;
KW keratin-9.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN WO2005061537-A2.
XX
PD 07-JUL-2005.
XX
PF 22-DEC-2004; 2004WO-EP014634.
XX
PR 22-DEC-2003; 2003DE-01060456.
XX
PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.
PA (VAEC-) VAECGENE BIOTECH GMBH.
XX
PI Gires O, Zeidler R, Muenz M, Schaffrik M;
XX
WPI; 2005-479443/48.
XX
PT Antigen for skin tumors in the nose and throat, uses at least one protein
PT from a selected sequence or their variants with a hybridized isolated
PT nucleic acid encoding the transcribed product.
XX
PS Claim 1; SEQ ID NO 5; 54pp; German.
XX
CC This invention describes the detection of novel antigens associated with
CC squamous cell carcinomas using autoantibody-mediated identification of
CC antigens (AMIDA). The invention also describes methods for producing
CC antigen-presenting cells and T cells that are specific for the antigens
CC described. The antigens can be used in a diagnostic formulation or as a
CC pharmaceutical product for therapy or as a vaccine, for diagnosis and
CC therapy of squamous cell tumors and skin tumors associated with the ear,
CC nose and throat (ENT). The tumor antigen is an improved diagnostic marker
CC for tumor identification, and is also an effective therapeutic agent.
CC This sequence represents the tumor-associated antigen corresponding to a
CC mutant keratin-9.
XX
SQ Sequence 622 AA;

Query Match      100.0%; Score 87; DB 9; Length 622;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIETHNLLGGQEDF 16
    |||||
Db 449 EIETHNLLGGQEDF 464

RESULT 6
ADF55631
ID ADF55631 standard; protein; 600 AA.
```

```

XX ADF55631;
AC
XX
XX 12-FEB-2004 (first entry)
XX
XX Protein (SEQ ID 1) related to oyster pearl keratin protein.
XX
XX pearl protein composite; PPC; mother of pearl manufacture; jewellery;
KW nanotechnology; oyster; keratin.
XX
XX Unidentified.
OS
XX
XX JP2003012696-A.
PN
XX
XX 15-JAN-2003.
PD
XX
XX 03-JUL-2001; 2001JP-00202033.
PF
XX
XX 03-JUL-2001; 2001JP-00202033.
PR
XX
XX (MATS/) MATSUSHIRO A.
PA
XX
XX WPI; 2003-451748/43.
DR
XX
XX Pearl protein composite useful in manufacture of mother of pearl,
PT comprises at least two protein components having preset molecular weight
PT as determined by sodium dodecyl sulfate gel electrophoresis.
XX
XX Example 4; SEQ ID NO 1; 25pp; Japanese.
XX
XX The invention relates to a novel pearl protein composite (PPC) comprising
CC at least two protein components as determined by sodium dodecyl sulphate
CC (SDS) gel electrophoresis. The composite of the invention may be useful
CC for the manufacture of mother of pearl for jewellery and also in
CC nanotechnology. The pearl protein composite (PPC) is effectively utilised
CC in manufacture of artificial pearls. The current sequence is that of the
CC protein (SEQ ID 1) of the invention which is related to oyster pearl
CC keratin protein and is homologous to a human keratin.
XX
XX
SQ Sequence 600 AA;
Query Match 86.2%; Score 75; DB 7; Length 600;
Best Local Similarity 87.5%; Pred. No. 0.00059;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIETHNLLGGQEDF 16
Db ||||| |||||
449 EIETHNKKGGQEDF 464

RESULT 7
ABR58600
ID ABR58600 standard; protein; 152 AA.
XX
XX ABR58600;
AC
XX
XX 09-JUL-2003 (first entry)
DT
XX
XX Human cancer related protein SEQ ID NO:257.
DE
XX
XX Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW heart disease; atherosclerosis; endometriosis.
XX
XX Homo sapiens.
OS
XX
XX WO2003025138-A2.
PN
XX
XX 27-MAR-2003.
PD
XX
XX 17-SEP-2002; 2002WO-US029560.
PF
XX
XX 17-SEP-2001; 2001US-0323469P.
PR 20-SEP-2001; 2001US-0323887P.
PR

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PR 13-NOV-2001; 2001US-0350666P.
PR 08-FEB-2002; 2002US-0355145P.
PR 08-FEB-2002; 2002US-0355257P.
PR 12-APR-2002; 2002US-0372246P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
PI Zlotnick A;
XX
XX WPI; 2003-354600/33.
DR N-PSDB; ACC72736.
XX
XX New genes that are up-regulated or down-regulated in cancers, useful as
PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT therapeutic targets for screening drugs for treating these diseases.
XX
XX Claim 12; Page 745; 767pp; English.
XX
XX The present invention describes an isolated nucleic acid molecule, which
CC comprises the sequence of any of the genes that are up-regulated or down-
CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC related gene nucleotide sequences which encode the proteins given in
CC ABR58521 to ABR58709. Also described: (1) determining the presence or
CC absence of a pathological cell in a patient; (2) an expression vector
CC comprising a nucleic acid molecule described above; (3) a host cell
CC comprising the vector; (4) an isolated polypeptide, which is encoded by
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC of (4); (6) specifically targeting a compound to a pathological cell in a
CC patient by administering to the patient the antibody above; and (7) a
CC drug screening assay. The nucleic acid is useful as diagnostic markers or
CC therapeutic targets. In particular, the nucleic acid is useful for
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC atherosclerosis and endometriosis. The nucleic acid is also useful in
CC drug screening, particularly for identifying agents for treating these
CC pathologies
XX
XX
SQ Sequence 152 AA;
Query Match 60.9%; Score 53; DB 6; Length 152;
Best Local Similarity 75.0%; Pred. No. 0.78;
Matches 12; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 1 EIETHNLL--EGQOE 14
Db ||||| || |||
129 EIETHYRLGEGGSE 144

RESULT 8
AAM21022
ID AAM21022 standard; protein; 96 AA.
XX
XX AAM21022;
AC
XX
XX 12-OCT-2001 (first entry)
DT
XX
XX Peptide #7456 encoded by probe for measuring cervical gene expression.
DE
XX
XX Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer.
XX
XX Homo sapiens.
OS
XX
XX WO200157278-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US000670.
PF
XX
XX 04-FEB-2000; 2000US-0180312P.
PR

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PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human cervical epithelial cells.
XX Claim 27; SEQ ID NO 25848; 487pp; English.
XX The present invention relates to human single exon nucleic acid probes
CC (SENP: see AA110068-AA128459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human Hela cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 96 AA;
XX Query Match 60.3%; Score 52.5; DB 4; Length 96;
XX Best Local Similarity 75.0%; Pred. No. 0.56;
XX Matches 12; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
XX QY 1 EITYHNLLEGGQEDF 16
XX ||||| ||||| |||||
XX 42 EIATYHRLLEDG-EDF 56
XX Db
XX RESULT 9
XX ABB43190
XX ID ABB43190 standard; peptide; 96 AA.
XX AC ABB43190;
XX DT 04-FEB-2002 (first entry)
XX DE Peptide #10696 encoded by human foetal liver single exon probe.
XX Human; foetal liver; gene expression; single exon nucleic acid probe.
XX Homo sapiens.
XX WO200157277-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000669.
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX
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```
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX Claim 27; SEQ ID NO 35825; 639pp + Sequence Listing; English.
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC part of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 96 AA;
XX Query Match 60.3%; Score 52.5; DB 4; Length 96;
XX Best Local Similarity 75.0%; Pred. No. 0.56;
XX Matches 12; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
XX QY 1 EITYHNLLEGGQEDF 16
XX ||||| ||||| |||||
XX 42 EIATYHRLLEDG-EDF 56
XX Db
XX RESULT 10
XX AAM37030
XX ID AAM37030 standard; protein; 96 AA.
XX AC AAM37030;
XX DT 17-OCT-2001 (first entry)
XX DE Peptide #11067 encoded by probe for measuring placental gene expression.
XX Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder.
XX Homo sapiens.
XX WO200157272-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000663.
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX Claim 27; SEQ ID NO 37299; 654pp; English.
XX The present invention relates to single exon nucleic acid probes (SENP:
CC see AA131315-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
```


KW	chronic obstructive pulmonary disease; interstitial lung disease;
KW	familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW	tuberos sclerosis; Gaucher's disease; Niemann-Pick disease;
KW	Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW	pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW	pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW	primary ciliary dyskinesia; pulmonary hypertension;
KW	hyaline membrane disease.
XX	
XX	Homo sapiens.
OS	
PN	WO200186003-A2..
XX	
XX	15-NOV-2001.
PD	
XX	
XX	30-JAN-2001; 2001WO-US000665.
XX	
PR	04-FEB-2000; 2000US-0180312P.
PR	26-MAY-2000; 2000US-0207456P.
PR	30-JUN-2000; 2000US-00608408.
PR	03-AUG-2000; 2000US-00632366.
PR	21-SEP-2000; 2000US-0234687P.
PR	27-SEP-2000; 2000US-0236359P.
PR	04-OCT-2000; 2000GB-00024263.
XX	
XX	(MOLE-) MOLECULAR DYNAMICS INC.
PA	
XX	
PI	Penn SG, Hanzel DK, Chen W, Rank DR;
XX	
XX	WPI; 2002-114183/15.
DR	
XX	
PT	Spatially-addressable set of single exon nucleic acid probes, used to
PT	measure gene expression in human lung samples.
XX	
PS	Claim 27; SEQ ID NO 35698; 634pp; English.
XX	
CC	The invention relates to a spatially-addressable set of single exon
CC	nucleic acid probes for measuring gene expression in a sample derived
CC	from human lung comprising single exon nucleic acid probes having one of
CC	12614 nucleic acid sequences mentioned in the specification, or their
CC	complements or the 12387 open reading frames derived from the 12614
CC	probes. Also included are a microarray comprising the novel set of probes
CC	; the novel set of probes which hybridise at high stringency to a nucleic
CC	acid expressed in the human lung; measuring gene expression in a sample
CC	derived from human lung, comprising (a) contacting the array with a
CC	collection of detectably labeled nucleic acids derived from human lung
CC	mRNA, and (b) measuring the label detectably bound to each probe of the
CC	array; identifying exons in a eukaryotic genome, comprising (a)
CC	algorithmically predicting at least one exon from genomic sequences of
CC	the eukaryote; and (b) detecting specific hybridisation of detectably
CC	labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC	having a fragment identical to the predicted exon, the probe is included
CC	in the above mentioned microarray; assigning exons to a single gene,
CC	comprising (a) identifying exons from genomic sequence by the method
CC	above and (b) measuring the expression of each of the exons in several
CC	tissues and/or cell types using hybridisation to a single exon
CC	microarrays having a probe with the exon, where a common pattern of
CC	expression of the exons in the tissues and/or cell types indicates that
CC	the exons should be assigned to a single gene; a peptide comprising one
CC	of 12011 sequences, mentioned in the specification, or encoded by the
CC	probes/open reading frames (ORF). The probes are used for gene expression
CC	analysis, and for identifying exons in a gene, particularly using human
CC	lung derived mRNA and for the study of lung diseases such as asthma, lung
CC	cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC	disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC	tuberos sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC	Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC	histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC	Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC	dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC	present sequence is a peptide/protein encoded by a single exon probe of
CC	the invention. Note: The sequence data for this patent did not form part
CC	of the printed specification, but was obtained in electronic format

CC	directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 96 AA;
	Query Match 60.3%; Score 52.5; DB 5; Length 96;
	Best Local Similarity 75.0%; Pred. No. 0.56; 3; Indels 1;
	Matches 12; Conservative 0; Mismatches
QY	1 EIETHNLLGGQEDF 16
DB	42 EIATYHRLLEDG-EDF 56
RESULT 14	
ABO59061	ID ABO59061 standard; protein; 148 AA.
XX	
AC	ABO59061;
XX	
DT	29-JUL-2004 (first entry)
XX	
DE	Human genome derived single exon protein #5295.
XX	
KW	Human; gene expression; single exon probe; microarray;
KW	alternative splicing event; genomic alteration.
XX	
OS	Homo sapiens.
XX	
PN	US2003194704-A1.
XX	
PD	16-OCT-2003.
XX	
PF	03-APR-2002; 2002US-00029386.
XX	
PR	03-APR-2002; 2002US-00029386.
XX	
PA	(PENN/) PENN S G.
PA	(RANK/) RANK D R.
PA	(HANZ/) HANZEL D K.
XX	
PI	Penn SG, Rank DR, Hanzel DK;
XX	
DR	WPI; 2004-119264/12.
XX	
PT	New human genome-derived single exon nucleic acid probes useful
PT	gene expression analysis, for identifying or characterizing al
PT	splicing events, for assessing genomic alterations or as tools
XX	surveying tissues.
XX	
PS	Claim 45; SEQ ID NO 32695; 80pp; English.
XX	
CC	The invention relates to a nucleic acid probe for measuring hum
CC	expression, comprising any of the 27,400 fully defined nucleot
CC	sequences in the specification, or their complements or fragmen
CC	encoding at least 8 amino acids of any of the 6888 amino acid
CC	fully defined in the specification. The probe is a single exon
CC	hybridises under high stringency conditions to a nucleic acid
CC	expressed in human cells or tissues. Also included are a spat
CC	addressable set of single exon nucleic acid probes for measuri
CC	gene expression (comprising a plurality of single exon nucleic
CC	probes cited above, where each of the plurality of probes is s
CC	and addressably isolatable or amplifiable from the plurality),
CC	exon microarray for measuring human gene expression, a method
CC	measuring human gene expression a vector comprising the single
CC	probe cited above, an ORF-encoded peptide comprising at least
CC	contiguous amino acids of any of the above-mentioned amino ac
CC	sequences (optionally with conservative amino acid substitution
CC	isolated antibody that binds specifically to a peptide cited ab
CC	methods of selling and/or licensing single exon probes or micro
CC	a customer desiring to measure gene expression, a method of pro
CC	human gene expression data by subscription, and a computer-read
CC	storage medium which contains a database having a plurality of
CC	(each record including data on the expression of a single exon

CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterizing
 CC alternative splicing events, in detecting and characterizing gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe protein of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704
 XX

SQ Sequence 148 AA;

Query Match 60.3%; Score 52.5; DB 8; Length 148;
 Best Local Similarity 75.0%; Pred. No. 0.93;
 Matches 12; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 EIETVHNLEGGQEDF 16

||| ||| ||| ||| ||| ||| |||

Db 101 EITTYHRLLEDG-EDF 115

RESULT 15

ABG27716

ID ABG27716 standard; protein; 385 AA.

XX

AC ABG27716;

XX

DT 18-FEB-2002 (first entry)

XX

DE Novel human diagnostic protein #27707.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX

OS Homo sapiens.

XX

FN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

XX

PR 23-AUG-2000; 2000US-00649167.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;

XX

XX WPI; 2001-639362/73.

DR

DR N-PSDB; AAS91903.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX

PS Claim 20; SEQ ID NO 58075; 103pp; English.

XX

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 385 AA;

Query Match 60.3%; Score 52.5; DB 4; Length 385;

Best Local Similarity 75.0%; Pred. No. 2.9;

Matches 12; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 EIETVHNLEGGQEDF 16

||| ||| ||| ||| ||| ||| |||

Db 337 EITTYHRLLEDG-EDF 351

Search completed: July 5, 2006, 19:08:51

Job time : 149.667 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 20:52:16 ; Search time 84.6667 Seconds
(without alignments)
87.537 Million cell updates/sec

Title: US-10-774-928A-3

Perfect score: 87

Sequence: 1 E1ETHNLLGGQEDF 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /EMC_Celerra_SID33/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SID33/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SID33/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SID33/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	16	5	US-10-774-928-3
2	52.5	60.3	96	3	US-09-864-761-47444
3	52.5	60.3	148	4	US-10-029-386-32695
4	52.5	60.3	385	5	US-10-450-763-58075
5	52.5	60.3	417	5	US-10-479-764-11
6	47	54.0	294	4	US-10-424-599-253404
7	47	54.0	757	5	US-10-450-763-37062
8	47	54.0	887	5	US-10-450-763-54043
9	47	54.0	1113	5	US-10-450-763-37061
10	46	52.9	209	5	US-10-450-763-46908
11	46	52.9	209	5	US-10-450-763-47051
12	46	52.9	483	4	US-10-316-253-8
13	45.5	52.3	85	5	US-10-475-075-236
14	45.5	52.3	85	5	US-10-475-075-509
15	45.5	52.3	165	4	US-10-106-698-6571
16	45.5	52.3	256	3	US-09-997-003-36
17	45.5	52.3	400	3	US-09-922-217-1115
18	45.5	52.3	400	4	US-10-025-380-1115
19	45.5	52.3	400	4	US-10-734-564-118
20	45.5	52.3	400	5	US-10-733-969A-33
21	45.5	52.3	400	6	US-11-108-172-1115
22	45.5	52.3	428	5	US-10-450-763-40382
23	45	51.7	1184	4	US-10-437-963-183853
24	45	51.7	7465	6	US-11-087-099-7521
25	44.5	51.1	130	5	US-10-450-763-44463
26	44.5	51.1	130	5	US-10-450-763-44564
27	44.5	51.1	130	5	US-10-450-763-44828

28 44.5 51.1 130 5 US-10-450-763-48987 Sequence 48987, A
29 44.5 51.1 232 3 US-09-919-497-78 Sequence 78, Appl
30 44.5 51.1 332 5 US-10-450-763-49052 Sequence 49052, A
31 44.5 51.1 359 5 US-10-883-020-6 Sequence 6, Appli
32 44.5 51.1 364 5 US-10-450-763-58076 Sequence 58076, A
33 44.5 51.1 375 4 US-10-080-334-268 Sequence 268, App
34 44.5 51.1 423 4 US-10-080-334-269 Sequence 269, App
35 44.5 51.1 423 5 US-10-514-932-2 Sequence 2, Appli
36 44.5 51.1 424 4 US-10-080-334-266 Sequence 266, App
37 44.5 51.1 429 5 US-10-883-020-2 Sequence 2, Appli
38 44.5 51.1 430 3 US-09-919-039-105 Sequence 105, App
39 44.5 51.1 430 3 US-09-813-432-36 Sequence 36, Appli
40 44.5 51.1 430 4 US-10-026-001-1 Sequence 1, Appli
41 44.5 51.1 430 4 US-10-060-036-155 Sequence 155, App
42 44.5 51.1 430 4 US-10-174-364-36 Sequence 36, Appl
43 44.5 51.1 430 4 US-10-080-334-265 Sequence 265, App
44 44.5 51.1 430 4 US-10-080-334-267 Sequence 267, App
45 44.5 51.1 430 4 US-10-246-583-36 Sequence 36, Appl

ALIGNMENTS

RESULT 1

US-10-774-928-3
; Sequence 3, Application US/10774928

; Publication No. US20040241168A1
; GENERAL INFORMATION:

; APPLICANT: O'Daly, Jose

; TITLE OF INVENTION: Psoriasis

; FILE REFERENCE: 302178

; CURRENT APPLICATION NUMBER: US/10/774,928

; CURRENT FILING DATE: 2004-02-09

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 3

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Leishmania

US-10-774-928-3

Query Match 100.0%; Score 87; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 E1ETHNLLGGQEDF 16
|||
Db 1 E1ETHNLLGGQEDF 16

RESULT 2

US-09-864-761-47444

; Sequence 47444, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aemica-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

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; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47444
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008739.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.56
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.5
; OTHER INFORMATION: SWISSPROT HIT: P05783, EVALUE 1.00e-39
; OTHER INFORMATION: EST_HUMAN HIT: AA829451.1, EVALUE 7.00e-39
US-09-864-761-47444

Query Match      60.3%; Score 52.5; DB 3; Length 96;
Best Local Similarity 75.0%; Pred. No. 1.3;
Matches 12; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 BIETVHNLGGQEDF 16
DB 42 EIATVHRLLEDG-EDF 56

RESULT 3
US-10-029-386-32695
; Sequence 32695, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32695
; LENGTH: 148
; TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC000094.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.7
; OTHER INFORMATION: SWISSPROT HIT: P05783, EVALUE 1.00e-57
US-10-029-386-32695

Query Match      60.3%; Score 52.5; DB 4; Length 148;
Best Local Similarity 75.0%; Pred. No. 2;
Matches 12; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 BIETVHNLGGQEDF 16
DB 101 EITVHRLLEDG-EDF 115

RESULT 4
US-10-450-763-58075
; Sequence 58075, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790C1F3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-05-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 58075
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (306)..(353)
; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL00226D, p-value=8.535e-26, raw score of 19.10
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (169)..(352)
; OTHER INFORMATION: Intermediate filament proteins domain identified by Pfam,
; OTHER INFORMATION: accession name filament, E-value=5.5e-46, Pfam score of 166.2
US-10-450-763-58075

Query Match      60.3%; Score 52.5; DB 5; Length 385;
Best Local Similarity 75.0%; Pred. No. 5.5;
Matches 12; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 BIETVHNLGGQEDF 16
DB 337 EITVHRLLEDG-EDF 351

RESULT 5
US-10-479-764-11
; Sequence 11, Application US/10479764
; Publication No. US20050027103A1
; GENERAL INFORMATION:
; APPLICANT: TANG, Y. TOM; WARREN, Bridget A.;
; APPLICANT: HONCHELL, Cynthia D.; RICHARDSON, Thomas W.;
; APPLICANT: ELLIOTT, Vicki S.; CHAWLA, Narinder K.;
; APPLICANT: YUE, Henry; BATRA, Sajeev;
; APPLICANT: GRIFFIN, Jennifer A.; BAUGHN, Mariah R.;
```


; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 54043
; LENGTH: 887
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (547)..(567)
; OTHER INFORMATION: kw ALLERGEN POLLEN CIM1 HOL-II domain identified by eMATRIX,
; OTHER INFORMATION: accession number DM01724, p-value=8.091e-11, raw score of 8.14
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (84)..(857)
; OTHER INFORMATION: Intermediate filament proteins domain identified by Pfam,
; OTHER INFORMATION: accession name filament, E-value=2e-247, Pfam score of 835.4
US-10-450-763-54043

Query Match 54.0%; Score 47; DB 5; Length 887;
Best Local Similarity 81.8%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIETHNLLLEG 11
||| ||| ||| |||
Db 394 EITVHRLLEG 404

RESULT 9

US-10-450-763-37061
; Sequence 37061, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 37061
; LENGTH: 1113
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1004)..(1024)
; OTHER INFORMATION: kw ALLERGEN POLLEN CIM1 HOL-II domain identified by eMATRIX,
; OTHER INFORMATION: accession number DM01724, p-value=3.045e-11, raw score of 8.14
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (84)..(1104)
; OTHER INFORMATION: Intermediate filament proteins domain identified by Pfam,
; OTHER INFORMATION: accession name filament, E-value=3.3e-277, Pfam score of 934.3
US-10-450-763-37061

Query Match 54.0%; Score 47; DB 5; Length 1113;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIETHNLLLEG 11
||| ||| ||| |||
Db 394 EITVHRLLEG 404

RESULT 10

US-10-450-763-46908

; Sequence 46908, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 46908
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (124)..(171)
; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL00226D, p-value=3.250e-25, raw score of 19.10
US-10-450-763-46908

Query Match 52.9%; Score 46; DB 5; Length 209;
Best Local Similarity 64.3%; Pred. No. 33;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIETHNLLLEGQ 14
||| ||| ||| |||
Db 155 EITVHCLLEDGKD 168

RESULT 11

US-10-450-763-47051
; Sequence 47051, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 47051
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (124)..(171)
; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL00226D, p-value=3.250e-25, raw score of 19.10
US-10-450-763-47051

Query Match 52.9%; Score 46; DB 5; Length 209;
Best Local Similarity 64.3%; Pred. No. 33;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIETHNLLLEGQ 14

Db 155 EITVHCLLEDGKD 168

US-10-450-763-47051

Query Match 52.9%; Score 46; DB 5; Length 209;
Best Local Similarity 64.3%; Pred. No. 33;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIETHNLEGGQE 14
||| ||| ||| ||| ::
Db 155 EITTHCLLEDGKD 168

RESULT 12

US-10-316-253-8
; Sequence 8, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-316-253-8

Query Match 52.9%; Score 46; DB 4; Length 483;
Best Local Similarity 64.3%; Pred. No. 80;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIETHNLEGGQE 14
||| ||| ||| ||| :
Db 418 EITTHRLLEDGSDQ 431

RESULT 13

US-10-475-075-236
; Sequence 236, Application US/10475075
; Publication No. US2006003498A1
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
; FILE REFERENCE: G-081US03PCT
; CURRENT APPLICATION NUMBER: US/10/475,075
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/IB01/00914
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 918
; SOFTWARE: Patent.pm
; SEQ ID NO 236
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -32..-1
US-10-475-075-236

Query Match 52.3%; Score 45.5; DB 5; Length 85;
Best Local Similarity 73.3%; Pred. No. 15;

Matches 11; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 EIETHNLEGGQE 15
||| ||| ||| ||| |||
Db 61 EIATYRSLLLE-GQED 74

RESULT 14

US-10-475-075-509
; Sequence 509, Application US/10475075
; Publication No. US20060053498A1
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
; FILE REFERENCE: G-081US03PCT
; CURRENT APPLICATION NUMBER: US/10/475,075
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/IB01/00914
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 918
; SOFTWARE: Patent.pm
; SEQ ID NO 509
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -32..-1
US-10-475-075-509

Query Match 52.3%; Score 45.5; DB 5; Length 85;

Best Local Similarity 73.3%; Pred. No. 15;
Matches 11; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 EIETHNLEGGQE 15
||| ||| ||| ||| |||
Db 61 EIATYRSLLLE-GQED 74

RESULT 15

US-10-106-698-6571
; Sequence 6571, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: Patent in Ver. 3.0
; SEQ ID NO 6571
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (4)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (6)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE

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; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC FEATURE
; LOCATION: (22)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC FEATURE
; LOCATION: (25)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6571
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Query Match      52.3%; Score 45.5; DB 4; Length 165;
Best Local Similarity 73.3%; Pred. No. 31;
Matches 11; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
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Qy      1 EIETHNLLGGQED 15
         ||||:|||||
Db      141 EIATYRSLLE-QQED 154
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Search completed: July 5, 2006, 20:57:19
Job time : 85.6667 secs
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 20:53:13 ; Search time 7.3333 Seconds
(without alignments)
58.543 Million cell updates/sec

Title: US-10-774-928A-3

Perfect score: 87

Sequence: 1 EIETHNLLGGQEDF 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 112942

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pap.*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pap.*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45.5	52.3	400	7	US-11-105-233-182
2	44.5	51.1	430	7	US-11-105-233-181
3	42	48.3	209	7	US-11-274-634-19
4	42	48.3	422	7	US-11-105-233-176
5	40	46.0	172	7	US-11-293-697-4778
6	40	46.0	356	6	US-10-953-349-38914
7	40	46.0	356	7	US-11-174-307B-4934
8	40	46.0	358	6	US-10-953-349-38913
9	40	46.0	491	7	US-11-293-697-4603
10	40	46.0	586	6	US-10-505-928-314
11	40	46.0	977	6	US-10-449-902-50081
12	39	44.8	356	6	US-10-953-349-24114
13	39	44.8	403	7	US-11-270-040-2
14	39	44.8	423	6	US-10-953-349-24113
15	39	44.8	424	7	US-11-105-233-183
16	39	44.8	443	6	US-10-953-349-24112
17	39	44.8	450	7	US-11-293-697-4090
18	39	44.8	466	7	US-11-289-102-289
19	39	44.8	469	6	US-10-505-928-457
20	39	44.8	483	7	US-11-105-233-180
21	39	44.8	520	7	US-11-293-697-3712
22	39	44.8	551	7	US-11-270-040-4
23	39	44.8	864	6	US-10-449-902-41176
24	38	43.7	91	6	US-10-953-349-29533
25	38	43.7	151	6	US-10-953-349-29532

26 38 43.7 254 6 US-10-449-902-33071 Sequence 33071, A
27 38 43.7 309 7 US-11-178-538-55 Sequence 55, Appl
28 38 43.7 309 7 US-11-178-538-62 Sequence 62, Appl
29 38 43.7 319 6 US-10-953-349-16459 Sequence 16459, A
30 38 43.7 386 6 US-10-953-349-16458 Sequence 16458, A
31 38 43.7 390 6 US-10-953-349-16457 Sequence 16457, A
32 38 43.7 557 7 US-11-233-089-46 Sequence 46, Appl
33 38 43.7 578 6 US-10-449-902-43188 Sequence 43188, A
34 38 43.7 599 6 US-10-449-902-49534 Sequence 49534, A
35 38 43.7 929 7 US-11-165-586-55 Sequence 55, Appl
36 38 43.7 2937 6 US-10-480-962-18 Sequence 18, Appl
37 38 43.7 2969 6 US-10-480-962-19 Sequence 19, Appl
38 37 42.5 195 6 US-10-449-902-43488 Sequence 43488, A
39 37 42.5 339 6 US-10-449-902-45912 Sequence 45912, A
40 37 42.5 339 6 US-10-449-902-29389 Sequence 29389, A
41 37 42.5 401 6 US-10-449-902-32420 Sequence 32420, A
42 37 42.5 504 6 US-10-449-902-56324 Sequence 56324, A
43 37 42.5 504 6 US-10-449-902-33553 Sequence 33553, A
44 37 42.5 827 6 US-10-449-902-56545 Sequence 56545, A
45 37 42.5 845 6 US-10-449-902-54753 Sequence 54753, A

ALIGNMENTS

RESULT 1
US-11-105-233-182
; Sequence 182, Application US/11105233
; Publication No. US20060134653A1
; GENERAL INFORMATION:
; APPLICANT: Thiagalingam et al
; TITLE OF INVENTION: Differential Expression of Genes in MSI
; FILE REFERENCE: 1657/2001
; CURRENT APPLICATION NUMBER: US/11/105,233
; CURRENT FILING DATE: 2005-04-13
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-233-182

Query Match 52.3%; Score 45.5; DB 7; Length 400;
Best Local Similarity 73.3%; Pred. No. 2.9;
Matches 11; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 EIETHNLLGGQED 15
DB 376 EIATYRSLLG-QED 389

RESULT 2
US-11-105-233-181
; Sequence 181, Application US/11105233
; Publication No. US20060134653A1
; GENERAL INFORMATION:
; APPLICANT: Thiagalingam et al
; TITLE OF INVENTION: Differential Expression of Genes in MSI
; FILE REFERENCE: 1657/2001
; CURRENT APPLICATION NUMBER: US/11/105,233
; CURRENT FILING DATE: 2005-04-13
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 181
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-233-181

Query Match 51.1%; Score 44.5; DB 7; Length 430;

```

Best Local Similarity 68.8%; Pred.No. 4.7;
Matches 11; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy      1 EIETHNLLGGQEDF 16
      ||||| |||||
Db      376 EIATYRLLDGG-EDF 390

RESULT 3
US-11-274-634-19
; Sequence 19, Application US/11274634
; Publication No. US20060134658A1
; GENERAL INFORMATION:
; APPLICANT: MARKOWITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
; FILE REFERENCE: CWRU-P02-044
; CURRENT APPLICATION NUMBER: US/11/274,634
; CURRENT FILING DATE: 2005-11-14
; PRIOR APPLICATION NUMBER: 10/650,112
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 10/274,177
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 10/229,345
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/406,296
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 11/041,788
; PRIOR FILING DATE: 2005-01-21
; PRIOR APPLICATION NUMBER: 10/649,591
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 10/087,080
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/272,206
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/281,149
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/284,555
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-274-634-19

Query Match      48.3%; Score 42; DB 7; Length 209;
Best Local Similarity 64.3%; Pred.No. 5.6;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 EIETHNLLGGQGE 14
      ||||| |||||
Db      154 EITTYRLLGESE 167

RESULT 4
US-11-105-233-176
; Sequence 176, Application US/11105233
; Publication No. US20060134653A1
; GENERAL INFORMATION:
; APPLICANT: Thiagalingam et al
; TITLE OF INVENTION: Differential Expression of Genes in MSI
; FILE REFERENCE: Tumors
; FILE REFERENCE: 1657/2001
; CURRENT APPLICATION NUMBER: US/11/105,233
; CURRENT FILING DATE: 2005-04-13
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-233-176

```



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US-10-449-902-50081
; Sequence 50081, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50081
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-50081

Query Match          46.0%; Score 40; DB 6; Length 977;
Best Local Similarity 70.0%; Pred. No. 67;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IETVHNLLGG 11
   :|:|:|:|:|
Db 255 LELYNNLLGG 264

RESULT 12
US-10-953-349-24114
; Sequence 24114, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24114
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-24114

Query Match          44.8%; Score 39; DB 6; Length 356;
Best Local Similarity 70.0%; Pred. No. 33;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 TVHNLGGQ 13
   |:|:|:|:|
Db 334 TINNLGGQ 343

RESULT 13
US-11-270-040-2
; Sequence 2, Application US/11270040
; Publication No. US20060110762A1
; GENERAL INFORMATION:
; APPLICANT: Kapil, Sanjay
; APPLICANT: Kim, Jeong-Ki
; TITLE OF INVENTION: PORCINE REPRODUCTIVE AND RESPIRATORY
; FILE REFERENCE: 14337/004001
; CURRENT APPLICATION NUMBER: US/11/270,040
; CURRENT FILING DATE: 2005-11-09
; ;
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US-10-449-902-50081
; PRIOR APPLICATION NUMBER: 60/680,297
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/626,788
; PRIOR FILING DATE: 2004-11-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Sus scrofa
US-11-270-040-2

Query Match          44.8%; Score 39; DB 7; Length 403;
Best Local Similarity 72.7%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIETHNLLGG 11
   |||:|:|:|
Db 266 EIATYRKLLGG 276

RESULT 14
US-10-953-349-24113
; Sequence 24113, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24113
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-24113

Query Match          44.8%; Score 39; DB 6; Length 423;
Best Local Similarity 70.0%; Pred. No. 39;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 TYHNLGGQ 13
   |:|:|:|:|
Db 401 TINNLGGQ 410

RESULT 15
US-11-105-233-183
; Sequence 183, Application US/11105233
; Publication No. US20060134653A1
; GENERAL INFORMATION:
; APPLICANT: Thigalingam et al
; TITLE OF INVENTION: Differential Expression of Genes in MSI
; FILE REFERENCE: 1657/2001
; CURRENT APPLICATION NUMBER: US/11/105,233
; CURRENT FILING DATE: 2005-04-13
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 183
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-233-183

Query Match          44.8%; Score 39; DB 7; Length 424;
Best Local Similarity 72.7%; Pred. No. 39;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIETHNLLGG 11
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Db || || || || ||
 366 E1ATYRELLEG 376

Search completed: July 5, 2006, 20:57:47
Job time : 7.33333 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 5, 2006, 19:24:38 ; Search time 28.3333 Seconds
(without alignments)
49.429 Million cell updates/sec

Title: US-10-774-928A-3

Perfect score: 87
Sequence: 1 EIETHNLLGGQEDF 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SID33/ptodata/2/iaa/5 COMB.pap:*
- 2: /EMC_Celerra_SID33/ptodata/2/iaa/6 COMB.pap:*
- 3: /EMC_Celerra_SID33/ptodata/2/iaa/7 COMB.pap:*
- 4: /EMC_Celerra_SID33/ptodata/2/iaa/H COMB.pap:*
- 5: /EMC_Celerra_SID33/ptodata/2/iaa/PCTUS COMB.pap:*
- 6: /EMC_Celerra_SID33/ptodata/2/iaa/RE COMB.pap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	100.0	16	US-09-809-003A-3	Sequence 3, Appli
2	45.5	52.3	400	US-07-730-953-2	Sequence 2, Appli
3	45.5	52.3	442	US-09-949-016-8625	Sequence 8625, Ap
4	44.5	51.1	232	US-09-919-497-78	Sequence 78, Appl
5	44.5	51.1	430	US-09-919-039-105	Sequence 105, App
6	44.5	51.1	447	US-09-949-016-11032	Sequence 11032, A
7	44	50.6	728	US-08-475-844-5	Sequence 5, Appli
8	44	50.6	728	PCT-US95-08429-5	Sequence 5, Appli
9	43	49.4	323	US-09-248-796A-24078	Sequence 24078, A
10	43	49.4	593	US-09-538-092-919	Sequence 919, App
11	43	49.4	911	US-08-928-692-59	Sequence 59, Appl
12	43	49.4	911	US-09-339-972-59	Sequence 59, Appl
13	43	49.4	916	US-08-928-692-58	Sequence 58, Appl
14	43	49.4	916	US-09-339-972-58	Sequence 58, Appl
15	42	48.3	422	US-09-067-351-3	Sequence 3, Appli
16	42	48.3	422	US-09-360-490-3	Sequence 3, Appli
17	42	48.3	428	US-09-248-796A-14834	Sequence 14834, A
18	41	47.1	235	US-09-620-405B-487	Sequence 487, App
19	41	47.1	235	US-09-604-287A-487	Sequence 487, App
20	41	47.1	235	US-09-834-759-487	Sequence 487, App
21	41	47.1	235	US-10-076-622-487	Sequence 487, App
22	41	47.1	235	US-10-124-805-487	Sequence 487, App
23	41	47.1	274	US-09-949-016-9095	Sequence 9095, App
24	41	47.1	335	US-09-810-506-2	Sequence 2, Appli
25	41	47.1	493	US-09-949-016-6203	Sequence 6203, Ap
26	41	47.1	505	US-09-620-405B-478	Sequence 478, App

27	41	47.1	505	2	US-09-620-405B-485	Sequence 485, App
28	41	47.1	505	2	US-09-604-287A-478	Sequence 478, App
29	41	47.1	505	2	US-09-604-287A-485	Sequence 485, App
30	41	47.1	505	2	US-09-834-759-478	Sequence 478, App
31	41	47.1	505	2	US-09-834-759-485	Sequence 485, App
32	41	47.1	505	2	US-09-590-751A-478	Sequence 478, App
33	41	47.1	505	2	US-09-551-621A-478	Sequence 478, App
34	41	47.1	505	2	US-09-551-621A-478	Sequence 478, App
35	41	47.1	505	2	US-10-076-622-485	Sequence 485, App
36	41	47.1	505	2	US-10-076-622-485	Sequence 485, App
37	41	47.1	505	2	US-10-124-805-478	Sequence 478, App
38	41	47.1	505	2	US-10-124-805-485	Sequence 485, App
39	41	47.1	615	1	US-08-484-105-6	Sequence 6, Appli
40	41	47.1	615	1	US-08-484-105-6	Sequence 6, Appli
41	40.5	46.6	634	2	US-10-164-595-69	Sequence 69, Appl
42	40.5	46.6	725	2	US-10-164-595-30	Sequence 30, Appl
43	40.5	46.6	1031	2	US-09-914-259-24	Sequence 24, Appl
44	40	46.0	185	2	US-09-543-681A-6449	Sequence 6449, Ap
45	40	46.0	251	2	US-09-252-991A-32188	Sequence 32188, A

ALIGNMENTS

RESULT 1

US-09-809-003A-3
; Sequence 3, Application US/09809003A
; Patent No. 6673351

; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose

; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 302178

; CURRENT APPLICATION NUMBER: US/09/809,003A
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 16

; TYPE: PRT
; ORGANISM: Leishmania

US-09-809-003A-3

Query Match 100.0%; Score 87; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIETHNLLGGQEDF 16
DB 1 EIETHNLLGGQEDF 16

RESULT 2

US-07-730-953-2
; Sequence 2, Application US/07730953
; Patent No. 5286614

; GENERAL INFORMATION:
; APPLICANT: BODENMULLER, Heinz

; APPLICANT: DESSAUER, Andreas
; TITLE OF INVENTION: METHOD FOR THE DETECTION OF MALIGNANT

; TITLE OF INVENTION: DISEASES
; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram

; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington

; STATE: D.C.
; COUNTRY: U.S.A.

; ZIP: 20005-5701
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/07/730,953
; FILING DATE: 19910723
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 39 42 999.7
; FILING DATE: 21-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitts, Monica C.
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P564-1119
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 400 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-730-953-2

Query Match 52.3%; Score 45.5; DB 1; Length 400;
Best Local Similarity 73.3%; Pred. No. 19;
Matches 11; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 EIETHNLLGGQED 15
||| :||| ||||
Db 376 EIATYRSLLG-QED 389

RESULT 3
US-09-949-016-8625
; Sequence 8625, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8625
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8625

Query Match 52.3%; Score 45.5; DB 2; Length 442;
Best Local Similarity 73.3%; Pred. No. 21;
Matches 11; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 EIETHNLLGGQED 15
||| :||| ||||
Db 418 EIATYRSLLG-QED 431

RESULT 4
US-09-919-497-78
; Sequence 78, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER

; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 78
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-78

Query Match 51.1%; Score 44.5; DB 2; Length 232;
Best Local Similarity 68.8%; Pred. No. 15;
Matches 11; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 EIETHNLLGGQEDF 16
||| :||| ||||
Db 178 EIATYRRLLEDG-EDF 192

RESULT 5
US-09-919-039-105
; Sequence 105, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 105
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. 6727066 1272969CD1
US-09-919-039-105

Query Match 51.1%; Score 44.5; DB 2; Length 430;
Best Local Similarity 68.8%; Pred. No. 30;
Matches 11; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 EIETHNLLGGQEDF 16
||| :||| ||||
Db 376 EIATYRRLLEDG-EDF 390

RESULT 6
US-09-949-016-11032
; Sequence 11032, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11032
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11032

Query Match 51.1%; Score 44.5; DB 2; Length 447;
Best Local Similarity 68.8%; Pred. No. 31;
Matches 11; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 EIETHNLLGGQEDF 16
||| ||| ||| ||| |||

Db 393 EIATYRLLLEDG-EDF 407

RESULT 7

US-08-475-844-5
; Sequence 5, Application US/08475844
; Patent No. 5972643

GENERAL INFORMATION:

; APPLICANT: Lobanenkov, Victor V.
; APPLICANT: Neiman, Paul E.
; APPLICANT: Klenova, Elena M.
; APPLICANT: Goodwin, Graham H.
; APPLICANT: Filippova, Galina N.
; APPLICANT: Collins, Steven J.
; TITLE OF INVENTION: CTCF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,844
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,680
FILING DATE: 17-JUN-1994

CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14538A-11-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:
LENGTH: 728 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-475-844-5

Query Match 50.6%; Score 44; DB 1; Length 728;
Best Local Similarity 60.0%; Pred. No. 65;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIETHNLLGGQED 15
| : ||| ||| |||

Db 21 ERKTYQRREGGQED 35

RESULT 8

PCT-US95-08429-5
; Sequence 5, Application PC/TUS9508429
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: CTCF
; NUMBER OF SEQUENCES: 21
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08429
FILING DATE: 15-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/261,680
FILING DATE: 17-JUN-1994

CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14538A-11-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 728 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

PCT-US95-08429-5

Query Match 50.6%; Score 44; DB 5; Length 728;
Best Local Similarity 60.0%; Pred. No. 65;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14538A-11-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 728 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

PCT-US95-08429-5

QY 1 EIETHNLLGGQED 15
| : ||| ||| |||

Db 21 ERKTYQRREGGQED 35

RESULT 9

US-09-248-796A-24078
; Sequence 24078, Application US/09248796A
; Patent No. 6747137

GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 24078
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Candida albicans

US-09-248-796A-24078

Query Match 49.4%; Score 43; DB 2; Length 323;
Best Local Similarity 53.8%; Pred. No. 39;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 ETYHNLLGGQED 15
: ||| | ||| :

Db 229 KTYHOWLNGKKE 241

```
RESULT 10
US-09-538-092-919
; Sequence 919, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Manefield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 919
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P13645
US-09-538-092-919

Query Match      49.4%; Score 43; DB 2; Length 593;
Best Local Similarity 72.7%; Pred. No. 76;
Matches      8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RIETVHNLEG 11
Db      445 EIQYRSLEGG 455

RESULT 11
US-08-928-692-59
; Sequence 59, Application US/08928692
; Patent No. 5958727
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Yaver, Deborah S.
; APPLICANT: Lamsa, Michael
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958727o No. 5958727disk of No. 5958727th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,692
; FILING DATE: 12-SEPT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/928,692
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 59:
; LENGTH: 911 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6323002e
US-09-339-972-59

Query Match      49.4%; Score 43; DB 2; Length 911;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches      8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      5 YHNLEGGQEDF 16
Db      171 YRNDLEGGSEEF 182

RESULT 12
US-09-339-972-59
; Sequence 59, Application US/09339972
; Patent No. 6323002
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Yaver, Deborah S.
; APPLICANT: Lamsa, Michael
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6323002o No. 6323002disk of No. 6323002th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/339,972
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/928,692
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 59:
; LENGTH: 911 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6323002e
US-09-339-972-59

Query Match      49.4%; Score 43; DB 2; Length 911;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches      8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      5 YHNLEGGQEDF 16
Db      171 YRNDLEGGSEEF 182
```

RESULT 13
US-08-928-692-58
; Sequence 58, Application US/08928692
; Patent No. 5958727
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Yaver, Deborah S.
; APPLICANT: Lamsa, Michael
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; TITLE OF INVENTION: a Polypeptide
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958727o No. 5958727disk of No. 5958727th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,692
; FILING DATE: 12-SEPT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 916 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5958727e
US-08-928-692-58
Query Match 49.4%; Score 43; DB 1; Length 916;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 5 YNNLLEGGQEDF 16
Db 176 YRNDLEGGSEEF 187
RESULT 14
US-09-339-972-58
; Sequence 58, Application US/09339972
; Patent No. 6323002
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Yaver, Deborah S.
; APPLICANT: Lamsa, Michael
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; TITLE OF INVENTION: a Polypeptide
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6323002o No. 6323002disk of No. 6323002th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,351
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0511 US
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422 amino acids

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/339,972
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/928,692
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 916 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6323002e
US-09-339-972-58
Query Match 49.4%; Score 43; DB 2; Length 916;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 5 YNNLLEGGQEDF 16
Db 176 YRNDLEGGSEEF 187
RESULT 15
US-09-067-351-3
; Sequence 3, Application US/09067351
; Patent No. 5994081
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN KERATINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,351
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0511 US
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422 amino acids

```

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRSTNOT07
; CLONE: 2124178
US-09-067-351-3

Query Match      48.3%; Score 42; DB 1; Length 422;
Best Local Similarity 64.3%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 EIETYHNLLEGQE 14
          |||||
Db      367 EITTYRLLGESE 380

```

Search completed: July 5, 2006, 19:26:43
Job time : 29.3333 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 19:09:18 ; Search time 10.9223 Seconds
(without alignments)
79.283 Million cell updates/sec

Title: US-10-774-928A-4

Perfect score: 45

Sequence: 1 AQVEDAIQK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*

1: Pirl:*

2: Pirl2:*

3: Pirl3:*

4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	82.2	785	2 AB1582	MutS protein (MutS)
2	35	77.8	174	2 S39790	male-enhanced anti
3	35	77.8	174	2 B34421	male-enhanced anti
4	35	77.8	185	2 A34421	male-enhanced anti
5	35	77.8	401	2 A96941	hypothetical prote
6	35	77.8	449	2 G87789	protein C34G6.7 li
7	35	77.8	785	2 AH1228	MutS protein (MutS)
8	35	77.8	875	2 S70115	ZiP1 protein - yea
9	35	77.8	2327	2 T31733	hypothetical prote
10	34	75.6	416	2 T37196	hypothetical prote
11	33	73.3	142	2 T28386	hypothetical prote
12	33	73.3	356	2 T27172	hypothetical prote
13	33	73.3	477	2 A49937	50k outer membrane
14	33	73.3	485	2 F83593	outer membrane pro
15	33	73.3	591	2 T03602	probable asparagin
16	33	73.3	708	2 T18779	transposase contai
17	33	73.3	854	2 S02003	neurofilament trip
18	33	73.3	908	2 C70168	DNA polymerase I (
19	33	73.3	1072	1 A37221	neurofilament trip
20	33	73.3	1087	1 QFM5H	neurofilament trip
21	32	71.1	98	2 D64005	hypothetical prote
22	32	71.1	105	2 T10152	hypothetical prote
23	32	71.1	173	2 JC5982	preylated protein
24	32	71.1	182	2 C75220	hypothetical prote
25	32	71.1	195	2 F71202	hypothetical prote
26	32	71.1	227	2 D86631	transposase of IS1
27	32	71.1	227	2 G86704	transposase of IS1
28	32	71.1	246	2 E97161	conserved membrane
29	32	71.1	272	2 C86642	transposase of IS1

30	32	71.1	272	2 C86884	transposase of IS1
31	32	71.1	272	2 D86671	transposase of IS1
32	32	71.1	293	2 T37465	probable prolyl am
33	32	71.1	370	2 A25004	keratin, 53K type
34	32	71.1	381	2 A69689	response regulator
35	32	71.1	387	2 T47632	hypothetical prote
36	32	71.1	411	2 T01471	hypothetical prote
37	32	71.1	461	2 A43782	keratin, type II -
38	32	71.1	512	2 T20350	hypothetical prote
39	32	71.1	629	2 A29666	keratin, 65K type
40	32	71.1	629	2 S42629	keratin K3 - rabbi
41	32	71.1	631	2 E71933	hypothetical prote
42	32	71.1	784	2 H64487	eIF-4A family prob
43	32	71.1	843	2 T13334	probable tail-host
44	32	71.1	1154	2 T15650	hypothetical prote
45	32	71.1	1168	2 T15890	hypothetical prote

ALIGNMENTS

RESULT 1

AB1582

MutS protein (MutS2) homolog lin1195 [imported] - Listeria innocua (strain Clip11262)

C:Species: Listeria innocua

C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004

C/Accession: AB1582

R/Glauser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.,

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat

ok, C.; Schlueter, T.; Simoes, N.; Tietz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A/Title: Comparative genomics of Listeria species.

A/Reference number: AB1077; MUID:21537279; PMID:11679669

A/Accession: AB1582

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-785 <GLA>

A/Cross-references: UNIPROT:Q92CH6; UNIPARC:UPI000012FA23; GB:AL592022; PIDN:CAC96426.1;

A/Experimental source: strain Clip11262

C/Genetics:

A/Gene: lin1195

C/Supfamily: DNA mismatch repair protein, bacterial/plant types

Query Match 82.2%; Score 37; DB 2; Length 785;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYEDAIQK 9

DB 716 RYEDAIQK 723

RESULT 2

S39790

male-enhanced antigen - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 19-May-1994 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

C/Accession: S39790

R/Kondo, M.; Sato, S.; Sutou, S.

Biochim. Biophys. Acta 1216, 483-486, 1993

A/Title: Cloning and sequence analysis of cDNA encoding the bovine testis-derived male-e-

A/Reference number: S39790; MUID:94092744; PMID:8268232

A/Accession: S39790

A/Molecule type: mRNA

A/Residues: 1-174 <KON>

A/Cross-references: UNIPROT:Q29407; UNIPARC:UPI000012EE9F; EMBL:DI7340; MUID:9560052; PIDN:

A/Note: it is uncertain whether Met-1 or Met-11 is the initiator

Query Match 77.8%; Score 35; DB 2; Length 174;
Best Local Similarity 66.7%; Pred. No. 8.7;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDAIQK 9
|:|:|:|:
Db 154 AQWEDVQK 162

RESULT 3
B34421
male-enhanced antigen - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Jun-1990 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
C:Accession: B34421
R: Lau, Y.F.C.; Chan, K.; Sparkes, R.
Proc. Natl. Acad. Sci. U.S.A. 86, 8462-8466, 1989
A:Title: Male-enhanced antigen gene is phylogenetically conserved and expressed at late
A:Reference number: A34421; MUID:90046817; PMID:2813404
A:Accession: B34421
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-174 <LAU>
A:CROSS-References: UNIPROT:Q64327; UNIPARC:UPI0000001930; GB:M27938; NID:gl187507; PIDN:
A:Note: the authors translated the codon GCA for residue 31 as Ser, and ACA for residue

Query Match 77.8%; Score 35; DB 2; Length 174;
Best Local Similarity 66.7%; Pred. No. 8.7;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDAIQK 9
|:|:|:|:
Db 154 AQWEDVQK 162

RESULT 4
A34421
male-enhanced antigen - human
C:Species: Homo sapiens (man)
C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 09-Jul-2004
C:Accession: A34421
R: Lau, Y.F.C.; Chan, K.; Sparkes, R.
Proc. Natl. Acad. Sci. U.S.A. 86, 8462-8466, 1989
A:Title: Male-enhanced antigen gene is phylogenetically conserved and expressed at late
A:Reference number: A34421; MUID:90046817; PMID:2813404
A:Accession: A34421
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-185 <LAU>
A:CROSS-References: UNIPROT:Q9BV01; UNIPARC:UPI000007291B; GB:M27937; NID:gl187507; PIDN:

Query Match 77.8%; Score 35; DB 2; Length 185;
Best Local Similarity 66.7%; Pred. No. 9.3;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDAIQK 9
|:|:|:|:
Db 165 AQWEDVQK 173

RESULT 5
A96941
hypothetical protein CAC0335 [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: A96941
R: Nolling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: A96941
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-401 <KUR>
A:CROSS-References: UNIPROT:Q97M63; UNIPARC:UPI00000C9E2B; GB:AE001437; PIDN:AAK78316.1;

A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC0335

Query Match 77.8%; Score 35; DB 2; Length 401;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQYEDAIQK 9
|:|:|:|:
Db 290 AEFEDAIEK 298

RESULT 6
G87789
protein C34G6.7 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G87789
R: anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_eleg
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: G87789
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-449 <STO>
A:CROSS-References: UNIPROT:O01498; UNIPARC:UPI000017A544; GB:chr_I; PIDN:AABS2480.1; PII
A:Note: contains similarity to an SH3 domain
C:Genetics:
A:Gene: C34G6.7
A:Map position: 1

Query Match 77.8%; Score 35; DB 2; Length 449;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDAIQK 9
|:|:|:|:
Db 357 ALYDDAIQK 365

RESULT 7
AH1228
MutS protein (MutS2) homolog lmo1232 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
C:Accession: AH1228
R: Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Krest, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1228
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-785 <GLA>
A:CROSS-References: UNIPROT:Q8Y7P1; UNIPARC:UPI000005509F; GB:NC_003210; PIDN:CAC99310.1;
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo1232
C:Superfamily: DNA mismatch repair protein, bacterial/plant types

Query Match 77.8%; Score 35; DB 2; Length 785;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYEDAIQK 9

Db 716 RYEDALQK 723
:||||:|

RESULT 8
S70115
N;Alternate names: protein D9819.9; protein YDR285w
C;Species: Saccharomyces cerevisiae
C;Date: 24-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: S70115; A45173; S30868
R;Fulton, L.
submitted to the EMBL Data Library, May 1996
A;Description: The sequence of *S. cerevisiae* cosmid 9819.
A;Reference number: S70115
A;Accession: S70115
A;Molecule type: DNA
A;Residues: 1-875 <FUL>
A;Cross-references: UNIPROT:P31111; UNIPARC:UPI0000013C3E2; EMBL:U51031; NID:gl332635; PI
R;Sym^m M.; Engbrecht, J.A.; Roeder, G.S.
Cell 72, 365-378, 1993
A;Title: Zif1 is a synaptonemal complex protein required for meiotic chromosome synapsis
A;Reference number: A45173; MUID:93161412; PMID:7916652
A;Accession: A45173
A;Molecule type: DNA
A;Residues: 1-54, 'A', 56-875 <SYM>
A;Cross-references: UNIPARC:UPI00000168FB9; EMBL:L06487; NID:gl73240; PIDN:AAA35239.1; PI
A;Note: sequence extracted from NCBI backbone (NCBIP:124844)
C;Genetics:
A;Gene: SGD:ZIF1
A;Cross-references: SGD:S0002693; MIPS:YDR285w
A;Map position: 4R

Query Match 77.8%; Score 35; DB 2; Length 875;
Best Local Similarity 66.7%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDAIQK 9
|||||:|
Db 529 AQYEDLVKK 537

RESULT 9
T31733
hypothetical protein T05C3.2 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 03-Nov-2003
C;Accession: T31733
R;Blanchard, M.; Bradshaw, H.; Kramer, J.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of *C. elegans* cosmid T05C3.
A;Reference number: Z21076
A;Accession: T31733
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2327 <BLA>
A;Cross-references: UNIPARC:UPI000017BB60; EMBL:AF016428; PIDN:AAB65359.1; GSPDB:GN00023
A;Experimental source: strain Bristol N2; clone T05C3
C;Genetics:
A;Gene: CESP:T05C3.2
A;Map position: 5
A;Introns: 4/1; 45/2; 77/1; 130/3; 184/2; 283/3; 388/1; 431/1; 492/1; 549/1; 645/3; 678/
1771/1; 1835/3; 1897/3; 2008/2; 2094/3; 2150/3; 2198/3; 2238/1; 2325/2
C;Superfamily: phospholipase D, chodopox type

Query Match 77.8%; Score 35; DB 2; Length 2327;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDAIQK 8
|||||
Db 1475 ADYEDAIQ 1482

RESULT 10
T37196

hypothetical protein F49D11.4 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37196
R;Hinds, K.; Graves, T.; Duckels, G.; Ozersky, P.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of *C. elegans* cosmid F49D11.
A;Reference number: Z21632
A;Accession: T37196
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-416 <HIN>
A;Cross-references: UNIPROT:O44723; UNIPARC:UPI000005C8F6; EMBL:AF039711; PIDN:AAB96710.1
C;Genetics:
A;Map position: 1
A;Introns: 189/1; 282/3; 372/1
A;Note: F49D11.4

Query Match 75.6%; Score 34; DB 2; Length 416;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDAIQK 9
|||||:|
Db 349 ANYEALQK 357

RESULT 11
T28386

hypothetical protein 225 - *Melanoplus sanguinipes entomopoxvirus*
C;Species: *Melanoplus sanguinipes entomopoxvirus*
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T28386
R;Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A;Title: The genome of *Melanoplus sanguinipes entomopoxvirus*.
A;Reference number: Z20484; MUID:99102612; PMID:9847359
A;Accession: T28386
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-142 <AFO>
A;Cross-references: UNIPROT:Q9YVL7; UNIPARC:UPI00000F658C; EMBL:AF063866; NID:g4049647; I
C;Genetics:
A;Note: MSV225

C;Superfamily: *Melanoplus sanguinipes entomopoxvirus* hypothetical protein 225

Query Match 73.3%; Score 33; DB 2; Length 142;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYEDAIQ 8
|||||:|
Db 84 QYEDAIQ 90

RESULT 12
T27172

hypothetical protein Y54G11A.8 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27172
R;Wallis, J.
submitted to the EMBL Data Library, December 1998

A;Reference number: Z20322
A;Accession: T27172
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-396 <WIL>
A;Cross-references: UNIPROT:Q9XW00; UNIPARC:UPI00000753C5; EMBL:AL034488; NID:e1359895; I
A;Experimental source: clone Y54G11A

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 18:28:56 ; Search time 92.0971 Seconds
(without alignments)

90.395 Million cell updates/sec

Title: US-10-774-928A-4

Perfect score: 45

Sequence: 1 AQYEDAIQK 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	82.2	785	1 MUTS2_LISIN	Q92ch6 listeria in
2	36	80.0	484	2 Q9F1L5_ARATH	Q9fil5 arabidopsis
3	36	80.0	559	2 Q8GZW0_ARATH	Q8gwz0 arabidopsis
4	36	80.0	681	1 AC0XZ2_RAT	P97562 r acyl-coen
5	36	80.0	788	2 Q5E2X9_VIBF1	Q5e2x9 vibrio fisc
6	35	77.8	131	2 Q9S387_LISMO	Q9s387 listeria mo
7	35	77.8	172	1 MEAL_HUMAN	Q16626 homo sapien
8	35	77.8	173	2 Q4R952_MACFA	Q4r952 macaca fasc
9	35	77.8	174	1 MEAL_BOVIN	Q29407 bos taurus
10	35	77.8	174	1 MEAL_MOUSE	Q64327 mus musculus
11	35	77.8	174	2 Q3T097_BOVIN	Q3t097 bos taurus
12	35	77.8	174	2 Q5FVH7_RAT	Q5fvh7 rattus norv
13	35	77.8	174	2 Q793G4_MOUSE	Q793g4 m male-enha
14	35	77.8	174	2 Q9DQO0_MOUSE	Q9dqo0 mus musculus
15	35	77.8	174	2 Q9DB93_MOUSE	Q9db93 mus musculus
16	35	77.8	258	2 Q8SW28_ENCCU	Q8sw28 encephalito
17	35	77.8	378	1 CAAL_BUEBA	Q6mkw4 bdellovibri
18	35	77.8	397	2 Q8I7I2_CABEL	Q8i7i2 caenorhabdi
19	35	77.8	401	2 Q97M63_CLOAB	Q97m63 clostridium
20	35	77.8	457	2 Q01498_CABEL	Q01498 caenorhabdi
21	35	77.8	594	2 Q3UV17_MOUSE	Q3uv17 mus musculus
22	35	77.8	607	2 Q6BIU4_DEBHA	Q6biu4 debaryomyce
23	35	77.8	678	2 Q90WB4_BRARE	Q90wb4 brachydanio
24	35	77.8	681	1 AC0XZ2_MOUSE	Q9qxd1 m acyl-coen
25	35	77.8	681	2 Q3UNF3_MOUSE	Q3unf3 mus musculus
26	35	77.8	681	2 Q8VCH0_MOUSE	Q8vch0 mus musculus
27	35	77.8	752	2 Q6LXF6_METMP	Q6lxf6 methanococc
28	35	77.8	762	2 Q90XS6_BRARE	Q90xs6 brachydanio
29	35	77.8	768	2 Q2T154_PECOC	Q2t154 pectobacter
30	35	77.8	768	2 Q6D3F4_ERWCT	Q6d3f4 erwinia car
31	35	77.8	785	1 MUTS2_LISMF	Q720j7 listeria mo

RESULT 1

ID	MUTS2_LISIN	STANDARD;	PRT;	785 AA.
AC	Q92CH6;			
DT	27-MAY-2002,	integrated into UniProtKB/Swiss-Prot.		
DT	01-DEC-2001,	sequence version 1.		
DT	07-MAR-2006,	entry version 23.		
DE	MutS2 protein.			
GN	Name=MutS2; OrderedLocusNames=lin1195;			
OS	Listeria innocua.			
OC	Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.			
OX	NCBI_TaxID=1642;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=CLIP 11262 / Serovar 6a;			
RX	MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;			
RA	Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,			
RA	Baquerio F., Berche P., Bloeker H., Brandt P., Chakraborty T.,			
RA	Charbit A., Chetoui F., Couve E., de Daruvar A., Dehoux P.,			
RA	Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,			
RA	Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,			
RA	Gautier L., Gobel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,			
RA	Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurapkat G.,			
RA	Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,			
RA	Nordiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,			
RA	Rommel B., Rose M., Schlueter T., Simoes N., Tierrez A.,			
RA	Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;			
RT	"Comparative genomics of Listeria species.";			
RL	Science 294:849-852(2001).			
CC	-!- FUNCTION: Not known.			
CC	-!- SIMILARITY: Belongs to the DNA mismatch repair mutS family.			
CC	-!- SIMILARITY: Contains 1 Smr domain.			
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NoDerivs License			
DR	EMBL; AL596167; CAC96426.1; -; Genomic_DNA.			
DR	PIR; AB1582; AB1582.			
DR	HSSP; Q56215; LEWR.			
DR	GenomeReviews; AL592022_GR; lin1195.			
DR	ListiList; LIN01195; -;			
DR	BioCyc; LINN1642:LIN1195-MONOMER; -;			
DR	HAMAP; MF_00092; -; 1.			
DR	InterPro; IPR005747; MutS2.			
DR	InterPro; IPR000432; MutS C.			
DR	InterPro; IPR007696; MutS III.			
DR	InterPro; IPR002625; Smr/MutS2_C.			
DR	Pfam; PF00488; MutS_V; 1.			
DR	Pfam; PF01713; Smr; 1.			
DR	PIRSP; PIRSF005814; MutS_ysd; 1.			
DR	ProDom; PD001263; MutS_C; 1.			
DR	SMART; SM00534; MUTSAC; 1.			
DR	SMART; SM00533; MUTSD; 1.			
DR	SMART; SM00463; SMR; 1.			

32	35	77.8	785	1	MUTS2_LISMO	Q8y7p1 listeria mo
33	35	77.8	785	2	Q4EEU4_LISMO	Q4eeu4 listeria mo
34	35	77.8	785	2	Q4ENE4_LISMO	Q4ene4 listeria mo
35	35	77.8	875	1	Z1P1_YEAST	P31111 saccharomyc
36	35	77.8	893	2	Q6NUY7_BRARE	Q6nuy7 brachydanio
37	35	77.8	893	2	Q7SZR3_BRARE	Q7szr3 brachydanio
38	35	77.8	918	2	Q54DV3_DICDI	Q54dv3 dictyosteli
39	35	77.8	1392	2	Q3VFA6_9SPHN	Q3vfa6 sphingopyxi
40	35	77.8	1729	2	Q61KG0_CABER	Q61kg0 caenorhabdi
41	35	77.8	1735	2	O16302_CABEL	O16302 caenorhabdi
42	35	77.8	4421	2	Q4RK60_TETNG	Q4rk60 tetraodon n
43	34	75.6	101	2	Q8DBR4_VIBVU	Q8db4 vibrio vuln
44	34	75.6	124	2	Q5NGF8_FRATT	Q5ngf8 franciella
45	34	75.6	155	2	Q7VP20_HAEDU	Q7vp20 haemophilus

ALIGNMENTS

TIGRFAMS; TIGR01069; mutS2; 1.
 DR PROSITE: PS00486; DNA MISMATCH_REPAIR_2; 1.
 DR PROSITE: PS00828; SMR; 1.
 KW ATP-binding; Complete proteome; DNA-binding; Nucleotide-binding.
 FT CHAIN 1 785 /FTID-PRO_0000115224.
 FT FT 710 785 Smr.
 FT NP BIND 335 342 ATP (Potential).
 SQ SEQUENCE 785 AA; 86679 MW; E5548422FB87CA17 CRC64;

Query Match 82.2%; Score 37; DB 1; Length 785;
 Best Local Similarity 87.5%; Pred. No. 1.9e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYEDAIQK 9
 DB 716 RYEDAIQK 723

RESULT 2

Q3FIL5 ARATH PRELIMINARY; PRT; 484 AA.
 ID Q3FIL5 ARATH PRELIMINARY; PRT; 484 AA.
 AC Q3FIL5;
 DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 12.
 DE Gb|AAB92637.1 (AT5G58960/k19m22_160).
 GN OrderedLocustNames=AT5G58960;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99156233; PubMed=10048488; DOI=10.1093/dnares/5.6.379;
 RA Asanizu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5, VIII.
 RT Sequence features of the regions of 1,081,958 bp covered by seventeen
 RT physically assigned P1 and TAC clones.";
 RL DNA Res. 5:379-391(1998).
 RN [2]

NUCLEOTIDE SEQUENCE.
 RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Banh J., Bowser L.,
 RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
 RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

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 CC -----
 DR EMBL; AB016885; BAB09639.1; -; Genomic DNA.
 DR EMBL; AY075634; AAL91642.1; -; mRNA.
 DR EMBL; BT002623; AAO11539.1; -; mRNA.
 DR TAIR; AT5G58960; -;
 DR InterPro; IPR006943; DUF641_pln.
 DR Pfam; PF04859; DUF641; 1.
 SQ SEQUENCE 484 AA; 54071 MW; FDCEFE146D40782F CRC64;

Query Match 80.0%; Score 36; DB 2; Length 484;
 Best Local Similarity 75.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYEDAIQK 9
 DB 53 QYEDALEK 60

RESULT 3

Q8GWZ0 ARATH PRELIMINARY; PRT; 559 AA.
 ID Q8GWZ0 ARATH PRELIMINARY; PRT; 559 AA.
 AC Q8GWZ0;
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 8.
 DE Hypothetical protein At5G58960/k19m22_160.
 GN Name=At5G58960/k19m22_160;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
 RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
 RA Hayashizaki Y., Shinozaki K.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; AK118548; BAC43150.1; -; mRNA.
 DR InterPro; IPR006943; DUF641_pln.
 DR Pfam; PF04859; DUF641; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 559 AA; 62668 MW; 3C0FCAE17FD0F801 CRC64;

Query Match 80.0%; Score 36; DB 2; Length 559;
 Best Local Similarity 75.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYEDAIQK 9
 DB 128 QYEDALEK 135

RESULT 4

ACOX2 RAT STANDARD; PRT; 681 AA.
 ID ACOX2 RAT STANDARD; PRT; 681 AA.
 AC P97562;
 DT 02-NOV-2001, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAY-1997, sequence version 1.
 DT 07-MAR-2006, entry version 41.
 DE Acyl-coenzyme A oxidase 2, peroxisomal (EC 1.17.99.3) (3-alpha,7-
 DE alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (3-
 DE alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase).
 DE (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase).
 GN Name=Acox2; Synonyms=Thcox;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Rodentia; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA], PROTEIN SEQUENCE OF 27-33; 74-83; 128-137;
 RP 265-270; 328-336; 454-464 AND 656-667, AND FUNCTION.
 RC TISSUE=Liver;
 RX MEDLINE=97103103; PubMed=8947475;
 RA Baumgart E., Vanhooren J.C.T., Franssen M., Van Leuven F., Fahimi H.D.,
 RA Van Veldhoven P.P., Mannaerts G.P.;


```

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=EGD;
RA Borovok I., Mislovati M., Cohen G., Aharonowitz Y.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=EGD;
RA Borovok I., Aharonowitz Y., Cohen G.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=EGD;
RA Borovok I.A.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AJ133006; CAB40814.2; -; Genomic_DNA.
DR InterPro; IPR002625; Smr/MutS2_C.
DR Pfam; PF01713; Smr; 1.
DR SMART; SM00463; Smr; 1.
DR PROSITE; PS50828; Smr; 1.
FT NON TER 1
SQ SEQUENCE 131 AA; 14481 MW; 7C401C6035798066 CRC64;

Query Match 77.8%; Score 35; DB 2; Length 131;
Best Local Similarity 75.0%; Pred. No. 73;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QVEDAIQK 9
DB 62 RYEDALQK 69
:|||||:
:|||||:

RESULT 7
MEAL HUMAN
ID MEAL STANDARD; PRT; 172 AA.
AC Q16626; QSTC36; Q9BV01.
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997, sequence version 1.
DT 07-FEB-2006, entry version 34.
DE Male-enhanced antigen 1 (Mea-1).
GN Name=MEAL; Synonyms=MEA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [RNA].
RC TISSUE=Testis;
RX MEDLINE=90046817; PubMed=2813404;
RA Lau Y.-F.C., Chan K., Sparkes R.S.;
RT "Male-enhanced antigen gene is phylogenetically conserved and
RT expressed at late stages of spermatogenesis.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8462-8466(1989).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) system donor
RT vector.";
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;
RA Murgall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,
RA Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,
RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,
RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,
RA Babbage A.K., Bagguley C.L., Bailey J., Banerjee R., Barker D.J.,

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RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,
RA Burford D.C., Burrill W., Burton J., Carder C., Carter N.P.,
RA Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Cobley V.,
RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,
RA Culley K.M., Dhani P., Davies J., Dunn M., Earthrowl M.E.,
RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,
RA Frankland J., French L., Garner P., Garnett J., Ghori M.J.,
RA Gibby L.M., Gillson C.J., Glithero R.J., Grafham D.V., Grant M.,
RA Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Hallis K.S.,
RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcote R.,
RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,
RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,
RA Maslen G.L., Mathews L., McCann O.T., McLaren S.J., McIlroy K.,
RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,
RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,
RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,
RA Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Seagle S.M.,
RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L.,
RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,
RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,
RA Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,
RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
RA Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.;
RT "The DNA sequence and analysis of human chromosome 6.";
RN Nature 425:805-811(2003).
[4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May play an important role in spermatogenesis and/or
CC testis development.
CC -!- INTERACTION:
CC P63010:AP2B1; NbExp=1; IntAct=EBI-744921; EBI-432924;
CC -!- TISSUE SPECIFICITY: Highly expressed in testis.
CC -!- CAUTION: Was originally thought to be the H-Y antigen.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-11 is the initiator.
CC -----
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CC -----
DR EMBL; M27937; AAA36208.1; ALT_INIT; mRNA.
DR EMBL; L10400; AAA36209.1; ALT_INIT; mRNA.
DR EMBL; BT009831; AAP88833.1; ALT_INIT; mRNA.
DR EMBL; AL136304; CAI19794.1; -; Genomic DNA.
DR EMBL; BC001754; AAH01754.1; ALT_INIT; mRNA.
DR PIR; A34421; A34421.
DR IntAct; Q16626; ...
DR Ensembl; ENSG00000124733; Homo sapiens.

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DR H-InvDB; HIX0005890; -.
DR HGNC; HGNC:6986; MEAL.
DR MIM; 143170; Gene.
DR LinkHub; Q16626; -.
DR GO; GO:0008584; P:male gonad development; TAS.
DR GO; GO:0007283; P:spermatogenesis; TAS.
DR InterPro; IPR009685; MEAL.
DR PANTHER; PTHR17005; MEAL; 1.
DR Pfam; PF06910; MEAL; 1.
DR CHAIN 1 172
KW Developmental protein; Differentiation; Spermatogenesis.
FT Male-enhanced antigen 1.
FT /FTid=PRO 0000096341.
SQ SEQUENCE 172 AA; 18544 MW; 9342AFAD2C96FF25 CRC64;

Query Match 77.8%; Score 35; DB 1; Length 172;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQVEDAIQK 9
Db 152 AQWEDVVQK 160

RESULT 8
Q4R992_MACFA PRELIMINARY; PRT; 173 AA.
AC Q4R992;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 5.
DE Testis cDNA clone: Q5A-10511, similar to human male-enhanced antigen (MEAL).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15944441; DOI=10.1093/molbev/msi187;
RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen C.-K.J., Wu C.I., Hashimoto K.;
RT "Substitution Rate and Structural Divergence of 5'UTR Evolution:
RT Comparative Analysis Between Human and Cynomolgus Monkey cDNAs.";
RL Mol. Biol. Evol. 22:1976-1982(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG International consortium for macaque cDNA sequencing and analysis;
RT "DNA sequences of macaque genes expressed in brain or testis and its
RT evolutionary implications.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC
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CC
CC EMBL; AB168204; BAE00329.1; -; mRNA.
DR GO; GO:0007283; P:spermatogenesis; IEA.
DR InterPro; IPR009685; MEAL.
DR PANTHER; PTHR17005; MEAL; 1.
DR Pfam; PF06910; MEAL; 1.
SQ SEQUENCE 173 AA; 18641 MW; 8B048AB82C0F4E3E CRC64;

Query Match 77.8%; Score 35; DB 2; Length 173;
Best Local Similarity 66.7%; Pred. No. 99;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQVEDAIQK 9
Db 153 AQWEDVVQK 161

RESULT 9
MEAL_BOVIN
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ID MEAL_BOVIN STANDARD; PRT; 174 AA.
AC Q29407;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE Male-enhanced antigen 1 (Mea-1).
GN Name=MEAL; Synonyms=MEA;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX TISSUE=Testis;
RX MEDLINE=94092744; PubMed=8268232; DOI=10.1016/0167-4781(93)90019-A;
RA Kondo M., Sato S., Sutoh S.;
RT "Cloning and sequence analysis of cDNA encoding the bovine testis-
RT derived male-enhanced antigen (Mea).";
RL Biochim. Biophys. Acta 1216:483-486(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=97063437; PubMed=8907304;
RA Kondo M., Terouchi S., Tsukasa N., Sato S., Ishida N., Sutoh S.;
RT "Genomic sequence analysis of the bovine male-enhanced antigen-1 (Mea-
RT 1) and differential localization of its transcripts and products
RT during spermatogenesis.";
RL DNA Seq. 6:75-85(1996).
CC -!- FUNCTION: May play an important role in spermatogenesis and/or
CC testis development.
CC -!- TISSUE SPECIFICITY: Highly expressed in testis. Transcripts can be
CC found in primary and secondary spermatocytes, and spermatids, but
CC the protein itself is only detected in spermatids. No expression
CC in Leydig cells, spermatogonia, or sperm. Very weak expression in
CC the heart, kidney, spleen, thymus and ovary.
CC -!- DEVELOPMENTAL STAGE: Expressed in the stages from 8-cell embryos
CC to hatched blastocysts.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-11 is the initiator.
CC
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CC
CC EMBL; D17340; BAA04158.1; -; mRNA.
DR EMBL; D30811; BAA06488.1; -; Genomic DNA.
DR PIR; S39790; S39790.
DR InterPro; IPR009685; MEAL.
DR PANTHER; PTHR17005; MEAL; 1.
DR Pfam; PF06910; MEAL; 1.
KW Developmental protein; Differentiation; Spermatogenesis.
FT Male-enhanced antigen 1.
FT CHAIN 1 174 /FTid=PRO 0000096340.
SQ SEQUENCE 174 AA; 18751 MW; E0E7CE95C0CB3530 CRC64;

Query Match 77.8%; Score 35; DB 1; Length 174;
Best Local Similarity 66.7%; Pred. No. 99;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQVEDAIQK 9
Db 154 AQWEDVVQK 162

RESULT 10
MEAL_MOUSE STANDARD; PRT; 174 AA.
AC Q64327;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997, sequence version 1.
DT 07-FEB-2006, entry version 33.
DE Male-enhanced antigen 1 (Mea-1).
GN Name=Meal; Synonyms=Mea;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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ID Q5FVH7_RAT PRELIMINARY; PRT; 174 AA.
AC Q5FVH7;
DT 01-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2005, sequence version 1.
DE 07-FEB-2006, entry version 7.
DE Hypothetical protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeng B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Director MGC Project;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC089978; AAH89978.1; -; mRNA.
DR GO; GO:0007283; P:spexmatogenesis; IEA.
DR InterPro; IPR009685; MEAL.
DR PANTHER; PTHR17005; MEAL; 1.
DR Pfam; PF06910; MEAL; 1.
KW Hypothetical protein.
SQ SEQUENCE 174 AA; 18584 MW; C3B16361635B176F CRC64;
Query Match 77.8%; Score 35; DB 2; Length 174;
Best Local Similarity 66.7%; Pred. No. 99;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 AQVEDAIQK 9
||:|:|:
Db 154 AQWEDVVQK 162
RESULT 13
Q793G4_MOUSE PRELIMINARY; PRT; 174 AA.
ID Q793G4_MOUSE
AC Q793G4;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 10.
DE Male-enhanced antigen-1 (Adult male cerebellum cDNA, RIKEN full-length
DE enriched library, clone:1500038006 product:male enhanced antigen 1,
DE full insert sequence) (Adult male small intestine cDNA, RIKEN full-
DE length enriched library, clone:2010011M24 product:male enhanced
DE antigen 1, full insert sequence) (Adult male small intestine cDNA,

DE RIKEN full-length enriched library, clone:2010103G23 product:male
DE enhanced antigen 1, full insert sequence) (13 days embryo liver cDNA,
DE RIKEN full-length enriched library, clone:2500003F22 product:MALE-
DE ENHANCED ANTIGEN-1 (MEA-1) homolog) (13 days embryo liver cDNA, RIKEN
DE full-length enriched library, clone:2510004F20 product:MALE-ENHANCED
DE ANTIGEN-1 (MEA-1) homolog) (13 days embryo liver cDNA, RIKEN full-
DE length enriched library, clone:2510012G06 product:MALE-ENHANCED
DE ANTIGEN-1 (MEA-1) homolog) (11 days embryo whole body cDNA, RIKEN
DE full-length enriched library, clone:2700096H08 product:male enhanced
DE antigen 1, full insert sequence).
GN Name=Meal; Synonyms=meal;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129SvJ;
RX MEDLINE=22330726; PubMed=12444059; DOI=10.1095/biolreprod.101.002550;
RA Ohinata Y., Sutou S., Kondo M., Takahashi T., Mitsui Y.;
RT "Male-enhanced antigen-1 gene flanked by two overlapping genes is
RL expressed in late spermatogenesis.";
RL Biol. Reprod. 67:1824-1831(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, Liver, Small intestine, and Whole
RC body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, Liver, Small intestine, and Whole
RC body;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilmong L.G., Aldin J.E., Allen J.E.,
RA Ambesi-Imbimbato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA Di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemmgis T., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottaugli-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Inamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shitaki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,

RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [4]
 RC NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, Liver, Small intestine, and Whole
 RC body;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [5]
 RC NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, Liver, Small intestine, and Whole
 RC body;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Bruscia V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Nunata K., Okido T., Pavan W.J., Pertele G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyszyn-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hitzane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [6]
 RC NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, Liver, Small intestine, and Whole
 RC body;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant H.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa T.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyszyn-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [7]
 RC NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum, Liver, Small intestine, and Whole
 RC body;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [8]
 RC NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, Liver, Small intestine, and Whole
 RC body;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [9]
 RC NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, Liver, Small intestine, and Whole
 RC body;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RL -----
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AB074009; BAB91440.1; -; Genomic DNA.
 Query Match 77.8%; Score 35; DB 2; Length 174;
 Best Local Similarity 66.7%; Pred. No. 99;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AQVEDAIQK 9
 Db 154 AQMEDVQX 162
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 AC Q9D0Q0;
 DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2001, sequence version 1.
 DT 07-FEB-2006, entry version 19.
 DE 10 days embryo whole body cDNA, RIKEN full-length enriched library,
 DE clone:2600013A18 product:hypothetical protein, full insert sequence.
 GN Name=Meal;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

- RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [2]
- RC NUCLEOTIDE SEQUENCE.
RX STRAIN=C57BL/6J; TISSUE=Whole body;
RA PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
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RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
- RC NUCLEOTIDE SEQUENCE.
RX STRAIN=C57BL/6J; TISSUE=Whole body;
RA PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
- RC NUCLEOTIDE SEQUENCE.
RX STRAIN=C57BL/6J; TISSUE=Whole body;
RA MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Negami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
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RA Konoaga A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numa K., Okido T., Pavan W.J., Perte G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
- RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
- RC NUCLEOTIDE SEQUENCE.
RX STRAIN=C57BL/6J; TISSUE=Whole body;
RA MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Klei Schmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bono M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Monbaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
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- RC NUCLEOTIDE SEQUENCE.
RX STRAIN=C57BL/6J; TISSUE=Whole body;
RA MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
- RC NUCLEOTIDE SEQUENCE.
RX STRAIN=C57BL/6J; TISSUE=Whole body;
RA MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishida T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
- RC NUCLEOTIDE SEQUENCE.
RX STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito K., Saito R., Sakai K., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: AK01189; BAB27454.1; -; mRNA.
DR Ensembl: ENSMUSG0000002768; Mus musculus.
DR MGI: MG1:96957; Mea1.
DR GO: GO:0005737; C:cytoplasm; IDA.
DR InterPro: IPR009685; MEAL1.
DR PANTHER: PTHR17005; MEAL1.
DR Pfam: PF06910; MEAL1.
DR KW Hypothetical protein.
SQ SEQUENCE 174 AA; 18556 MW; C3B25352635B176F CRC64;

Query Match 77.8%; Score 35; DB 2; Length 174;
Best Local Similarity 66.7%; Pred. No. 99;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYDAIQK 9
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Db 154 AQMEDVQK 162

RESULT 15
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AC Q9DB93;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE Adult male cerebellum cDNA, RIKEN full-length enriched library,
DE clone:1500002806 product:male enhanced antigen 1, full insert
DE sequence.
GN Name=Meal;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilmong L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impombato A., Anweiler K., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Belsel R.W., Bersano T., Bono H., Chalk A.M.,
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RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
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RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
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RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
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RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reid J., Ring B.Z., Ringwald M.,
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RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
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RA Kuehl P., Lewis S., Mateau Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
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RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
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RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
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RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakauchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: AK005106; BAB23822.1; -; mRNA.
DR Ensembl: ENSMUSG0000002768; Mus musculus.
DR MGI: MG1:96957; Mea1.
DR GO: GO:0005737; C:cytoplasm; IDA.
DR InterPro: IPR009685; MEA1.
DR PANTHER: PTHR17005; MEA1; 1.
DR Pfam: PF06910; MEA1; 1.
SQ SEQUENCE 174 AA; 18597 MW; C3B173BB0F736B9D CRC64;

Query Match 77.8%; Score 35; DB 2; Length 174;
Best Local Similarity 66.7%; Pred. No. 99;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 AQYEDAIQK 9
DB 154 AQWEDVVQK 162
|||:|:|

Search completed: July 5, 2006, 19:01:27
Job time : 95.1971 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 18:28:26 ; Search time 78.2039 Seconds
(without alignments)
52.618 Million cell updates/sec

Title: US-10-774-928A-4
Perfect score: 45
Sequence: 1 AQVEDAIQK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 8:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*
10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	6	AAO26384 Psoriasis
2	45	100.0	9	9	ADV04409 Leishmania
3	35	77.8	9	6	AAO26382 Psoriasis
4	35	77.8	9	9	ADV04407 Leishmania
5	35	77.8	164	2	AAR67587 Bovine ma
6	35	77.8	172	7	ADE62272 Human Pro
7	35	77.8	174	2	AAR67586 Murine ma
8	35	77.8	185	6	ABU07424 Protein d
9	35	77.8	185	9	ADU07373 Cyclin-de
10	35	77.8	644	9	AEAL5501 Human pol
11	35	77.8	785	5	ABBA48335 Listeria
12	35	77.8	785	6	ABU32679 Protein e
13	35	77.8	875	8	ADNI19018 Bacterial
14	34	75.6	9	4	AAM99474 Vaccine r
15	34	75.6	124	8	ADH12886 Francisel
16	34	75.6	233	4	AAU35049 Enterococ
17	34	75.6	233	6	ABU29360 Protein e
18	33	73.3	117	7	ADM04300 Human pro
19	33	73.3	117	9	AEC87230 Human cdn
20	33	73.3	228	4	AAB94159 Human pro
21	33	73.3	396	6	AAO19957 C elegans
22	33	73.3	420	4	ABU52997 Human tes
23	33	73.3	527	7	ABO68208 Pseudomon

24	33	73.3	590	5	AAU74362	Aau74362 Human cyt
25	33	73.3	808	6	ABU24980	Abu24980 Protein e
26	33	73.3	831	7	ADE63406	Ade63406 Rat Prote
27	33	73.3	831	7	ADE58908	Ade58908 Rat Prote
28	33	73.3	831	7	ADD46632	Add46632 Rat Prote
29	33	73.3	808	6	ABU19261	Abu19261 Protein e
30	33	73.3	1072	5	ABBS7023	Abbs7023 Mouse isc
31	33	73.3	1072	9	ADX26395	Adx26395 Novel cel
32	32	71.1	10	10	AEF10781	Aef10781 Human PRL
33	32	71.1	126	4	AAU41376	Aau41376 Propionib
34	32	71.1	126	6	ABM37895	Abm37895 Propionib
35	32	71.1	129	8	ADO08004	Ado08004 Fusobacte
36	32	71.1	129	8	ADP70200	Adp70200 Fusobacte
37	32	71.1	148	7	ADC99072	Adc99072 Human KPP
38	32	71.1	149	7	ADC99073	Adc99073 Human KPP
39	32	71.1	173	2	AAW37914	Aaw37914 Disease a
40	32	71.1	173	3	AAV92174	Aav92174 Human car
41	32	71.1	173	5	ABB90758	Abb90758 Human Tum
42	32	71.1	173	6	ABU54465	Abu54465 Human Tum
43	32	71.1	173	7	ADE95438	Ade95438 Human PRL
44	32	71.1	173	7	ADE95441	Ade95441 Human PRL
45	32	71.1	173	8	ADI28335	Adi28335 Human pro

ALIGNMENTS

RESULT 1
AAO26384
ID AAO26384 standard; peptide; 9 AA.
XX
AC AAO26384;
XX
DT 30-JAN-2003 (first entry)
DE Psoriasis treating immunotherapeutic peptide, SEQ ID No 4.
XX
KW Antipsoriatic; immunostimulant; gene therapy; pharmaceutical composition;
KW vaccine; immunogenic variant; immunotherapeutic agent; psoriasis;
KW gene therapy.
XX
OS Leishmania sp.
XX
PN WO200274239-A2.
XX
PD 26-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006496.
XX
PR 16-MAR-2001; 2001US-00809003.
XX
(AKIV-) AKIVA LLC.
XX
O'daly JA;
XX
WPI; 2003-018763/01.
XX
New polypeptide and immunogenic variants comprising amino acid sequences of particulate antigens, useful for the treatment and clinical remission of psoriasis.
XX
Claim 1; Page 43; 56pp; English.
XX
The invention relates to a polypeptide comprising an isolated amino acid sequence or immunogenic variants selected from any of 14 fully defined sequences of 7-16 amino acids, given in the specification. The immunotherapeutic agents and a pharmaceutical compositions comprising polynucleotides and vectors of the invention are useful for the treatment and clinical remission of psoriasis. The isolated nucleic acids are useful as probes. The sequences of the invention can be used in the treatment of disorders by gene therapy. This sequence represents one of the 14 immunotherapeutic peptides of the invention

```

SQ      Sequence 9 AA;
Query Match      100.0%; Score 45; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AQYEDAIQK 9
      |||||
Db      1 AQYEDAIQK 9

RESULT 2
ADV04409
ID      AAO26382 standard; peptide; 9 AA.
XX
AC      ADV04409;
XX
DT      24-FEB-2005 (first entry)
XX
DE      Leishmania immunotherapeutic peptide SEQ ID NO:4.
XX
KW      T-lymphocyte; immunogenicity; antigen; antipsoriatic; immunostimulant;
KW      psoriasis.
XX
OS      Leishmania sp.
XX
PN      US2004241168-A1.
XX
PD      02-DEC-2004.
XX
PF      09-FEB-2004; 2004US-00774928.
XX
PR      16-MAR-2001; 2001US-00809003.
PR      17-OCT-2003; 2003US-00687892.
XX
PA      (ODAL/) ODALY J A.
PI      Odaly JA;
XX
PI      WPI; 2005-011563/01.
XX
DR      WPI; 2005-011563/01.
XX
PT      Inhibiting selectively T-cell rolling in human, by administering compound
PT      interfering with cutaneous lymphocyte antigen-E selectin interaction and
PT      leukocyte function associated antigen-1 interaction.
XX
PS      Claim 9; SEQ ID NO 4; 21pp; English.
XX
CC      The invention relates to a novel method for selectively inhibiting T-cell
CC      rolling in a human host, comprising administering a compound that
CC      selectively interferes with the cutaneous lymphocyte antigen (CLA)-E
CC      selectin interaction and leukocyte function associated antigen (LFA)-
CC      1/intercellular adhesion molecule (ICAM) and very late antigen
CC      (VLA)/vascular cell adhesion molecule (VCAM) interactions. The compound
CC      includes an immunotherapeutic agent, which comprises a purified protein
CC      extract that is isolated by diethylaminoethyl Sephadex chromatography of
CC      a Nonidet P-40 insoluble particulate antigen fraction derived from
CC      isolated killed cells of anastigotes from one or more species of the
CC      Leishmania genus, where the particulate antigen fraction is solubilized
CC      with 8M urea and 0.025 M Tris(hydroxymethyl)aminomethane pH 8.3 applied
CC      to diethylaminoethyl Sephadex and is eluted with a solution comprising
CC      0.1 M sodium chloride, 8 M urea and 0.025 M
CC      Tris(hydroxymethyl)aminomethane pH 8.3, and the purified protein extract
CC      includes polypeptides having apparent molecular weights of 73, 80 and 82
CC      kDa, after total reduction and alkylation. The species is L. amazonensis,
CC      L. venezuelensis, L. brasiliensis and/or L. chagasi. A compound of the
CC      invention has antipsoriatic and immunostimulant activity, and inhibits T-
CC      cell rolling by interfering with CLA-E selectin interaction and LFA-
CC      1/ICAM and VLA/VCAM interactions. The method is useful for selectively
CC      inhibiting T-cell rolling in a human host, and for treating psoriasis.
CC      The present sequence represents a Leishmania peptide used in the
CC      invention.
XX
SQ      Sequence 9 AA;
Query Match      77.8%; Score 35; DB 6; Length 9;
Best Local Similarity 77.8%; Pred. No. 2.1e+06;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 AQYEDAIQK 9
      |||||
Db      1 AQYEDAIQK 9

RESULT 4
ADV04407
ID      ADV04407 standard; peptide; 9 AA.
XX
AC      ADV04407;
XX

```

DT 24-FEB-2005 (first entry)
 XX Leishmania immunotherapeutic peptide SEQ ID NO:2.
 DE T-lymphocyte; immunogenicity; antigen; antipsoriatic; immunostimulant;
 XX psoriasis.
 KW Leishmania sp.
 XX US2004241168-A1.
 PN 02-DEC-2004.
 PD 09-FEB-2004; 2004US-00774928.
 XX 16-MAR-2001; 2001US-00809003.
 XX 17-OCT-2003; 2003US-00687892.
 XX (ODAL/) ODALY J A.
 PA Odaly JA;
 PI WPI; 2005-011563/01.
 DR Inhibiting selectively T-cell rolling in human, by administering compound
 XX interfering with cutaneous lymphocyte antigen-E selectin interaction and
 PT leukocyte function associated antigen-1 interaction.
 XX Claim 9; SEQ ID NO 2; 21pp; English.
 PS The invention relates to a novel method for selectively inhibiting T-cell
 CC rolling in a human host, comprising administering a compound that
 CC selectively interferes with the cutaneous lymphocyte antigen (CLA)-E
 CC selectin interaction and leukocyte function associated antigen (LFA)-
 CC 1/intercellular adhesion molecule (ICAM) and very late antigen
 CC (VLA)/vascular cell adhesion molecule (VCAM) interactions. The compound
 CC includes an immunotherapeutic agent, which comprises a purified protein
 CC extract that is isolated by diethylaminoethyl Sephadex chromatography of
 CC a Nonidet P-40 insoluble particulate antigen fraction derived from
 CC isolated killed cells of amastigotes from one or more species of the
 CC Leishmania genus, where the particulate antigen fraction is solubilized
 CC with 8M urea and 0.025 M Tris(hydroxymethyl)aminomethane pH 8.3 applied
 CC to diethylaminoethyl Sephadex and is eluted with a solution comprising
 CC 0.1 M sodium chloride, 8 M urea and 0.025 M
 CC Tris(hydroxymethyl)aminomethane pH 8.3, and the purified protein extract
 CC includes polypeptides having apparent molecular weights of 73, 80 and 82
 CC kDa, after total reduction and alkylation. The species is L. amazonensis,
 CC L. venezuelensis, L. brasiliensis and/or L. chagasi. A compound of the
 CC invention has antipsoriatic and immunostimulant activity, and inhibits T-
 CC cell rolling by interfering with CLA-E selectin interaction and LFA-
 CC 1/ICAM and VLA/VCAM interactions. The method is useful for selectively
 CC inhibiting T-cell rolling in a human host, and for treating psoriasis.
 CC The present sequence represents an Leishmania peptide used in the
 CC invention.
 XX Sequence 9 AA;
 SQ

Query Match 77.8%; Score 35; DB 9; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2.1e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AQVEDAIQK 9
 DB 1 AQVEDAIQK 9
 RESULT 5
 AAR67587
 ID AAR67587 standard; protein; 164 AA.
 XX AAR67587;
 AC AAR67587;
 XX 06-OCT-1995 (first entry)
 DT

XX Bovine male enhanced antigen (Mea).
 DE Bovine male enhanced antigen; Mea; gender discrimination; cow; primers;
 XX probes.
 KW Bos taurus.
 XX JP06319546-A.
 PN 22-NOV-1994.
 PD 07-MAY-1993; 93JP-00130055.
 XX 07-MAY-1993; 93JP-00130055.
 PR (KACH-) KACHIKU JUSEIRAN ISHOKU GIKUTSU KENKYUKU.
 XX WPI; 1995-040314/06.
 DR N-PSDB; AAQ79135, AAQ79136, AAQ79137.
 XX DNA sequences from mice and cattle - used as primers and probes for the
 PT discrimination of gender.
 PS Claim 7; Page 9; 12pp; Japanese.
 XX AAQ79136 encodes AAR67587 bovine male enhanced antigen (Mea), the cDNA
 CC can be used to produce probes and primers for the discrimination of
 CC genders from tissue samples and embryos
 XX Sequence 164 AA;
 SQ

Query Match 77.8%; Score 35; DB 2; Length 164;
 Best Local Similarity 66.7%; Pred. No. 92;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AQVEDAIQK 9
 DB 144 AQWEDVVQK 152
 RESULT 6
 ADE62272
 ID ADE62272 standard; protein; 172 AA.
 XX ADE62272;
 AC ADE62272;
 XX 29-JAN-2004 (first entry)
 DT Human Protein Q16626, SEQ ID NO 8201.
 DE Human; pain; neuronal tissue; gene therapy;
 XX spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX Homo sapiens.
 OS WO2003016475-A2.
 PN 27-FEB-2003.
 PD 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 XX 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 PI WPI; 2003-268312/26.
 DR

DR GENBANK; Q16626.

XX New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

XX

PS Claim 1; Page; 1017pp; English.

XX

CC The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,

CC derivative or allelic variation of the nucleic acid sequence. Also

CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence

CC which is differentially regulated in an animal subjected to pain and a

CC kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal

CC subjected to pain, a method for identifying a compound which regulates

CC the expression of a polynucleotide sequence which is differentially

CC expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the

CC activity in an animal of one or more of the polypeptides given in the

CC specification, a method for identifying a compound useful in treating

CC pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that

CC modulates its activity is useful for preparing a medicament for treating

CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene

CC therapy). The sequence presented is a human protein (shown in Table 2 of

CC the specification) which is differentially expressed during pain. Note:

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

XX

XX Sequence 172 AA;

XX

Query Match 77.8%; Score 35; DB 7; Length 172;

Best Local Similarity 66.7%; Pred. No. 97;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDAIQK 9

Db 152 AQWEDVVQK 160

RESULT 7

AA067586

ID AAR67586 standard; protein; 174 AA.

XX

AC AAR67586;

XX

XX 06-OCT-1995 (first entry)

DT Murine male enhanced antigen (Mea).

DE Murine male enhanced antigen (Mea).

XX

XX Murine male enhanced antigen; Mea; gender discrimination; mouse; primers;

KW probes.

XX

XX Mus musculus.

OS

XX JP06319546-A.

PN

XX 22-NOV-1994.

PD

XX 07-MAY-1993; 93JP-00130055.

PF

XX 07-MAY-1993; 93JP-00130055.

PR

XX (KACH-) KACHIKU JUSETRAN ISHOKU GIKUTSU KENKYUKU.

PA

XX WPI; 1995-040314/06.

DR N-PSDB; AAR67586.

XX DNA sequences from mice and cattle - used as primers and probes for the

PT discrimination of gender.

XX

PS Claim 2; Page 6-7; 12pp; Japanese.

XX

CC AA079134 encodes AAR67586 murine male enhanced antigen (Mea), the cDNA

CC can be used to produce probes and primers for the discrimination of

CC genders from tissue samples and embryos

XX

XX Sequence 174 AA;

XX

Query Match 77.8%; Score 35; DB 2; Length 174;

Best Local Similarity 66.7%; Pred. No. 98;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDAIQK 9

Db 154 AQWEDVVQK 162

RESULT 8

ABU07424

ID ABU07424 standard; protein; 185 AA.

XX

AC ABU07424;

XX

XX 28-JAN-2003 (first entry)

DT Protein differentially regulated in prostate cancer #27.

DE

XX Prostate cancer; gene expression; differential regulation;

KW molecular marker; drug target; cancer detection; cancer diagnosis;

KW cancer staging; cancer grading; cancer assessing; cancer monitoring.

XX

XX Homo sapiens.

OS

XX WO200281638-A2.

PN

XX 17-OCT-2002.

PD

XX 08-APR-2002; 2002WO-US010824.

PF

XX 06-APR-2001; 2001US-0281731P.

PR

XX 06-APR-2001; 2001US-0281732P.

XX

XX (ORIG-) ORIGENE TECHNOLOGIES INC.

PA

XX Sun Z, Jay G;

PI

XX WPI; 2003-058520/05.

DR

XX Novel genes which are differentially regulated in prostate cancer, useful

PT for diagnosing prostate cancer in prostate tissue sample and assessing

PT therapeutic or preventive intervention in prostate cancer patients.

XX

XX Claim 1; Page 262-263; 416pp; English.

PS

XX The invention describes genes (I) which are differentially regulated in

CC prostate cancer. (I) is useful for diagnosing a prostate cancer in a

CC sample comprising prostate tissue, which involves determining the number

CC of target genes which are differentially-regulated in the sample, where

CC the number is indicative of the probability that the sample comprises

CC prostate cancer. (I) is useful for assessing a therapeutic or preventive

CC intervention in a subject having a prostate cancer, which involves

CC determining the expression levels in a sample comprising prostate tissue

CC of target genes which are differentially-regulated in prostate cancer.

CC Preferably, the expression levels of at least 10 genes are determined.

CC (I) is also useful for identifying agents that modulate a biological

CC activity of a polypeptide differentially-regulated in prostate cancer

CC cells, which involves contacting a polypeptide differentially-regulated

CC in prostate cancer cells with a test agent under conditions effective for

CC the test agent to modulate a biological activity of the polypeptide, and

CC determining whether the test agent modulates the biological activity. (I)
 CC is useful as molecular markers, as drug targets, and for detecting,
 CC diagnosing, staging, grading, assessing, monitoring, prognosticating,
 CC preventing or treating, determining predisposition to diseases and
 CC conditions especially relating to prostate cancer. (I) and its expression
 CC products are used in the diagnostic test to assay for presence of cancer
 CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
 CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
 CC of cancer, its stage of development, the nature of genetic defect, etc.
 CC The polypeptide encoded by (I) can be used as target for therapy or drug
 CC discovery. (I) can also be used for expressing the polypeptide and thus
 CC for searching specific binding partners of the polypeptide. (I) is useful
 CC in therapeutic applications to treat prostate cancer. The identification
 CC of specific genes, and groups of genes, expressed in pathways
 CC physiologically relevant to prostate cancer permits the definition of
 CC functional and disease pathways and the delineation of targets in these
 CC pathways which are useful in diagnostic, therapeutic, and clinical
 CC applications. This is the amino acid sequence of a protein differentially
 CC regulated in prostate cancer

XX Sequence 185 AA;

Query Match 77.8%; Score 35; DB 6; Length 185;
 Best Local Similarity 66.7%; Pred. No. 1e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQVEDAIQK 9
 Db 165 AQWEDVVQK 173
 ||:||:|

RESULT 9
 ADX07373
 ID ADX07373 standard; protein; 185 AA.

AC ADX07373;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 1938.

XX cytotstatic; cyclin-dependent kinase; cdk; biomarker.

XX Homo sapiens.

XX WO2005012875-A2.

XX 10-FEB-2005.

XX 29-JUL-2004; 2004WO-US024424.

XX 29-JUL-2003; 2003US-0490890P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;

XX WPI; 2005-163068/17.

XX N-PSDB; ADX07372.

XX Biomarkers useful for predicting or determining the response of a mammal
 PT to a cancer treatment comprising administration of a modulator of cyclin-
 PT dependent kinase activity.

PS Claim 5; SEQ ID NO 1938; 141pp; English.

XX This invention describes a novel method of predicting or determining
 CC whether a mammal will respond or is responding to an anti-cancer agent
 CC that modulates cyclin-dependent kinase (cdk) activity. The method
 CC comprises measuring the level of one or more biomarkers selected from
 CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
 CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the
 CC invention is utilized in a kit for determining or predicting whether

CC patient would be susceptible or resistant to treatment by an agent
 CC modulating cdk activity. The invention also describes a method for
 CC utilizing individualized genetic profiles for treating diseases and
 CC disorders based on patient's response and molecular level, specialized
 CC microarrays comprising the biomarkers described, antibodies directed
 CC against the biomarkers and a cell culture model to identify biomarkers.
 CC The cdk modulator is preferably N-5-([5-(1,1-Dimethylethyl)-2-oxazolyl]
 CC oxazolyl)methylthiol-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
 CC tartaric acid salt. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at fip.wipo.int/pub/published pct sequences. This
 CC sequence represents a biomarker used in the method of the invention.

XX Sequence 185 AA;

Query Match 77.8%; Score 35; DB 9; Length 185;
 Best Local Similarity 66.7%; Pred. No. 1e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQVEDAIQK 9
 Db 165 AQWEDVVQK 173
 ||:||:|

RESULT 10
 AEA15501
 ID AEA15501 standard; protein; 644 AA.

AC AEA15501;

DT 28-JUL-2005 (first entry)

XX Human polypeptide #120.

XX Diagnosis; prognosis; cancer; breast tumor; ovary tumor; stomach tumor;
 KW colon tumor; esophagus tumor; bladder tumor; non-small-cell lung cancer;
 KW cytostatic; neoplasm.

OS Homo sapiens.

PN WO2005047534-A2.

PD 26-MAY-2005.

PF 15-OCT-2004; 2004WO-BF011599.

PR 28-OCT-2003; 2003EP-00024565.

XX (FARB) BAYER HEALTHCARE AG.

XX Wirtz R, Munnes M;

XX WPI; 2005-372393/38.

XX N-PSDB; AEA15423.

XX Predicting a response to cancer treatment by detecting at least 2
 PT markers, which are genes or genomic nucleic acid sequences that are
 PT located on one chromosomal region, which is altered in malignant
 PT neoplasia.

XX Claim 7; SEQ ID NO 463; 464pp; English.

XX The invention relates to a method of predicting response to cancer
 CC treatment comprising detection of at least 2 markers, where the markers
 CC are genes and fragments or genomic nucleic acid sequences that are
 CC located on one chromosomal region, which is altered in malignant
 CC neoplasia. The invention also relates to a method for the prediction,
 CC diagnosis or prognosis of malignant neoplasia, methods for detecting,
 CC deregulations in malignant neoplasia and breast cancer, a method of
 CC determining the phenotype of a cell or tissue, a method for identifying
 CC genomic regions which are altered on the chromosomal level and encode
 CC genes that are linked by function and are differentially expressed in
 CC malignant neoplasia and breast cancer, methods of screening for agents

CC which regulate the activity of a polypeptide or a polynucleotide and
CC antibodies that specifically bind to a full length or partial
CC polypeptide. The method is useful for predicting response to cancer
CC treatment. The methods and compositions are useful for predicting,
CC diagnosing, prognosing, preventing or treating malignant neoplasia
CC including breast cancer, ovarian cancer, gastric cancer, colon cancer,
CC esophageal cancer, mesenchymal cancer, bladder cancer or non-small-cell
CC lung cancer. This sequence represents a human polypeptide used in the
CC scope of the invention.

XX
SQ Sequence 644 AA;

Query Match 77.8%; Score 35; DB 9; Length 644;
Best Local Similarity 77.8%; Pred. No. 4.3e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AQYEDAIQK 9
|||||
DB 356 AQYEDAIQK 364

RESULT 11
ABB48335
ID ABB48335 standard; protein; 785 AA.

XX
AC ABB48335;
XX
DT 05-FEB-2002 (first entry)

XX
DE Listeria monocytogenes protein #1039.

XX
KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW vitamin B12; bacterial infection; disease.

XX
OS Listeria monocytogenes.

XX
PN WO200177335-A2.

XX
PD 18-OCT-2001.

XX
PF 11-APR-2001; 2001WO-FR001118.

XX
PR 11-APR-2000; 2000FR-00004629.

XX
PA (INSP) INST PASTEUR.

XX
PI Buchrieser C, Frangeul L, Couve E, Rueniok C, Fsihi H, Dehoux P;
PI Dussurget O, Chetoui F, Nedjari H, Glaser P, Kunst F, Cossart P;
PI Daniels J, Goebel W, Kref J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Madueno E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;

XX
WPI; 2002-010914/01.

XX
Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
PT and prevention of Listeria and related bacterial infections, and related
PT polypeptides.

XX
Claim 6; SEQ ID NO 1040; 192pp; French.

XX
The present invention relates to the genome sequence of Listeria
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in L.
CC monocytogenes and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present invention is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies. Identification of L. monocytogenes and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for

CC selecting compounds that regulate gene expression and cell replication
CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccine compositions for the treatment or prevention of infections by L.
CC monocytogenes and related organisms. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 785 AA;

Query Match 77.8%; Score 35; DB 5; Length 785;
Best Local Similarity 75.0%; Pred. No. 5.3e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYEDAIQK 9
|||||
DB 716 QYEDAIQK 723

RESULT 12
ABU32679

ID ABU32679 standard; protein; 785 AA.

XX
AC ABU32679;

XX
DT 19-JUN-2003 (first entry)

XX
DE Protein encoded by Prokaryotic essential gene #18206.

XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX
OS Listeria monocytogenes.

XX
PN WO200277183-A2.

XX
PD 03-OCT-2002.

XX
PF 21-MAR-2002; 2002WO-US009107.

XX
PR 21-MAR-2001; 2001US-00815242.

XX
PR 06-SEP-2001; 2001US-00948993.

XX
PR 25-OCT-2001; 2001US-0342923P.

XX
PR 08-FEB-2002; 2002US-00072851.

XX
PR 06-MAR-2002; 2002US-0362699P.

XX
PA (ELIT-) ELITRA PHARM INC.

XX
Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX
WPI; 2003-029926/02.

XX
N-PSDB; ACA36549.

XX
New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

XX
Claim 25; SEQ ID NO 60603; 1766pp; English.

XX
The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 785 AA;

Query Match 77.8%; Score 35; DB 6; Length 785;

Best Local Similarity 75.0%; Pred. No. 5.3e+02;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYEDAIQK 9

Db 716 RYEDALQK 723

RESULT 13

ADN19018
 ID ADN19018 standard; protein; 875 AA.

AC ADN19018;

DT 02-DEC-2004 (first entry)

DE Bacterial polypeptide #1671.

XX Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.

OS Bacteria.

XX US2003233675-A1.

PN 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 1671; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 875 AA;

Query Match 77.8%; Score 35; DB 8; Length 875;

Best Local Similarity 66.7%; Pred. No. 6e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDAIQK 9

Db 529 AQYEDLVKK 537

RESULT 14

AAM99474

ID AAM99474 standard; peptide; 9 AA.

AC AAM99474;

DT 07-DEC-2001 (first entry)

XX Vaccine related MHC ligand peptide SEQ ID NO:577.

XX Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC;
 KW immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal;
 KW bactericidal; antiparasitic; fungicidal; cytostatic; medicine;
 KW pharmaceutical; immune disorder; immune deficiency; autoimmune;
 KW hypersensitivity; allergy; graft rejection; infection; hormonal disorder;
 KW central nervous system disease; cancer; melanoma; anti-melanoma vaccine;
 KW human immunodeficiency virus.

XX Homo sapiens.

XX WO200170772-A2.

XX 27-SEP-2001.

XX 22-MAR-2001; 2001WO-FR000872.

XX 23-MAR-2000; 2000FR-00003711.

XX (FABR-) FABRE MEDICAMENT SA PIERRE.

XX Klinguer-Hamour C, Corvaia N, Beck A, Goetsch L;

XX WPI; 2001-611470/70.

XX Stabilized pharmaceutical containing N-terminal glutamic acid or
 PT glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt

PT with strong acid.
 XX Claim 9; Page 129; 149pp; French.
 PS
 XX The present invention describes a pharmaceutical compound (I) that contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in the form of an addition salt with a strong, physiologically acceptable acid (II). Also described are: (a) a pharmaceutical composition containing at least one (I); (b) a vaccine containing at least one (I) where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a method for in vitro diagnosis of diseases associated with the presence of (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process for preparing (I). (I) has immunomodulator, endocrine, antiallergic, neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and cytostatic activities. (I) are useful, in human or veterinary medicine, in pharmaceutical compositions (for treating immune disorders, e.g. immune deficiency, autoimmune states, hypersensitivity, allergy, graft rejection, infection, hormonal disorders and central nervous system diseases), also, where (I) is a MHC ligand (Ia), in vaccines for treatment or prevention of: (i) viral, bacterial, parasitic or fungal infections; or (ii) of cancers. A particular application is in anti-melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases associated with interactions between MHC and (I), e.g. melanoma and human immunodeficiency virus infection. AAM98898 to AAM99592 represent peptides which can be used in pharmaceutical compounds from the present invention

XX
 XX Sequence 9 AA;
 SQ

Query Match 75.6%; Score 34; DB 4; Length 9;
 Best Local Similarity 62.5%; Pred. No. 2.1e+06;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QYEDAIQK 9
 ||:|:|:
 Db 1 QYDDAVEK 8

RESULT 15
 ADH12886
 ID ADH12886 standard; protein; 124 AA.
 XX
 AC ADH12886;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Francisella tularensis immunogenic protein 67, SEQ ID NO:67.
 XX
 KW Immunogenic protein; protective immune response; vaccine;
 KW genetic vaccine; antibacterial.
 XX
 OS Francisella tularensis.
 XX
 PN WO2004003009-A2.
 XX
 PD 08-JAN-2004.
 XX
 PF 26-JUN-2003; 2003WO-GB002718.
 XX
 PR 28-JUN-2002; 2002GB-00014942.
 XX
 PA (MINA) UK SEC FOR DEFENCE.
 XX
 PI Titball RW, Mayers CN, Duffield ML, Miller J, Rowe SC;
 XX
 DR WPI: 2004-083016/08.
 DR N-PSDB; ADH12886.
 XX
 XX New protein, useful as a vaccine for producing a protective immune response in a mammal against infection by Francisella tularensis, or preventing or treating Francisella tularensis infection in a mammal.
 PT
 PT
 PS Claim 1; SEQ ID NO 67; 217pp; English.

CC The invention relates to 100 potentially immunogenic proteins from Francisella tularensis (ADH12820-ADH12919) and nucleic acids encoding them (ADH12920-ADH13019) which may be used in vaccines. The nucleic acids may be contained within a vaccine, bacterial or plasmid vector. The invention also relates to a pharmaceutical composition comprising the protein or the nucleic acid in combination with a pharmaceutical carrier or excipient. The proteins and nucleic acids are useful in vaccine compositions for producing a protective immune response against Francisella tularensis infection in a mammal, or for preventing or treating Francisella tularensis infection in a mammal. The present sequence represents a Francisella tularensis protein of the invention.

XX
 XX Sequence 124 AA;
 SQ

Query Match 75.6%; Score 34; DB 8; Length 124;
 Best Local Similarity 87.5%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AQYEDAIQ 8
 |||||:
 Db 76 AQYESAIQ 83

Search completed: July 5, 2006, 18:43:47
 Job time : 80.2039 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 20:38:52 ; Search time 65.8835 Seconds
(without alignments)
63.277 Million cell updates/sec

Title: US-10-774-928A-4

Perfect score: 45

Sequence: 1 AQVEDAIQK 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SID33/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SID33/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SID33/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SID33/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	45	100.0	9	5	US-10-774-928-4
2	35	77.8	9	5	US-10-774-928-2
3	35	77.8	258	5	US-10-732-923-14076
4	35	77.8	785	4	US-10-282-122A-60603
5	35	77.8	785	6	US-11-045-004-1040
6	35	77.8	875	4	US-10-369-493-1671
7	34	75.6	9	4	US-10-239-313A-577
8	34	75.6	77	4	US-10-424-599-214479
9	34	75.6	148	4	US-10-767-701-57385
10	34	75.6	233	3	US-09-815-242-10642
11	34	75.6	233	4	US-10-282-122A-57284
12	34	75.6	366	4	US-10-437-963-181853
13	33	73.3	117	4	US-10-108-260A-2985
14	33	73.3	396	4	US-10-179-766-7
15	33	73.3	530	4	US-10-437-963-197053
16	33	73.3	590	4	US-10-275-595A-33
17	33	73.3	591	4	US-10-437-963-197054
18	33	73.3	808	4	US-10-282-122A-52904
19	33	73.3	908	4	US-10-282-122A-47185
20	33	73.3	1132	4	US-10-437-963-160810
21	32	71.1	10	6	US-11-129-104-74
22	32	71.1	60	4	US-10-425-115-186946
23	32	71.1	129	5	US-10-737-288-13
24	32	71.1	129	5	US-10-891-825-13
25	32	71.1	148	5	US-10-491-467-25
26	32	71.1	149	5	US-10-491-467-26
27	32	71.1	162	4	US-10-767-701-52156

28	32	71.1	173	3	US-09-918-715-248	Sequence 248, App
29	32	71.1	173	4	US-10-427-887-3	Sequence 3, Appli
30	32	71.1	173	4	US-10-427-887-6	Sequence 6, Appli
31	32	71.1	173	4	US-10-444-795B-799	Sequence 799, App
32	32	71.1	173	4	US-10-474-794-248	Sequence 248, App
33	32	71.1	173	5	US-10-979-159-248	Sequence 248, App
34	32	71.1	173	6	US-11-129-104-88	Sequence 88, Appli
35	32	71.1	199	4	US-10-767-701-35473	Sequence 35473, A
36	32	71.1	200	4	US-10-437-963-140077	Sequence 140077, A
37	32	71.1	221	4	US-10-291-190-36	Sequence 36, Appl
38	32	71.1	229	4	US-10-425-115-193806	Sequence 193806,
39	32	71.1	235	6	US-11-129-104-90	Sequence 90, Appl
40	32	71.1	235	4	US-10-335-977-8903	Sequence 8903, Ap
41	32	71.1	243	6	US-11-129-104-91	Sequence 91, Appl
42	32	71.1	293	4	US-10-163-214-10	Sequence 10, Appl
43	32	71.1	358	4	US-10-727-936-38	Sequence 38, Appl
44	32	71.1	385	4	US-10-369-493-3196	Sequence 3196, Ap
45	32	71.1	405	4	US-10-335-977-8905	Sequence 8905, Ap

ALIGNMENTS

RESULT 1

US-10-774-928-4
; Sequence 4, Application US/10774928
; Publication No. US20040241168A1
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 302178
; CURRENT APPLICATION NUMBER: US/10/774,928
; CURRENT FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Leishmania
US-10-774-928-4

Query Match 100.0%; Score 45; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQVEDAIQK 9
Db 1 AQVEDAIQK 9

RESULT 2

US-10-774-928-2
; Sequence 2, Application US/10774928
; Publication No. US20040241168A1
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 302178
; CURRENT APPLICATION NUMBER: US/10/774,928
; CURRENT FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Leishmania
US-10-774-928-2

Query Match 77.8%; Score 35; DB 5; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.9e+06;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 AQYEDAIQK 9
    |||||
Db 1 AQYEDAIQK 9

RESULT 3
US-10-732-923-14076
; Sequence 14076, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 14076
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Encephalitozoon cuniculi
US-10-732-923-14076

Query Match 77.8%; Score 35; DB 5; Length 258;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYEDAIQK 9
    |||||
Db 5 QYEEALQK 12

RESULT 4
US-10-282-122A-60603
; Sequence 60603, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Lianguo
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
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; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60603
; LENGTH: 785
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-10-282-122A-60603

Query Match 77.8%; Score 35; DB 4; Length 785;
Best Local Similarity 75.0%; Pred. No. 5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYEDAIQK 9
    |||||
Db 716 RYEDALQK 723

RESULT 5
US-11-045-004-1040
; Sequence 1040, Application US/11045004
; Publication No. US20060078901A1
; GENERAL INFORMATION:
; APPLICANT: BUCHRIESER, CARMEN
; APPLICANT: FRANGEUL, LIONEL
; APPLICANT: COUVE, ELISABETH
; APPLICANT: RUSNIOK, CHRISTOPHE
; APPLICANT: FSIHI, HAFIDA
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: DUSSURGET, OLIVIER
; APPLICANT: CHETOUANI, FARID
; APPLICANT: NEDJARI, HAFED
; APPLICANT: GLASER, PHILIPPE
; APPLICANT: KUNST, FRANCK
; APPLICANT: COSSART, PASCALE
; APPLICANT: DANIELS, JUSTIN
; APPLICANT: GORBEL, WERNER
; APPLICANT: KREFT, JURGEN
; APPLICANT: KUHN, MICHAEL
; APPLICANT: NG, EVA
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
; APPLICANT: GARRIDO-GARCIA, PATRICIA
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
; APPLICANT: AMEND, ALEXANDRA
; APPLICANT: CHAKRABORTY, TRINAD
; APPLICANT: DOWANN, EUGEN
; APPLICANT: HAIN, THORSTEN
; APPLICANT: BERCHE, PATRICK
; APPLICANT: CHARBIT, ALAIN
; APPLICANT: DURANT, LIONEL
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
; APPLICANT: BAQUERO, FERNANDO
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
; APPLICANT: GOMEZ-LOPEZ, NURIA
; APPLICANT: MADUENIO, ENCARN
; APPLICANT: PABLOS, BETRIZ DE
; APPLICANT: WEHLAND, JURGEN
; APPLICANT: KARST, UWE
; APPLICANT: ENTIAN, KARL-DIETER
; APPLICANT: HAUF, JORG
; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; FILE REFERENCE: 05394.0018-02
; CURRENT APPLICATION NUMBER: US/11/045,004
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/637,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/257,023
; PRIOR FILING DATE: 2002-10-08
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; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1040
; LENGTH: 785
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-045-004-1040

Query Match 77.8%; Score 35; DB 6; Length 785;
Best Local Similarity 75.0%; Pred. No. 5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYEDAIQK 9
Db 716 RYEDALQK 723

RESULT 6

US-10-369-493-1671
; Sequence 1671, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1671
; LENGTH: 875
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-1671

Query Match 77.8%; Score 35; DB 4; Length 875;
Best Local Similarity 66.7%; Pred. No. 5.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDAIQK 9
Db 529 AQYEDLVKK 537

RESULT 7

US-10-239-313A-577
; Sequence 577, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22

; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 577
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-577

Query Match 75.6%; Score 34; DB 4; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.9e+06;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYEDAIQK 9
Db 1 QYDDAVEK 8

RESULT 8

US-10-424-599-214479
; Sequence 214479, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 214479
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(77)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_35701C.1.pap
US-10-424-599-214479

Query Match 75.6%; Score 34; DB 4; Length 77;
Best Local Similarity 66.7%; Pred. No. 65;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQYEDAIQK 9
Db 67 AQHEDALQK 75

RESULT 9

US-10-767-701-57385
; Sequence 57385, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 57385
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 30966480.pap

US-10-767-701-57385

Query Match 75.6%; Score 34; DB 4; Length 148;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YEDAIQK 9
||||:|
Db 67 YEDALQK 73

RESULT 10

US-09-815-242-10642
; Sequence 10642, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10642
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10642

Query Match 75.6%; Score 34; DB 3; Length 233;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YEDAIQK 9
||||:|
Db 36 YEDALQK 42

RESULT 11

US-10-282-122A-57284
; Sequence 57284, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57284
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-10-282-122A-57284

Query Match 75.6%; Score 34; DB 4; Length 233;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YEDAIQK 9
||||:|
Db 36 YEDALQK 42

RESULT 12

US-10-437-963-181853
; Sequence 181853, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 181853
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_79094C.1.pap
US-10-437-963-181853

Query Match 75.8%; Score 34; DB 4; Length 366;
Best Local Similarity 77.8%; Pred. No. 3.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQVEDAIQK 9
DB 244 AQKEDALQK 252
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RESULT 13

US-10-108-260A-2985
; Sequence 2985, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2985
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-2985

Query Match 73.3%; Score 33; DB 4; Length 117;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQVEDAIQK 9
DB 49 AQVEDAIQK 57
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RESULT 14

US-10-179-766-7
; Sequence 7, Application US/10179766
; Publication No. US20030190312A1
; GENERAL INFORMATION:
; APPLICANT: Kenyon, Cynthia
; APPLICANT: Apfeld, Javier
; APPLICANT: Dillin, Andrew
; APPLICANT: Garigan, Delia
; APPLICANT: Hsu, Ao-Lin A.
; APPLICANT: Lehrer-Graiwer, Josh
; APPLICANT: Murphy, Coleen
; TITLE OF INVENTION: The Regents of the University of California
; FILE REFERENCE: 023070-119930US
; CURRENT APPLICATION NUMBER: US/10/179,766
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/300,577
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/301,052
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/373,975
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; OTHER INFORMATION: llw-1 (long-lived worm protein), gene Y54G11A.8
US-10-179-766-7

Query Match 73.3%; Score 33; DB 4; Length 396;
Best Local Similarity 85.7%; Pred. No. 5.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYEDAIQK 8
DB 108 QYDDAIQK 114
||:|

RESULT 15

US-10-437-963-197053
; Sequence 197053, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 197053
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_92848C.1.pap
US-10-437-963-197053

Query Match 73.3%; Score 33; DB 4; Length 530;
Best Local Similarity 66.7%; Pred. No. 7.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AQVEDAIQK 9
DB 491 AAYEDTLQK 499
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OM protein - protein search, using sw model

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(without alignments)
46.842 Million cell updates/sec

Title: US-10-774-928A-4

Perfect score: 45

Sequence: 1 AQVEDAIQK 9

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Searched: 112942 seqs, 26832045 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

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- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	75.6	447	6	US-10-449-902-51639
2	33	73.3	117	7	US-11-293-697-2985
3	33	73.3	591	6	US-10-449-902-53151
4	32	71.1	173	6	US-10-537-303-10
5	32	71.1	321	6	US-10-449-902-41051
6	31	68.9	167	6	US-10-537-303-4
7	31	68.9	167	6	US-10-537-303-6
8	31	68.9	173	6	US-10-537-303-2
9	31	68.9	250	6	US-10-449-902-32999
10	31	68.9	351	6	US-10-449-902-46480
11	31	68.9	691	6	US-10-953-349-1322
12	31	68.9	705	6	US-10-953-349-1321
13	31	68.9	713	6	US-10-953-349-1320
14	31	68.9	723	6	US-10-449-902-53379
15	31	68.9	809	6	US-10-449-902-54024
16	30	66.7	23	7	US-11-134-871-3360
17	30	66.7	103	6	US-10-953-349-26513
18	30	66.7	324	6	US-10-953-349-25046
19	30	66.7	329	6	US-10-953-349-25045
20	30	66.7	330	6	US-10-953-349-25044
21	30	66.7	335	6	US-10-953-349-32983
22	30	66.7	351	6	US-10-953-349-32982
23	30	66.7	462	6	US-10-196-749-298
24	30	66.7	553	6	US-10-449-902-52615
25	30	66.7	1180	6	US-10-505-928-459

26	64.4	130	6	US-10-953-349-525	Sequence 525, App
27	64.4	161	6	US-10-953-349-19502	Sequence 19502, A
28	64.4	173	6	US-10-953-349-19501	Sequence 19501, A
29	64.4	181	7	US-11-174-307B-5276	Sequence 5276, Ap
30	64.4	232	6	US-10-953-349-19523	Sequence 19523, A
31	64.4	265	6	US-10-953-349-27010	Sequence 27010, A
32	64.4	279	6	US-10-449-902-49131	Sequence 49131, A
33	64.4	297	6	US-10-953-349-19522	Sequence 19522, A
34	64.4	317	6	US-10-953-349-27009	Sequence 27009, A
35	64.4	347	6	US-10-953-349-19521	Sequence 19521, A
36	64.4	349	6	US-10-953-349-20252	Sequence 20252, A
37	64.4	467	6	US-10-953-349-20251	Sequence 20251, A
38	64.4	485	6	US-10-953-349-25060	Sequence 25060, A
39	64.4	490	6	US-10-953-349-20250	Sequence 20250, A
40	64.4	500	6	US-10-953-349-25059	Sequence 25059, A
41	64.4	507	6	US-10-953-349-25058	Sequence 25058, A
42	64.4	599	6	US-10-449-902-53037	Sequence 53037, A
43	64.4	627	6	US-10-471-571A-3090	Sequence 3090, Ap
44	64.4	649	6	US-10-449-902-37545	Sequence 37545, A
45	64.4	732	6	US-10-756-047-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-10-449-902-51639
; Sequence 51639, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205V1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51639
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-51639

Query Match 75.6%; Score 34; DB 6; Length 447;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AQVEDAIQK 9

Db 364 AQKDALQK 372

RESULT 2

US-11-293-697-2985
; Sequence 2985, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 2985
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-2985

Query Match      73.3%; Score 33; DB 7; Length 117;
Best Local Similarity 77.8%; Pred. No. 7.1;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 AQVEDAIQK 9
Db      49 AQVERAIQE 57

RESULT 3
US-10-449-902-53151
; Sequence 53151, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53151
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-53151

Query Match      73.3%; Score 33; DB 6; Length 591;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 AQVEDAIQK 9
Db      552 AYEDTLQK 560

RESULT 4
US-10-537-303-10
; Sequence 10, Application US/10537303
; Publication No. US20060135419A1
; GENERAL INFORMATION:
; APPLICANT: Meise, Martin
; APPLICANT: Eulenber, Karsten
; APPLICANT: Nguyen, Tri
; APPLICANT: Tsetsenis, Theodoros
; TITLE OF INVENTION: Proteins Involved in the Regulation of Energy Homeostasis
; FILE REFERENCE: 2923-703
; CURRENT APPLICATION NUMBER: US/10/537,303
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: PCT/EP03/013655
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: EP 02 026 921.3
; PRIOR FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-537-303-10

Query Match      71.1%; Score 32; DB 6; Length 173;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYEDAIQK 8
Db      125 KYEDAIQK 131

RESULT 5
US-10-449-902-41051
; Sequence 41051, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41051
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-41051

Query Match      71.1%; Score 32; DB 6; Length 321;
Best Local Similarity 62.5%; Pred. No. 34;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYEDAIQK 9
Db      181 KYEAVQK 188

RESULT 6
US-10-537-303-4
; Sequence 4, Application US/10537303
; Publication No. US20060135419A1
; GENERAL INFORMATION:
; APPLICANT: Meise, Martin
; APPLICANT: Eulenber, Karsten
; APPLICANT: Nguyen, Tri
; APPLICANT: Tsetsenis, Theodoros
; TITLE OF INVENTION: Proteins Involved in the Regulation of Energy Homeostasis
; FILE REFERENCE: 2923-703
; CURRENT APPLICATION NUMBER: US/10/537,303
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: PCT/EP03/013655
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: EP 02 026 921.3
; PRIOR FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-537-303-4

Query Match      69.9%; Score 31; DB 6; Length 167;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 2 QYEDAIQ 8
Db 122 KYEDAVQ 128

RESULT 7
US-10-537-303-6
; Sequence 6, Application US/10537303
; Publication No. US20060135419A1
; GENERAL INFORMATION:
; APPLICANT: Meise, Martin
; APPLICANT: Eulenbergh, Karsten
; APPLICANT: Nguyen, Tri
; APPLICANT: Tsetsenis, Theodoros
; TITLE OF INVENTION: Proteins Involved in the Regulation of Energy Homeostasis
; FILE REFERENCE: 2923-703
; CURRENT APPLICATION NUMBER: US/10/537,303
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: PCT/EP03/013655
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: EP 02 026 921.3
; PRIOR FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-537-303-6

Query Match 68.9%; Score 31; DB 6; Length 167;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYEDAIQ 8
Db 122 KYEDAVQ 128

RESULT 8
US-10-537-303-2
; Sequence 2, Application US/10537303
; Publication No. US20060135419A1
; GENERAL INFORMATION:
; APPLICANT: Meise, Martin
; APPLICANT: Eulenbergh, Karsten
; APPLICANT: Nguyen, Tri
; APPLICANT: Tsetsenis, Theodoros
; TITLE OF INVENTION: Proteins Involved in the Regulation of Energy Homeostasis
; FILE REFERENCE: 2923-703
; CURRENT APPLICATION NUMBER: US/10/537,303
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: PCT/EP03/013655
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: EP 02 026 921.3
; PRIOR FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-537-303-2

Query Match 68.9%; Score 31; DB 6; Length 173;
Best Local Similarity 71.4%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYEDAIQ 8
Db 125 KYEDAVQ 131

RESULT 9
US-10-449-902-32999
; Sequence 32999, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32999
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-32999

Query Match 68.9%; Score 31; DB 6; Length 250;
Best Local Similarity 44.4%; Pred. No. 41;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AOYEDAIQK 9
Db 10 ABYQEAVER 18

RESULT 10
US-10-449-902-46480
; Sequence 46480, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46480
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-46480

Query Match 68.9%; Score 31; DB 6; Length 351;
Best Local Similarity 85.7%; Pred. No. 59;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AOYEDAI 7
Db 251 AXYEDAI 257

RESULT 11
US-10-953-349-1322
; Sequence 1322, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

```
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1322
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1322

Query Match      68.9%; Score 31; DB 6; Length 691;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      2 QYEDAIQK 9
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Db      315 QYEDEVK 322

RESULT 12
US-10-953-349-1321
; Sequence 1321, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1321
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1321

Query Match      68.9%; Score 31; DB 6; Length 705;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      2 QYEDAIQK 9
      |||| :||
Db      329 QYEDEVK 336

RESULT 13
US-10-953-349-1320
; Sequence 1320, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1320
; LENGTH: 713
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1320

Query Match      68.9%; Score 31; DB 6; Length 713;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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Qy      2 QYEDAIQK 9
      |||| :||
Db      337 QYEDEVK 344

RESULT 14
US-10-449-902-53379
; Sequence 53379, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53379
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-53379

Query Match      68.9%; Score 31; DB 6; Length 723;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      2 QYEDAIQK 9
      |||| :||
Db      344 QYEDEVK 351

RESULT 15
US-10-449-902-54024
; Sequence 54024, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54024
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-54024

Query Match      68.9%; Score 31; DB 6; Length 809;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      2 QYEDAIQK 9
      |||| :||
Db      781 QYQAVTK 788
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OM protein - protein search, using sw model

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Title: US-10-774-928A-4
Perfect score: 45
Sequence: 1 AQYEDAIQK 9

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Gapop 10.0 , Gapext 0.5

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Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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- 4: /EMC_Celerra_SID33/ptodata/2/iaa/H COMB.pcp:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	9	2 US-09-809-003A-4	Sequence 4, Appli
2	35	77.8	9	2 US-09-809-003A-2	Sequence 2, Appli
3	35	77.8	637	2 US-09-949-016-8152	Sequence 8152, Ap
4	33	73.3	390	2 US-09-248-796A-17724	Sequence 17724, A
5	33	73.3	527	2 US-09-252-991A-16954	Sequence 16954, A
6	32	71.1	173	2 US-08-725-532A-3	Sequence 3, Appli
7	32	71.1	173	2 US-09-164-193-2	Sequence 2, Appli
8	32	71.1	173	2 US-09-221-448A-2	Sequence 2, Appli
9	32	71.1	293	2 US-10-163-214-10	Sequence 10, Appli
10	32	71.1	315	2 US-09-543-681A-6875	Sequence 6875, Ap
11	32	71.1	358	2 US-09-889-463A-38	Sequence 38, Appl
12	32	71.1	424	2 US-09-328-352-6614	Sequence 6614, Ap
13	32	71.1	812	2 US-09-689-065B-6	Sequence 6, Appli
14	32	71.1	812	2 US-10-210-296A-6	Sequence 6, Appli
15	32	71.1	914	2 US-10-163-214-12	Sequence 12, Appl
16	32	71.1	1729	2 US-09-134-000C-5675	Sequence 5675, Ap
17	31	68.9	29	2 US-09-270-767-56905	Sequence 56905, A
18	31	68.9	103	2 US-09-198-452A-1230	Sequence 1230, Ap
19	31	68.9	130	2 US-09-270-767-59805	Sequence 59805, A
20	31	68.9	167	2 US-08-725-532A-5	Sequence 5, Appli
21	31	68.9	170	2 US-08-725-532A-1	Sequence 1, Appli
22	31	68.9	173	2 US-08-725-532A-6	Sequence 6, Appli
23	31	68.9	173	2 US-09-164-193-20	Sequence 20, Appl
24	31	68.9	173	2 US-09-221-448A-20	Sequence 20, Appl
25	31	68.9	173	2 US-09-849-016-6368	Sequence 6368, Ap
26	31	68.9	175	2 US-09-949-016-8724	Sequence 8724, Ap

27	31	68.9	176	2 US-09-270-767-31748	Sequence 31748, A
28	31	68.9	176	2 US-09-270-767-46965	Sequence 46965, A
29	31	68.9	177	2 US-09-438-185A-867	Sequence 867, App
30	31	68.9	194	2 US-09-949-016-10907	Sequence 10907, A
31	31	68.9	227	2 US-09-252-991A-31164	Sequence 31164, A
32	31	68.9	230	2 US-09-270-767-41662	Sequence 41662, A
33	31	68.9	275	2 US-09-468-433C-24	Sequence 24, Appl
34	31	68.9	312	2 US-09-270-767-33539	Sequence 33539, A
35	31	68.9	312	2 US-09-270-767-48756	Sequence 48756, A
36	31	68.9	330	2 US-09-270-767-61311	Sequence 61311, A
37	31	68.9	451	2 US-09-270-767-45789	Sequence 45789, A
38	31	68.9	544	2 US-09-328-352-4446	Sequence 4446, Ap
39	31	68.9	581	2 US-10-104-047-3540	Sequence 3540, Ap
40	31	68.9	663	2 US-09-248-796A-19801	Sequence 19801, A
41	30	66.7	85	2 US-09-543-681A-5028	Sequence 5028, Ap
42	30	66.7	86	2 US-09-107-532A-5983	Sequence 5983, Ap
43	30	66.7	324	2 US-09-902-540-15215	Sequence 15215, A
44	30	66.7	355	2 US-09-328-352-5122	Sequence 5122, Ap
45	30	66.7	363	2 US-09-270-767-33628	Sequence 33628, A

ALIGNMENTS

RESULT 1

US-09-809-003A-4
; Sequence 4, Application US/09809003A
; Patent No. 6673351
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; FILE REFERENCE: Psoriasis
; CURRENT APPLICATION NUMBER: US/09/809,003A
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Leishmania
US-09-809-003A-4

Query Match 100.0%; Score 45; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQYEDAIQK 9
Db 1 AQYEDAIQK 9

RESULT 2

US-09-809-003A-2
; Sequence 2, Application US/09809003A
; Patent No. 6673351
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; FILE REFERENCE: Psoriasis
; CURRENT APPLICATION NUMBER: US/09/809,003A
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Leishmania
US-09-809-003A-2

Query Match 77.8%; Score 35; DB 2; Length 9;
Best Local Similarity 77.8%; Pred. No. 5e+05;

```
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AQYEDAIQK 9
Db 1 AQYEDIAQK 9

RESULT 3
US-09-949-016-8152
; Sequence 8152, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8152
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8152

Query Match 77.8%; Score 35; DB 2; Length 637;
Best Local Similarity 77.8%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AQYEDAIQK 9
Db 356 AQYEDIAQK 364

RESULT 4
US-09-248-796A-17724
; Sequence 17724, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17724
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17724

Query Match 73.3%; Score 33; DB 2; Length 390;
Best Local Similarity 75.0%; Pred. No. 98;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYEDIAQK 9
Db 288 QYHDSIQK 295

RESULT 5
```

```
US-09-252-991A-16954
; Sequence 16954, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16954
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16954

Query Match 73.3%; Score 33; DB 2; Length 527;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AQYEDIAQK 8
Db 415 AQYEDIAQK 422

RESULT 6
US-08-725-532A-3
; Sequence 3, Application US/08725532A
; Patent No. 6020179
; GENERAL INFORMATION:
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/725,532A
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0130 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 173 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
```

US-08-725-532A-3

Query Match 71.1%; Score 32; DB 2; Length 173;
Best Local Similarity 85.7%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYEDAIQ 8
Db 125 KYEDAIQ 131

RESULT 7

US-09-164-193-2
; Sequence 2, Application US/09164193C
; Patent No. 6258582

; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.

; TITLE OF INVENTION: NOVEL CSAPTF NUCLEIC ACID MOLECULES AND USES THEREFOR (as amended)

; FILE REFERENCE: MNI-051

; CURRENT APPLICATION NUMBER: US/09/164,193C

; CURRENT FILING DATE: 1998-09-30

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 173

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-164-193-2

Query Match 71.1%; Score 32; DB 2; Length 173;
Best Local Similarity 85.7%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYEDAIQ 8
Db 125 KYEDAIQ 131

RESULT 8

US-09-221-448A-2

; Sequence 2, Application US/09221448A

; Patent No. 6436685

; GENERAL INFORMATION:

; APPLICANT: Acton, Susan

; TITLE OF INVENTION: NOVEL CSAPTF PROTEIN MOLECULES AND USES THEREFOR (AS AMENDED)

; FILE REFERENCE: MNI-051DVI

; CURRENT APPLICATION NUMBER: US/09/221,448A

; CURRENT FILING DATE: 1998-12-28

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 173

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-221-448A-2

Query Match 71.1%; Score 32; DB 2; Length 173;
Best Local Similarity 85.7%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYEDAIQ 8
Db 125 KYEDAIQ 131

RESULT 9

US-10-163-214-10

; Sequence 10, Application US/10163214

; Patent No. 6849781

; GENERAL INFORMATION:

; APPLICANT: Allen, Stephen M.

; APPLICANT: Broglie, Karen E.

; APPLICANT: Butler, Karlene H.

; APPLICANT: Thorpe, Catherine J.
; TITLE OF INVENTION: Starch Synthase Isoform V
; FILE REFERENCE: BB1520 US NA
; CURRENT APPLICATION NUMBER: US/10/163,214
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/297,099
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 10
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-163-214-10

Query Match 71.1%; Score 32; DB 2; Length 293;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AQVEDAIQK 9
Db 276 SQVEDIYQK 284

RESULT 10

US-09-543-681A-6875

; Sequence 6875, Application US/09543681A

; Patent No. 6605709

; GENERAL INFORMATION:

; APPLICANT: GARY BRETON

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

; FILE REFERENCE: 2709.1002-001

; CURRENT APPLICATION NUMBER: US/09/543,681A

; CURRENT FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/128,706

; PRIOR FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 8344

; SEQ ID NO 6875

; LENGTH: 315

; TYPE: PRT

; ORGANISM: Proteus mirabilis

US-09-543-681A-6875

Query Match 71.1%; Score 32; DB 2; Length 315;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AQVEDAIQK 9
Db 105 AQVEDKAQR 113

RESULT 11

US-09-889-463A-38

; Sequence 38, Application US/09889463A

; Patent No. 6680185

; GENERAL INFORMATION:

; APPLICANT: Cahoon, Rebecca E.

; APPLICANT: Falco, Saverio C.

; APPLICANT: Kinney, Anthony J.

; APPLICANT: Miao, Guo-Hua

; TITLE OF INVENTION: Plant Polyphenol Oxidase Homologs

; FILE REFERENCE: BB1330

; CURRENT APPLICATION NUMBER: US/09/889,463A

; CURRENT FILING DATE: 2001-07-16

; PRIOR APPLICATION NUMBER: 60/119,590

; PRIOR FILING DATE: 1999-02-10

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 38

; LENGTH: 358

; TYPE: PRT

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; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (5)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (20)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (179)
; OTHER INFORMATION: Xaa = any amino acid
US-09-889-463A-38

Query Match      71.1%; Score 32; DB 2; Length 358;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 AQYEDAIQ 8
Db      43 AKYDDAVQ 50

RESULT 12
US-09-328-352-6614
; Sequence 6614, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6614
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6614

Query Match      71.1%; Score 32; DB 2; Length 424;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 YEDAIQK 9
Db      194 YEDAIAKK 200

RESULT 13
US-09-689-065B-6
; Sequence 6, Application US/09689065B
; Patent No. 6605696
; GENERAL INFORMATION:
; APPLICANT: Pfizer Products, Inc.
; TITLE OF INVENTION: LAWSONIA INTRACELLULARIS PROTEINS AND RELATED METHODS AND
; FILE REFERENCE: 3153.00187/PC10589A
; CURRENT APPLICATION NUMBER: US/09/689,065B
; CURRENT FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: US Prov. 60/160,922
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US Prov. 60/163,858
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-09-689-065B-6
```

```
Query Match      71.1%; Score 32; DB 2; Length 812;
Best Local Similarity 55.6%; Pred. No. 3.5e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AQYEDAIQK 9
Db      247 AEYEEALQK 255

RESULT 14
US-10-210-296A-6
; Sequence 6, Application US/10210296A
; Patent No. 6982114
; GENERAL INFORMATION:
; APPLICANT: Pfizer Products, Inc.
; TITLE OF INVENTION: LAWSONIA INTRACELLULARIS PROTEINS, AND RELATED METHODS AND
; FILE REFERENCE: 3153.00355/PC10589B
; CURRENT APPLICATION NUMBER: US/10/210,296A
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/689,065
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: US 60/160,922
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 60/163,858
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-10-210-296A-6
```

```
Query Match      71.1%; Score 32; DB 2; Length 812;
Best Local Similarity 55.6%; Pred. No. 3.5e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AQYEDAIQK 9
Db      247 AEYEEALQK 255

RESULT 15
US-10-163-214-12
; Sequence 12, Application US/10163214
; Patent No. 6849781
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Broglie, Karen E.
; APPLICANT: Butler, Karlene H.
; APPLICANT: Thorpe, Catherine J.
; TITLE OF INVENTION: Starch Synthase Isoform V
; FILE REFERENCE: BB1520 US NA
; CURRENT APPLICATION NUMBER: US/10/163,214
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/297,099
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 12
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-163-214-12

Query Match      71.1%; Score 32; DB 2; Length 914;
Best Local Similarity 66.7%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 AQYEDAIQK 9
Db      247 AEYEEALQK 255
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Db 897 SQYEDIYQK 905

Search completed: July 5, 2006, 19:24:24
Job time : 21.2718 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 19:20:41 ; Search time 6.41667 Seconds
(without alignments)
104.964 Million cell updates/sec

Title: US-10-774-928A-5
Perfect score: 33
Sequence: 1 AEASLY 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	553	2	IS9009
2	33	100.0	643	1	KRHU2
3	31	93.9	483	2	keratin 1, type II
4	30	90.9	243	2	keratin 8, type II
5	30	90.9	243	2	capsular polysacch
6	30	90.9	249	2	B87309
7	30	90.9	355	2	T47147
8	30	90.9	423	2	S54135
9	30	90.9	534	2	I37942
10	30	90.9	602	2	AF2771
11	30	90.9	629	2	AG2666
12	30	90.9	710	2	AG2285
13	29	87.9	268	2	C83104
14	29	87.9	351	2	T26840
15	29	87.9	364	2	T47698
16	29	87.9	386	2	T00589
17	29	87.9	444	2	E96905
18	29	87.9	494	2	A10964
19	29	87.9	585	2	T15995
20	29	87.9	591	2	A84765
21	29	87.9	629	2	T45829
22	29	87.9	669	2	A97443
23	29	87.9	669	2	AC2661
24	29	87.9	815	2	T19704
25	29	87.9	1758	2	T34393
26	28	84.8	216	2	JS0639
27	28	84.8	217	2	S38741
28	28	84.8	217	2	S45023
29	28	84.8	217	2	S41431

30	28	84.8	218	2	T06448
31	28	84.8	310	2	S43865
32	28	84.8	370	2	A25004
33	28	84.8	487	2	JT0407
34	28	84.8	489	2	S05474
35	28	84.8	490	2	JS0658
36	28	84.8	627	2	T25395
37	28	84.8	646	2	T34532
38	28	84.8	1055	2	A87364
39	27	81.8	214	2	T04872
40	27	81.8	238	2	G87267
41	27	81.8	257	2	I38025
42	27	81.8	266	2	C96913
43	27	81.8	298	2	C87417
44	27	81.8	346	2	S34165
45	27	81.8	384	2	I61769

ALIGNMENTS

RESULT 1

IS9009
epidermal keratin subunit II - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: IS9009; A61205
R:Steinert, P.M.; Parry, D.A.D.; Racoosin, E.L.; Idler, W.W.; Steven, A.C.; Trus, B.L.; F
Proc. Natl. Acad. Sci. U.S.A. 81, 5709-5713, 1984
A:Title: The complete cDNA and deduced amino acid sequence of a type II mouse epidermal
A:Reference number: IS9009; MUID:85014838; PMID:6207530
A:Accession: IS9009
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-553 <RES>
A:Cross-references: UNIPROT:P50446; UNIPARC:UPI000016CE87; GB:K02108; NID:g198634; PTDN:
R:Finch, J.; Andrews, K.; Krieg, P.; Fuerstenberger, G.; Slaga, T.; Ootsuyama, A.; Tanoo
Carcinogenesis 12, 1519-1522, 1991
A:Title: Identification of a cloned sequence activated during multi-stage carcinogenesis
A:Reference number: A61205; MUID:91316763; PMID:1713533
A:Accession: A61205
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 528-553 <FIN>
A:Cross-references: UNIPARC:UPI00001774C8
C:Genetics:
A:Gene: KER2
C:Superfamily: cytoskeletal keratin

Query Match 100.0%; Score 33; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEASLY 7

Db 339 AEASLY 345

RESULT 2

KRHU2
keratin 1, type II, cytoskeletal - human
N:Alternate names: 67K type II epidermal keratin; cytokeratin 1
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 22-Oct-1999 #text_change 10-Dec-1999
C:Accession: A22940; A02950; A43342
R:Johnson, L.D.; Idler, W.W.; Zhou, X.M.; Roop, D.R.; Steinert, P.M.
Proc. Natl. Acad. Sci. U.S.A. 82, 1896-1900, 1985
A:Reference number: A22940; MUID:85166239; PMID:2580302
A:Accession: A22940
A:Molecule type: DNA
A:Residues: 1-643 <JOH>
A:Cross-references: UNIPARC:UPI0000173D59; GB:M98776; GB:M11215; GB:M11845; GB:M11846; NJ

A>Note: translation of initiator Met is not shown

R;Steinert, P.M.; Parry, D.A.D.; Idler, W.W.; Johnson, L.D.; Steven, A.C.; Roop, D.R.
 J. Biol. Chem. 260, 7142-7149, 1985
 A>Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67,000 and human epidermal type I keratins of M-r 40,000
 A:Reference number: A92535; MUID:85207740; PMID:2581964
 A:Accession: A02950
 A:Molecule type: mRNA
 A:Residues: 151-183, 'K', 185-199, 'M', 201-204, 'K', 206-236, 'S', 238-239, 'R', 241-356, 'Y', 358-363, 'S', 638-643 <STE>
 A:Cross-references: UNIPARC:UPI000016ABD0; GB:M10938; NID:g186787; PIDN:AAA36153.1; PID:1000016ABD0
 A:Experimental source: tissue neonatal foreskin
 A>Note: the authors translated the codon CUG for residue 476 as Met
 R;Chipev, C.C.; Korge, B.P.; Markova, N.; Bale, S.J.; DiGiovanna, J.J.; Compton, J.G.; Scahill, W.; 821-828, 1992
 A>Title: A leucine----proline mutation in the H1 subdomain of keratin 1 causes epidermolysis bullosa
 A:Reference number: A43342; MUID:92386601; PMID:1381288
 A:Accession: A43342
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 144-146, 'P', 148-159, 'P', 161-183, 'K', 185-186 <CHI>
 A:Cross-references: UNIPARC:UPI0000173D5A; GB:M98776; GB:M11215; GB:M11845; GB:M11846; NID:g186787
 A>Note: sequence extracted from NCBI backbone (NCBIP:112784)
 C:Comment: The cytoskeletal and microfibrillar keratins are classified into two types, type I and type II. Type I keratins are usually found in the epidermis and type II keratins are found in the dermis.
 C:Comment: Keratin 1 is expressed in terminally differentiating epidermis.
 C:Genetics:
 A:Gene: GDB:KRT1
 A:Cross-references: GDB:128198; OMIM:139350
 A:Map position: 12q11-12q13
 A>Note: defects in this gene may result in epidermolytic hyperkeratosis
 C:Complex: heterotetramer of two type I, usually keratin 10 (see PIR:KRHU0), and two type II keratins
 C:Superfamily: cytoskeletal keratin
 C:Keywords: coiled coil; heterotetramer; intermediate filament
 F:4-179/Domain: head <HD>
 F:4-143/Region: E1 and V1 subdomains
 F:14-179/Region: H1 subdomain
 F:180-492/Domain: rod <RD>
 F:180-214/Region: coil 1A
 F:215-226/Region: linker 1
 F:227-327/Region: coil 1B
 F:328-344/Region: linker 12
 F:345-363/Region: coil 2A
 F:364-371/Region: linker 2
 F:372-492/Region: coil 2B
 F:430/Region: stutted
 F:493-643/Domain: tail <TD>
 F:493-512/Region: H2 subdomain
 F:513-643/Region: V2 and E2 subdomains

Query Match 100.0%; Score 33; DB 1; Length 643;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
 |||||
 Db 366 AEAESLY 372

RESULT 3
 A34720
 Keratin 8, type II cytoskeletal - human
 C:Species: Homo sapiens (man)
 C>Date: 06-Jul-1990 #sequence revision 06-Jul-1990 #text change 09-Jul-2004
 C:Accession: A34720; S06888; S12479; I37982; I37983; JS0487; A31942
 R.Yanamoto, R.; Kao, L.C.; McKnight, C.E.; Straus III, J.F.
 Mol. Endocrinol. 4, 370-374, 1990
 A>Title: Cloning and sequence of cDNA for human placental cyokeratin 8. Regulation of expression
 A:Reference number: A34720; MUID:90258929; PMID:1692965
 A:Accession: A34720
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-483 <YAM>
 A:Cross-references: UNIPROT:P05787; UNIPARC:UPI00001774C3; GB:M34225

R;Leube, R.E.; Bosch, F.X.; Romano, V.; Zimbelmann, R.; Hoefler, H.; Franke, W.W.
 Differentiation 33, 69-85, 1986
 A>Title: Cytokeratin expression in simple epithelia.
 A:Reference number: S06888; MUID:87134779; PMID:2434381
 A:Accession: S06888
 A:Molecule type: mRNA
 A:Residues: 205-483 <LEU>
 A:Cross-references: UNIPARC:UPI000016ABAL; EMBL:X12882
 R.Franke, W.W.
 submitted to the EMBL Data Library, September 1988
 A:Reference number: S12479
 A:Accession: S12479
 A:Molecule type: mRNA
 A:Residues: 205-309, 'I', 311-483 <PRA>
 A:Cross-references: UNIPARC:UPI000016A769; EMBL:X12882; NID:g30312; PIDN:CAA31376.1; PID:1000016A769
 R.Waseem, A.; Alexander, C.M.; Steel, J.B.; Lane, E.B.
 New Biol. 2, 464-478, 1990
 A>Title: Embryonic simple epithelial keratins 8 and 18: chromosomal location emphasizes a common evolutionary origin
 A:Reference number: I37982; MUID:91145351; PMID:1705144
 A:Accession: I37982
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-76, 'V', 78-416, 'S', 418-428, 'G', 430-431, 'S', 433-483 <RES>
 A:Cross-references: UNIPARC:UPI0000161B3E; EMBL:X74929; NID:g400415; PIDN:CAAS2882.1; PII:10000161B3E
 A:Accession: I37983
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 151-201, 'VD', 202-271 <RE2>
 A:Cross-references: UNIPARC:UPI000016ABCF; EMBL:X74981; NID:g400417; PIDN:CAAS2916.1; PII:1000016ABCF
 R.Krause, S.; Franke, W.W.
 Gene 86, 241-249, 1990
 A>Title: Organization and sequence of the human gene encoding cytokeratin 8.
 A:Reference number: JS0487; MUID:90215304; PMID:1691124
 A:Accession: JS0487
 A:Molecule type: DNA
 A:Residues: 1-76, 'V', 78-428, 'G', 'SQA', 434-483 <KRA>
 A:Cross-references: UNIPARC:UPI000016A82B; GB:M34482; NID:g181572; PIDN:AAA35763.1; PID:1000016A82B
 R.Kulesh, D.A.; Cecena, G.; Darmon, Y.M.; Vasseur, M.; Oshima, R.G.
 Mol. Cell. Biol. 9, 1553-1565, 1989
 A>Title: Posttranslational regulation of keratins: degradation of mouse and human keratins
 A:Reference number: A31942; MUID:89261783; PMID:2471065
 A:Accession: A31942
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-76, 'V', 78-231 <KUL>
 A:Cross-references: UNIPARC:UPI000016A354; GB:M26512; NID:g177796; PIDN:AAA51542.1; PID:1000016A354
 C:Comment: This protein is one of the type II cytokeratins.
 C:Genetics:
 A:Gene: GDB:KRT8
 A:Cross-references: GDB:118830; OMIM:148060
 A:Map position: 12p13.2-12q24.1
 A:Introns: 108/3; 178/2; 198/3; 230/3; 327/3; 401/2; 421/1
 C:Superfamily: cytoskeletal keratin
 C:Keywords: coiled coil; intermediate filament

Query Match 93.9%; Score 31; DB 2; Length 483;
 Best Local Similarity 85.7%; Pred. No. 26;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
 |||||
 Db 276 AEAESLY 282

RESULT 4
 JC5723
 capsular polysaccharide synthesis protein cpsB [similarity] - Streptococcus thermophilus
 C:Species: Streptococcus thermophilus
 A>Note: Streptococcus thermophilus is synonym to Streptococcus salivarius subsp. thermophilus
 C>Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 09-Jul-2004
 C:Accession: JC5723
 R.Griffin, A.M.; Morris, V.J.; Gasson, M.J.
 Gene 183, 23-27, 1996

A:Title: The cpsABCDE genes involved in polysaccharide production in *Streptococcus salivarius*
A:Reference number: JCS723; MUID:97149274; PMID:8996082
A:Accession: JCS723
A:Molecule type: DNA
A:Residues: 1-243 <CR1>
A:Cross-references: UNIPROT:O67929; UNIPROT:Q56039; UNIPROT:Q55203; UNIPROT:Q93E04; UNIPROT:Q93E05
A:Experimental source: strain NCBF 2393
C:Comment: This protein is required for polysaccharide biosynthesis.
C:Genetics:
A:Gene: cpsB
A:Start codon: GTG
C:Superfamily: Streptococcus pneumoniae capsular polysaccharide synthesis protein 14B

Query Match 90.9%; Score 30; DB 2; Length 243;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
Db 64 AEAELY 70
|||||

RESULT 5
B87309
hypothetical protein CC0483 [imported] - *Caulobacter crescentus*
C:Species: *Caulobacter crescentus*
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: B87309
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: B87309
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <STO>
A:Cross-references: UNIPROT:Q9AAW0; UNIPARC:UPI00000C706C; GB:AE005673; NID:gl3421660; F1152-464/Domain: head #status predicted <HEA>
C:Genetics:
A:Gene: CC0483

Query Match 90.9%; Score 30; DB 2; Length 249;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
Db 109 AEAELY 115
|||||

RESULT 6
T47147
hypothetical protein DKFZp761H229.1 - human (fragment)
C:Species: *Homo sapiens* (man)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47147
R:Blum, H.; Bauersachs, S.; Mewes, H.W.; Weil, B.; Wiemann, S.
submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24379
A:Accession: T47147
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-355 <AAA>
A:Cross-references: UNIPROT:Q9NSK0; UNIPARC:UPI000012DECE; EMBL:AL162078
A:Experimental source: adult amygdala; clone DKFZp761H229
C:Genetics:
A:Note: DKFZp761H229.1

Query Match 90.9%; Score 30; DB 2; Length 355;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
Db 132 AEAELY 138
|||||

RESULT 7
S54135
phytoene synthase (EC 2.5.1.-) - *Narcissus pseudonarcissus*
C:Species: *Narcissus pseudonarcissus*
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S54135
R:Schledz, M.; Lintig, J.; Albabili, S.; Kleinig, H.; Beyer, P.
submitted to the EMBL Data Library, April 1994
A:Reference number: S54135
A:Accession: S54135
A:Molecule type: mRNA
A:Residues: 1-423 <SCH>
A:Cross-references: UNIPROT:P53797; UNIPARC:UPI000013284A; EMBL:X78814; NID:g780274; PIDN:CAA30534.1; PID
C:Genetics:
A:Gene: PSY
C:Superfamily: Mycobacterium marinum phytoene synthase
C:Keywords: transferase

Query Match 90.9%; Score 30; DB 2; Length 423;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
Db 271 AEAESLY 277
|||||

RESULT 8
I37942
keratin 4, type II, cytoskeletal - human
N:Alternate names: basic cytokeratin; cytokeratin 4
C:Species: *Homo sapiens* (man)
C:Date: 12-Aug-1996 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
C:Accession: I37942; S01068; S21884; A30186; S31662
R:Wanner, R.; Forster, H.H.; Tilmans, I.; Mischke, D.
J. Invest. Dermatol. 100, 735-741, 1993
A:Title: Allelic variations of human keratins K4 and K5 provide polymorphic markers with
A:Reference number: I37942; MUID:93267125; PMID:7684424
A:Accession: I37942
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-127, 'I', 129-144 <WAN1>
A:Cross-references: UNIPROT:PI9013; UNIPARC:UPI000016AB8C; EMBL:X67683; NID:g34020; PIDN:CAA30534.1; PID
R:Leube, R.E.; Bader, B.L.; Bosch, F.X.; Zimbelmann, R.; Achtstaetter, T.; Franke, W.W.
J. Cell Biol. 106, 1249-1261, 1988
A:Title: Molecular characterization and expression of the stratification-related cytokera
A:Reference number: S01068; MUID:88198369; PMID:2452170
A:Accession: S01068
A:Molecule type: mRNA
A:Residues: 'S', 128-534 <LEU>
A:Cross-references: UNIPARC:UPI000016ABA3; EMBL:X07695; NID:g34072; PIDN:CAA30534.1; PID
R:Wanner, R.; Tilmans, I.; Mischke, D.
submitted to the EMBL Data Library, July 1991
A:Reference number: S21884
A:Accession: S21884
A:Molecule type: DNA
A:Residues: 411-534 <WAN2>
A:Cross-references: UNIPARC:UPI000016ABA5; EMBL:X61028; NID:g34076; PIDN:CAA43362.1; PID
A:Experimental source: allele K4a
C:Genetics:
A:Gene: GDB:KRT4; CVK4
A:Cross-references: GDB:120697; OMIM:123940
A:Map position: 12p11.2-12q11
A:Introns: 463/2; 475/1
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament
F1-152/Domain: head #status predicted <HEA>
F153-464/Domain: helical rod #status predicted <ROD>

F:465-534/Domain: tail #status predicted <TAI>

Query Match 90.9%; Score 30; DB 2; Length 534;

Best Local Similarity 85.7%; Pred. No. 49;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEAESLY 7

||||:|

338 AEAEALY 344

RESULT 9

E97551

A:Title: single-stranded-DNA-specific exonuclease recJ (recJ) rp528 [imported] - Agrobacterium tumefaciens

C:Species: Agrobacterium tumefaciens

C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C:Accession: E97551

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens

A:Reference number: A97359; MUID:21608551; PMID:11743194

A:Accession: E97551

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-602 <KUR>

A:Cross-references: UNIPROT:Q8UF16; UNIPARC:UPI00000D1BE7; GB:AE007869; PIDN:AAK87366.1;

C:Genetics: AGR_C_2915

A:Gene: AGR_C_2915

A:Map position: circular chromosome

C:Superfamily: single-stranded-DNA-specific exonuclease RecJ

Query Match

Best Local Similarity 90.9%; Score 30; DB 2; Length 602;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEAESLY 7

||||:|

363 AEAEALY 369

RESULT 10

AF2771

A:Title: single-stranded-DNA-specific exonuclease [imported] - Agrobacterium tumefaciens (strain AF2771)

C:Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C:Accession: AF2771

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.; E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; MUID:21608550; PMID:11743193

A:Accession: AF2771

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-602 <KUR>

A:Cross-references: UNIPROT:Q8UF16; UNIPARC:UPI00000D1BE7; GB:AE008688; PIDN:AAL42588.1;

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: recJ

A:Map position: circular chromosome

C:Superfamily: single-stranded-DNA-specific exonuclease RecJ

Query Match

Best Local Similarity 90.9%; Score 30; DB 2; Length 602;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEAESLY 7

||||:|

363 AEAEALY 369

RESULT 11

A29666

A:Title: 65K type II cytoskeletal - human

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 20-Apr-2001

C:Accession: A29666

R:Klinge, E.M.; Sylvestre, Y.R.; Freedberg, I.M.; Blumenberg, M.

J. Mol. Evol. 24, 319-329, 1987

A:Title: Evolution of keratin genes: different protein domains evolve by different pathways

A:Reference number: A29666; MUID:87254239; PMID:2499698

A:Accession: A29666

A:Molecule type: DNA

A:Residues: 1-629 <KLI>

A:Cross-references: UNIPARC:UPI00000161C35; GB:X05418; NID:934040; PIDN:CAA28991.1; PID:G34047; 92; PIDN:CAA28994.1; PID:G1335193; PIDN:CAA28995.1; PID:G1335194; GB:X03421; NID:G34047;

A>Note: the authors translated the codon AAC for residue 63 as Asp and ACA for residue 21; A>Note: the complete translation is not annotated in GenBank entries HSKER65A, HSKER65B, s mistranslated as a Met initiator codon

C:Genetics:

A:Introns: 215/3; 289/2; 309/3; 341/3; 396/3; 438/3; 512/2; 525/1

C:Superfamily: cytoskeletal keratin

C:Keywords: coiled coil

Query Match

Best Local Similarity 90.9%; Score 30; DB 2; Length 629;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEAESLY 7

||||:|

387 AEAEALY 393

RESULT 12

AG2285

A:Title: hypothetical protein all3838 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A>Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AG2285

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AG2285

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-710 <KUR>

A:Cross-references: UNIPROT:Q8Y015; UNIPARC:UPI00000CE918; GB:BA000019; PIDN:BA875537.1;

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: all3838

Query Match

Best Local Similarity 90.9%; Score 30; DB 2; Length 710;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEAESLY 7

||||:|

500 SEAESLY 506

RESULT 13

C83104

A:Title: hypothetical protein PA4327 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C:Accession: C83104

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Bri

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: C83104
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-268 <STO>
A;Cross-references: UNIPROT:Q9HW74; UNIPARC:UPI0000005CBF; GB:AE004849; GB:AE004091; NID
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA4327

Query Match 87.9%; Score 29; DB 2; Length 268;

Best Local Similarity 85.7%; Pred. No. 41;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AEAESELY 7

|||||

Db 70 AEAELLY 76

RESULT 14

T26840

hypothetical protein Y43F4B.2 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T26840

R;Matthews, L.

submitted to the EMBL Data Library, January 1998

A;Reference number: Z20276

A;Accession: T26840

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-351 <WIL>

A;Cross-references: UNIPROT:O45931; UNIPARC:UPI000017BC75; EMBL:AL021481; PIDN:CAA16331

A;Experimental source: clone Y43F4B

C;Genetics:

A;Gene: CESP:Y43F4B.2

A;Introns: 38/3; 125/3; 150/1; 200/1; 248/1; 274/3

Query Match 87.9%; Score 29; DB 2; Length 351;

Best Local Similarity 100.0%; Pred. No. 55;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EAESLY 7

|||||

Db 93 EAESLY 98

RESULT 15

T47698

mannose-1-phosphate guanylyltransferase-like protein - *Arabidopsis thaliana*

N;Alternate names: protein T22E16.250

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C;Accession: T47698

R;Renes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.H.

submitted to the Protein Sequence Database, February 2000

A;Reference number: Z24472

A;Accession: T47698

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-364 <BEN>

A;Cross-references: UNIPROT:Q9M2S0; UNIPARC:UPI000000A4F69; EMBL:AL132975

A;Experimental source: cultivar Columbia; BAC clone T22E16

C;Genetics:

A;Map position: 3

A;Introns: 37/3; 58/3; 141/3

A;Note: T22E16.250

C;Superfamily: mannose-1-phosphate guanylyltransferase

Query Match 87.9%; Score 29; DB 2; Length 364;

Best Local Similarity 85.7%; Pred. No. 57;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AEAESELY 7

|||||

Db 206 AEAELLY 212

Search completed: July 5, 2006, 19:25:13

Job time : 7.41667 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 19:01:48 ; Search time 81.375 Seconds
(without alignments)
79.571 Million cell updates/sec

Title: US-10-774-928A-5
Perfect score: 33
Sequence: 1 AEASLY 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	221	Q94J09_ORYSA	Q94J09 oryza sativ
2	33	100.0	311	Q2Y5H7_NITMU	Q2Y5H7 nitrospir
3	33	100.0	330	Q4K8B8_PSEF5	Q4K8B8 pseudomonas
4	33	100.0	340	Q92S23_RHIME	Q92S23 rhizobium m
5	33	100.0	643	K2C1_HUMAN	P04264 homo sapien
6	33	100.0	771	Q3VPN4_9CHLB	Q3VPN4 pelodictyon
7	33	100.0	5303	Q9V628_DROME	Q9V628 drosophila
8	31	93.9	98	Q42999_9CAUD	Q42999 staphylococ
9	31	93.9	220	Q75119_ORYSA	Q75119 oryza sativ
10	31	93.9	279	Q714M3_HUMAN	Q714M3 homo sapien
11	31	93.9	365	Q96910_HUMAN	Q96910 homo sapien
12	31	93.9	482	K2C8_HUMAN	P05787 homo sapien
13	31	93.9	483	Q53GJ0_HUMAN	Q53GJ0 homo sapien
14	31	93.9	483	Q6DHW5_HUMAN	Q6DHW5 homo sapien
15	31	93.9	483	Q6GMY0_HUMAN	Q6GMY0 homo sapien
16	31	93.9	483	Q5RB34_PONPY	Q5RB34 pongo pygma
17	31	93.9	499	Q9H552_HUMAN	Q9H552 homo sapien
18	31	93.9	505	Q6P4C7_HUMAN	Q6P4C7 homo sapien
19	31	93.9	667	Q351E8_9GAMM	Q351E8 alkaliimni
20	30	90.9	74	Q9Y9W7_NPVEP	Q9Y9W7 epiphyas po
21	30	90.9	120	Q53WA3_THET8	Q53WA3 thermus the
22	30	90.9	120	Q746N7_THET8	Q746N7 thermus the
23	30	90.9	147	Q4R3D5_MACFA	Q4R3D5 macaca fasc
24	30	90.9	151	Q510X7_HUMAN	Q510X7 homo sapien
25	30	90.9	157	Q46DA8_METBA	Q46DA8 methanosarc
26	30	90.9	176	Q44SN2_SOLUS	Q44SN2 solibacter
27	30	90.9	183	Q8GPD5_PSEAE	Q8GPD5 pseudomonas
28	30	90.9	184	Q5CHF8_CRYHO	Q5CHF8 cryptospori
29	30	90.9	184	Q5CTQ9_CRYPO	Q5CTQ9 cryptospori
30	30	90.9	243	Q87929_STRTR	Q87929 streptococc
31	30	90.9	243	Q55203_STRSL	Q55203 streptococc

32	30	90.9	243	2	Q56039_STRTR	Q56039 streptococc
33	30	90.9	243	2	Q7B099_STRTR	Q7B099 streptococc
34	30	90.9	243	2	Q8G954_STRTR	Q8G954 streptococc
35	30	90.9	243	2	Q8GMA7_STRTR	Q8GMA7 streptococc
36	30	90.9	243	2	Q8GP56_STRTR	Q8GP56 streptococc
37	30	90.9	243	2	Q8GP78_STRTR	Q8GP78 streptococc
38	30	90.9	243	2	Q8GP94_STRTR	Q8GP94 streptococc
39	30	90.9	243	2	Q8GPD9_STRTR	Q8GPD9 streptococc
40	30	90.9	243	2	Q5LZN2_STRTR	Q5LZN2 streptococc
41	30	90.9	243	2	Q5M488_STRTR	Q5M488 streptococc
42	30	90.9	249	2	Q9AAW0_CAUCR	Q9AAW0 caulobacter
43	30	90.9	254	2	Q4ZS06_PSEU2	Q4ZS06 pseudomonas
44	30	90.9	290	2	Q892J0_PSESM	Q892J0 pseudomonas
45	30	90.9	319	2	Q36NC9_MARHY	Q36NC9 marinobacte

ALIGNMENTS

RESULT 1
Q94J09_ORYSA PRELIMINARY; PRT; 221 AA.
AC Q94J09; Q7XJ38;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 21-FEB-2006, entry version 24.
DE GTP-binding protein GTP1.
GN Name=P0481E12.49-1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP Clade;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi C.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada M.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Ito S., Ito Y., Ito Y., Iwabuchi A., Kamiya K.,
RA Karsawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaka H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwana H., Endo T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Quanhong Y., Rihe P., Aisheng X.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Attached to the cytoplasmic side of the
CC membrane by a lipid-anchor (By similarity).
CC -!- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
CC
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DR EMBL; AP003076; BAB56054.1; -; Genomic_DNA.
DR EMBL; AX327044; AAP92129.1; -; mRNA.
DR HSSP; P07560; 1G16.
DR SMR; Q94J09; 13-180.
DR Gramene; Q94J09; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0015031; P:protein transport; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.

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DR InterPro; IPR003579; GTPase_Rab.
DR InterPro; IPR003577; GTPase_Rae.
DR InterPro; IPR003578; GTPase_Rho.
DR InterPro; IPR002041; RAN_GTP_bd.
DR InterPro; IPR001806; Ras_trnsfrmng.
DR InterPro; IPR005225; Small_GTP_bd.
DR Pfam; PF00071; Ras; 1.
DR PRINTS; PR00449; RASTRNSFRNG.
DR SMART; SM00175; RAB; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR GTP-binding; Membrane; Nucleotide-binding.
KW GTP-binding; Membrane; Nucleotide-binding.
SQ SEQUENCE 221 AA; 24193 MW; 075EB2A613B7B7F1 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
Db 150 AEAESLY 156

RESULT 2
Q2Y5H7 NITMU
ID Q2Y5H7 NITMU PRELIMINARY; PRT; 311 AA.
AC Q2Y5H7
DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 20-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Kinesin light chain precursor.
GN ORFNames=Nmul_A2707;
OS Nitrosospora multiformis (strain ATCC 25196 / NCIMB 11849).
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadales; Nitrosospora.
OX NCBI_TaxID=323848;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 25196;
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pittluck S., Chain P., Malfatti S., Shin M.,
RA Vergez L., Schmutz J., Larimer F., Land M., Hauser L., Kyrpides N.,
RA Lykidis A., Richardson P.;
RT "Complete sequence of Chromosome 1 of Nitrosospora multiformis ATCC
RT 25196".
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
KW SIGNAL.
FT SIGNAL. 1 22 Potential.
SQ SEQUENCE 311 AA; 34152 MW; AB10459D7863E758 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
Db 126 AEAESLY 132

RESULT 3
Q4K8B8 PSEFS
ID Q4K8B8 PSEFS PRELIMINARY; PRT; 330 AA.
AC Q4K8B8;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 21-FEB-2006, entry version 6.
DE Cobalamin biosynthesis protein CobC.
GN OrderedLocusNames=PFL_4427;

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OS Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=220664;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15980861; DOI=10.1038/nbt1110;
RA Paulsen I.T., Press C.M., Ravel J., Kobayashi D.Y., Myers G.S.A., Dodson R.J.,
RA Mavrodi D.V., Deboy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
RA Durkin A.S., Brinkac L.M., Daugherty S.C., Sullivan S.A.,
RA Rosovitz M.J., Gwinn M.L., Zhou L., Schneider D.J., Cartinhour S.W.,
RA Nelson W.C., Weidner J., Watkins K., Tran K., Khouri H., Pierson E.A.,
RA Pierson L.S. III, Thomashow L.S., Loper J.E.;
RT "Complete genome sequence of the plant commensal Pseudomonas
RT fluorescens Pf-5."
RT Nat. Biotechnol. 23:873-878 (2005).
RL CC -!- COPACTOR: Pyridoxal phosphate (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC -----
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CC -----
DR EMBL; CP000076; AAY93678.1; -; Genomic DNA.
DR GO; GO:0016769; P:transferase activity; transferring nitrogen. ; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR InterPro; IPR004838; NHtransf_1_BS.
DR Pfam; PF00155; Aminotran_1_2; 1.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; UNKNOWN_1.
KW Complete proteome; Pyridoxal phosphate.
SQ SEQUENCE 330 AA; 36974 MW; EBC4E27BF648D117 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 330;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
Db 279 AEAESLY 285

RESULT 4
Q92S23 RHIME
ID Q92S23 RHIME PRELIMINARY; PRT; 340 AA.
AC Q92S23
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DE Hypothetical protein.
GN OrderedLocusNames=R00202; ORFNames=SMC02877;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=1021;
RX MEDLINE=213196507; PubMed=11481430; DOI=10.1073/pnas.161294398;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masny D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Rampeger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).
CC -----
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CC -----
DR EMBL; AL591782; CAC41589.1; -; Genomic DNA.
DR BioCyc; SMEL382.SMC02877-MONOMER; -.
DR GO; GO:0005529; F:sugar binding; IEA.

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[14]
RP VARIANT NBPBK ILR-73.
RX MEDLINE=95096501; PubMed=7528239; DOI=10.1111/1523-1747.ep12412771;
RA Kimonis V., DiGiovanna J.J., Yang J.-M., Doyle S.Z., Bale S.J.,
RA Compton J.G.;
RT "A mutation in the VI end domain of keratin 1 in non-epidermolytic
RT palmar-plantar keratoderma.";
RL J. Invest. Dermatol. 103:764-769(1994).
RN [15]
RP VARIANT EHK VAL-339.
RX MEDLINE=99072666; PubMed=9856846;
RX DOI=10.1046/j.1523-1747.1998.00389.x;
RA Kremer H., Lavrijsen A.P., McLean W.H.I., Lane E.B., Melchers D.,
RA Rutter D.J., Mariman A.C., Steijlen P.M.;
RT "An atypical form of bullous congenital ichthyosiform erythroderma is
RT caused by a mutation in the L12 linker region of keratin 1.";
RL J. Invest. Dermatol. 111:1224-1226(1998).
RN [16]
RP VARIANTS AEI PHE-478 AND THR-478.
RX MEDLINE=99162195; PubMed=10053007;
RA Sybert V.P., Francis J.S., Corden L.D., Smith L.T., Weaver M.,
RA Stephens K., McLean W.H.I.;
RT "Cyclic ichthyosis with epidermolytic hyperkeratosis: a phenotype
RT conferred by mutations in the 2B domain of keratin K1.";
RL Am. J. Hum. Genet. 64:732-738(1999).
RN [17]
RP VARIANT EHK THR-187.
RX MEDLINE=99247363; PubMed=10232403;
RA Arin M.J., Longley M.A., Kuster W., Huber M., Hohl D., Rothnagel J.A.,
RA Roop D.R.;
RT "An asparagine to threonine substitution in the 1A domain of keratin
RT 1: a novel mutation that causes epidermolytic hyperkeratosis.";
RL Exp. Dermatol. 8:124-127(1999).
RN [18]
RP VARIANT AEI PHE-478.
RX MEDLINE=20062276; PubMed=10597140;
RA Michael E.J., Schneiderman P., Grossman M.E., Cristiano A.M.;
RT "Epidermolytic hyperkeratosis with polycyclic psoriasiform plaques
RT resulting from a mutation in the keratin 1 gene.";
RL Exp. Dermatol. 8:501-503(1999).
RN [19]
RP VARIANT EHK PRO-213.
RX MEDLINE=20305470; PubMed=10844506;
RX DOI=10.1046/j.1365-2230.2000.00625.x;
RA Cserhalmi-Friedman P.B., Squeo R., Gordon D., Garzon M.,
RA Schneiderman P., Grossman M.E., Cristiano A.M.;
RT "Epidermolytic hyperkeratosis in a Hispanic family resulting from a
RT mutation in the keratin 1 gene.";
RL Clin. Exp. Dermatol. 25:241-243(2000).
RN [20]
RP VARIANT EHK THR-478.
RX MEDLINE=20151078; PubMed=10688370;
RX DOI=10.1034/j.1600-0625.2000.00901016.x;
RA Arin M.J., Longley M.A., Epstein E.H. Jr., Rothnagel J.A., Roop D.R.;
RT "Identification of a novel mutation in keratin 1 in a family with
RT epidermolytic hyperkeratosis.";
RL Exp. Dermatol. 9:116-119(2000).
RN [21]
RP VARIANT EHK ASP-154.
RX MEDLINE=21423058; PubMed=11531804;
RX DOI=10.1046/j.1365-2133.2001.04327.x;
RA Whittock N.V., Ashton G.H.S., Griffiths W.A.D., Eady R.A.J.,
RA McGrath J.A.;
RT "New mutations in keratin 1 that cause bullous congenital
RT ichthyosiform erythroderma and keratin 2e that cause ichthyosis
RT bullosa of Siemens.";
RL Br. J. Dermatol. 145:330-335(2001).
RN [22]
RP INVOLVEMENT IN IHCM.
RX MEDLINE=21184521; PubMed=11286616;
RX DOI=10.1046/j.1523-1747.2001.01292.x;

Query Match

100.0%; Score 33; DB 1; Length 643;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AEASLY 7
Db 366 AEASLY 372
RESULT 6
Q3VFN4_9CHLB
ID Q3VFN4_9CHLB PRELIMINARY; PRT; 771 AA.
AC Q3VFN4;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE TPR repeat precursor.
GN ORFNames=PphaDRAFT_0572;
OS Pelodictyon phaeoclathratiforme BU-1.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/Pelodictyon group; Pelodictyon.
OX NCBI_TaxID=324925;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BU-1;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hamon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Pelodictyon
RT phaeoclathratiforme BU-1.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BU-1;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Pelodictyon
RT phaeoclathratiforme BU-1.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC EMBL; AAIK01000002; EAN26333.1; -; Genomic_DNA.
DR GO; GO:0005871; C:kinesin complex; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR InterPro; IPR002151; Kinesin_light.
DR InterPro; IPR01440; TPR_1.
DR InterPro; IPR013105; TPR_2.
DR InterPro; IPR013026; TPR_region.
DR Pfam; PF00515; TPR_1; 10.
DR PRINTS; PR00381; KINESINLIGHT.
DR SMART; SM00028; TPR; 13.
DR PROSITE; PS00005; TPR; 15.
DR PROSITE; PS50293; TPR_REGION; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 771 AA; 86933 MW; 8ECFC325793BAC93 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 771;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEASLY 7
Db 292 AEASLY 298

RESULT 7
Q9V628_DROME

ID Q9V628 DROME PRELIMINARY; PRT; 5303 AA.
 AC Q9V628; Q9V627;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 21-MAR-2001, sequence version 2.
 DT 21-FEB-2006, entry version 32.
 DE CG13185-PA.
 GN Name=CG13185; ORFNames=Dmel_CG13185;
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.P.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foeller C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Liang P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard M.S., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537558;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirkas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatic
 a genomics perspective."

RL Q9V628 DROME PRELIMINARY; PRT; 5303 AA.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kinkler J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RX Berkeley Drosophila Genome Project;
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacle J., Park S., Svirkas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RX FlyBase;
 RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
 CC -1- INTERACTION:
 CC Q9Y011:NRG15; NbExp=1; IntAct=EBI-93523; EBI-102665;
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
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 CC EMBL; AE003824; AAF58611.2; -; Genomic_DNA.
 CC IntAct; Q9V628;
 DR FlyBase; FBgn0033661; CG13185.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR InterPro; IPR011704; AAA_5.
 DR InterPro; IPR003593; AAA_Atpase.
 DR InterPro; IPR012099; Midasin.
 DR Pfam; PF07726; AAA_3; 1.
 DR Pfam; PF07728; AAA_5; 5.
 DR PIRSF; PIRSF010340; Midasin; 1.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS0234; VWFA; 1.
 KW ATP-binding; Nucleotide-binding; Transport.
 SQ SEQUENCE 5303 AA; 605199 MW; BF3D78FBAFBI6B6C CRC64;
 Query Match 100.0%; Score 33; DB 2; Length 5303;
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 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEAEESLY 7
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 DB 3378 AEAEESLY 3384
 RESULT 8
 Q4Z999 9CAUD
 ID Q4Z999 9CAUD PRELIMINARY; PRT; 98 AA.
 AC Q4Z999;
 DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
 DT 07-JUN-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE ORF129.
 OS Staphylococcus phage Twort.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
 OX NCBI_TaxID=55510;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15788529; DOI=10.1073/pnas.0501140102;
 RA Kwan T., Liu J., Dubow M., Gros P., Pelletier J.;
 RT "The complete genomes and proteomes of 27 *Staphylococcus aureus*

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RT bacteriophages."
RL Proc. Natl. Acad. Sci. U.S.A. 102:5174-5179(2005).
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AV954970; AAX92417.1; -; Genomic_DNA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR000119; Hist_DNA_bd_Bac.
DR Pfam; PF00216; Bac_DNA_binding; I.
DR ProDom; PD000945; Bac_DNABind; 1.
SQ SEQUENCE 98 AA; 11966 MW; 8CE5171F422EFDE3 CRC64;

Query Match 93.9%; Score 31; DB 2; Length 98;
Best Local Similarity 85.7%; Pred. No. 59;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
DB 28 AEAESIY 34
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RESULT 9
Q751I9 ORYSA PRELIMINARY; PRT; 220 AA.
AC Q751I9
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 10.
DE Putative GTP-binding protein RIC2.
GN Name=B1130610.13;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chow T.-Y., Haing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Lee P.-F., Chang S.-J., Chen H.-C., Chen S.-K.,
RA Chen T.-R., Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y.,
RA Hsiao S.-H., Hsiung J.-N., Hsu C.-H., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; AC130603; AAT01316.1; -; Genomic_DNA.
DR HSP; P10114; 1KAO.
DR SMR; Q751I9; 14-181.
DR -----
DR Gramene; Q751I9; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0015031; P:protein transport; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR003579; GTPase Rab.
DR InterPro; IPR003577; GTPase Ras.
DR InterPro; IPR003578; GTPase Rho.
DR InterPro; IPR002041; RAN GTP bd.
DR InterPro; IPR001806; Ras trnsfrmg.
DR InterPro; IPR002078; Sig54 interact.
DR InterPro; IPR005225; Small_GTP_bd.
DR Pfam; PF00071; Ras; 1.
DR SMART; SM00175; RAB; 1.
DR TIGRFAMs; TIGR00231; small GTP; 1.
DR PROSITE; PS00675; SIGMA54_INTERACT_1; 1.
SQ SEQUENCE 220 AA; 24146 MW; A4F728F377525145 CRC64;

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Query Match 93.9%; Score 31; DB 2; Length 220;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
DB 149 AEAESMY 155
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RESULT 10
Q7L4M3 HUMAN PRELIMINARY; PRT; 279 AA.
AC Q7L4M3
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE KR78 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BC008200; AAH08200.1; -; mRNA.
DR HSP; P08670; 1GK4.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893.SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PROSITE; PS00226; IF; 1.
SQ SEQUENCE 279 AA; 30820 MW; D9B2EB27FD985629 CRC64;

Query Match 93.9%; Score 31; DB 2; Length 279;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
DB 72 AEAESMY 78
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RESULT 11
Q96910 HUMAN PRELIMINARY; PRT; 365 AA.
ID Q96910; Q14099; Q14716; Q14717; Q96560;
AC P05787; Q14099; Q14716; Q14717; Q96560;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2005, sequence version 2.
DT 07-FEB-2006, entry version 23.
DE KRT8 protein (Fragment).
GN Name=KRT8; Synonyms=CVK8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RG NIH MGC Project;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
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CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC
CC EMBL; BC011373; AAH1373.2; -; mRNA.
DR Ensembl; ENSG00000170421; Homo sapiens.
DR GO; GO:0005982; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001684; IF.
DR InterPro; IPR002957; Keratin_I.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
DR KW Intermediate filament.
FT NON TER
SQ SEQUENCE 365 AA; 41108 MW; 57CD83091D0635E8 CRC64;
Query Match 93.9%; Score 31; DB 2; Length 365;
Best Local Similarity 85.4%; Pred. NO. 2.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AEAEASY 7
Db 158 AEAEASY 164
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RESULT 12
K2C8 HUMAN STANDARD; PRT; 482 AA.
ID K2C8; Q14099; Q14716; Q14717; Q96560;
AC P05787; Q14099; Q14716; Q14717; Q96560;
DT 01-NOV-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997, sequence version 5.
DT 07-FEB-2006, entry version 72.
DE Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keraton-8) (K8).
GN Name=KRT8; Synonyms=CVK8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=90258929; PubMed=1692965;
RA Yamamoto R., Kao L.C., McKnight C.E., Strauss J.F. III;
RT "Cloning and sequence of cDNA for human placental cytokeratin 8.
RT Regulation of the mRNA in trophoblastic cells by cAMP.";
RL Mol. Endocrinol. 4:370-374(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=90215304; PubMed=1691124; DOI=10.1016/0378-1119(90)90285-Y;
RA Krauss S., Franke W.W.;
RT "Organization and sequence of the human gene encoding cytokeratin 8.";
RL Gene 86:241-245(1990).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9114551; PubMed=1705144;
RA Waseem A., Alexander C.M., Steel J.B.;
RT "Embryonic simple epithelial keratins 8 and 18: chromosomal location
RT emphasizes difference from other keratin pairs.";
RL New Biol. 2:464-478(1990).
RN [4]
RP NUCLEOTIDE SEQUENCE, AND PHOSPHORYLATION SITES SER-23 AND SER-431.
RX MEDLINE=97207326; PubMed=9054461; DOI=10.1074/jbc.272.11.7556;
RA Ku N.-O., Omary M.B.;
RT "Phosphorylation of human keratin 8 in vivo at conserved head domain
RT serine 23 and at epidermal growth factor-stimulated tail domain serine
RT 431.";
RL J. Biol. Chem. 272:7556-7564(1997).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP NUCLEOTIDE SEQUENCE OF 1-230.
RX MEDLINE=89261783; PubMed=2471065;
RA Kulesh D.A., Cecena G., Darmon Y.M., Vasseur M., Oshima R.G.;
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"Posttranslational regulation of keratins: degradation of mouse and human keratins 18 and 8.";
Mol. Cell. Biol. 9:1553-1565(1989).
[7]
RN NUCLEOTIDE SEQUENCE OF 204-482.
RX MEDLINE=87134779; PubMed=2434381;
RA Leube R.E., Bosch F.X., Romano V., Zimbelmann R., Hofler H.,
RA Franke W.W.;
RT "Cyokeratin expression in simple epithelia. III. Detection of mRNAs encoding human cytokeratins nos. 8 and 18 in normal and tumor cells by hybridization with cDNA sequences in vitro and in situ.";
RL Differentiation 33:69-85(1986).
RN [8]
RP PARTIAL PROTEIN SEQUENCE.
RC TISSUE-Colon carcinoma;
RX MEDLINE=97295306; PubMed=9150948;
RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
RT "A two-dimensional gel database of human colon carcinoma proteins.";
RL Electrophoresis 18:605-613(1997).
RN [9]
RP INTERACTION WITH PNN.
RX PubMed=10809736; DOI=10.1074/jbc.275.20.14910;
RA Shi J., Sugrue S.P.;
RT "Dissection of protein linkage between keratins and pinin, a protein with dual location at desmosome-intermediate filament complex and in the nucleus.";
RL J. Biol. Chem. 275:14910-14915(2000).
RN [10]
RP PHOSPHORYLATION SITE SER-73.
RX PubMed=2190496; PubMed=11781324; DOI=10.1074/jbc.M111436200;
RA He T., Steplak A., Holmstrom T.H., Omary M.B., Eriksson J.E.;
RT "The intermediate filament protein keratin 8 is a novel cytoplasmic substrate for c-Jun N-terminal kinase.";
RL J. Biol. Chem. 277:10767-10774(2002).
RN [11]
RP PHOSPHORYLATION SITE SER-73, AND MUTAGENESIS OF LEU-71 AND SER-73.
RX MEDLINE=21909510; PubMed=11785853; DOI=10.1074/jbc.M107623200;
RA Ku N.O., Azhar S., Omary M.B.;
RT "Keratin 8 phosphorylation by p38 kinase regulates cellular keratin filament reorganization: modulation by a keratin 1-like disease causing mutation.";
RL J. Biol. Chem. 277:10775-10782(2002).
RN [12]
RP INTERACTION WITH HCV CORE PROTEIN.
RX PubMed=15846844; DOI=10.1002/emc.200401093;
RA Kang S.-M., Shin M.-J., Kim J.-H., Oh J.-W.;
RT "Proteomic profiling of cellular proteins interacting with the hepatitis C virus core protein.";
RL Proteomics 5:2227-2237(2005).
RN [13]
RP VARIANTS CRYPTOGENIC CIRRHOSIS VAL-52; CYS-53 AND CYS-61, AND VARIANT VAL-62.
RX PubMed=12724528; DOI=10.1073/pnas.0936165100;
RA Ku N.-O., Darling J.M., Krams S.M., Esquivel C.O., Keesfe E.B., Sibley R.K., Lee Y.M., Wright T.L., Omary M.B.;
RT "Keratin 8 and 18 mutations are risk factors for developing liver disease of multiple etiologies.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:6063-6068(2003).
CC -!- SUBUNIT: Heterotrimer of two type I and two type II keratins. Keratin 8 associates with keratin 18. Interacts with HCV core protein and PNN.
CC -!- PTM: Phosphorylation on serine residues is enhanced during EGF stimulation and mitosis. Ser-73 phosphorylation plays an important role in keratin filament reorganization.
CC -!- DISEASE: Defects in KRT8 are a cause of cryptogenic cirrhosis [MIM:215600].
CC -!- MISCELLANEOUS: There are two types of cytoskeletal and microfibrillar keratin: I (acidic; 40-55 kDa) [K9 to K20] and II (neutral to basic; 56-70 kDa) [K1 to K8].
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -!- DATABASE: NAME=Human Intermediate Filament Mutation Database; WWW="http://www.interfil.org".

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CC -----
DR EMBL; M34225; AA35748.1; -; mRNA.
DR EMBL; M34482; AA35763.1; -; Genomic_DNA.
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DR EMBL; X98614; CAA67203.1; -; mRNA.
DR EMBL; M26512; AAAS1542.1; -; mRNA.
DR EMBL; BC00654; AAH0654.2; ALT_INIT; mRNA.
DR EMBL; X12882; CAA31376.1; -; mRNA.
DR EMBL; X74981; CAA52916.1; -; Genomic_DNA.
DR PIR; A34720; A34720.
DR HSSP; P08670; 1GK7.
DR INACT; P05787; -.
DR GLYCOSUITEDB; P05787; -.
DR SWISS-2DPAGE; P05787; HUMAN.
DR SIENA-2DPAGE; P05787; -.
DR Ensembl; ENSG00000170421; Homo sapiens.
DR HGNC; HGNC:6446; KRT8.
DR MIM; 148050; gene.
DR MIM; 215600; phenotype.
DR LinkHub; P05787; -.
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DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; NAS.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
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DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Coiled coil; Direct protein sequencing; Disease mutation;
KW Intermediate filament; Keratin; Phosphorylation; Polymorphism.
FT INIT MET 0 0
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FT REGION 1 89 /FTid=PRO_0000063740.
FT REGION 90 397 Head.
FT REGION 90 125 Rod.
FT REGION 126 142 Coil 1A.
FT REGION 143 234 Linker 1.
FT REGION 235 258 Coil 1B.
FT REGION 259 397 Linker 12.
FT REGION 260 381 Coil 2.
FT REGION 398 482 Necessary for interaction with PNN.
FT SITE 341 341 Tail.
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FT MOD_RES 73 73 Phosphoserine (by MAPK).
FT MOD_RES 431 431 Phosphoserine (by CAMK2 and MAPK).
FT VARIANT 52 52 G -> V (in cryptogenic cirrhosis).
FT VARIANT 53 53 Y -> C (in cryptogenic cirrhosis).
FT VARIANT 61 61 G -> C (in cryptogenic cirrhosis).
FT /FTid=VAR_023058.
FT /FTid=VAR_023059.
FT /FTid=VAR_023060.
Query Match 93.9%; Score 31; DB 1; Length 482;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AEAESLY 7
DB 275 AEAESMY 281
RESULT 13
Q53GJ0 HUMAN
AC Q53GJ0_HUMAN PRELIMINARY; PRT; 483 AA.
ID Q53GJ0;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.

DT 24-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Keratin 8 variant (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=94171032; PubMed=8125298; DOI=10.1016/0378-1119(94)90802-8;
 RA Maruyama K., Sugano S.;
 RT "Oligo-capping: a simple method to replace the cap structure of
 RT eucaryotic mRNAs with oligoribonucleotides.";
 RL Gene 138:171-174 (1994).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=9803898; PubMed=9373149; DOI=10.1016/S0378-1119(97)00411-3;
 RA Suzuki Y., Yoshitomo K., Maruyama A., Sugano S.;
 RT "Construction and characterization of a full length-enriched and a 5'-
 RT end-enriched cDNA library.";
 RL Gene 200:149-156(1997).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
 RA Tanaka A., Yokoyama S.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the intermediate filament family.
 CC
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 CC
 CC EMBL; AK222941; BAD96661.1; -; mRNA.
 DR Ensembl; ENSG00000170421; Homo sapiens.
 DR GO; GO:0005882; C:intermediate filament; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR001664; IF.
 DR InterPro; IPR002957; Keratin I.
 DR InterPro; IPR003054; Keratin II.
 DR PANTHER; PTHR18893:SF5; Keratin_II; 1.
 DR Pfam; PF00038; Filament; 1.
 DR PRINTS; PR01248; TYPE1KERATIN.
 DR PRINTS; PR01276; TYPE2KERATIN.
 DR PROSITE; PS00226; IF; 1.
 DR PROSITE; PS00226; IF; 1.
 KW Intermediate filament; Keratin.
 FT NON TER 1 1
 SQ SEQUENCE 483 AA; 53738 MW; D4F01FEB859C93D3 CRC64;
 Query Match 93.9%; Score 31; DB 2; Length 483;
 Best Local Similarity 85.7%; Pred. NO. 3e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEASLY 7
 Db 276 AEASMY 282
 RESULT 14
 Q6DHW5 HUMAN
 ID Q6DHW5_HUMAN PRELIMINARY; PRT; 483 AA.
 AC Q6DHW5;
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE Keratin 8.
 GN Name=KRT8;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the intermediate filament family.
 CC
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 CC
 CC EMBL; BC075839; AAH75839.1; -; mRNA.
 DR Ensembl; ENSG00000170421; Homo sapiens.
 DR GO; GO:0005882; C:intermediate filament; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR001664; IF.
 DR InterPro; IPR002957; Keratin I.
 DR InterPro; IPR003054; Keratin II.
 DR PANTHER; PTHR18893:SF5; Keratin_II; 1.
 DR Pfam; PF00038; Filament; 1.
 DR PRINTS; PR01248; TYPE1KERATIN.
 DR PRINTS; PR01276; TYPE2KERATIN.
 DR PROSITE; PS00226; IF; 1.
 DR PROSITE; PS00226; IF; 1.
 KW Intermediate filament; Keratin.
 SQ SEQUENCE 483 AA; 53704 MW; B0BC730B65929D37 CRC64;
 Query Match 93.9%; Score 31; DB 2; Length 483;
 Best Local Similarity 85.7%; Pred. NO. 3e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEASLY 7
 Db 276 AEASMY 282
 RESULT 15
 Q6GMY0 HUMAN
 ID Q6GMY0_HUMAN PRELIMINARY; PRT; 483 AA.
 AC Q6GMY0;
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 13.
 DE Keratin 8.
 GN Name=KRT8;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;

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RN NUCLEOTIDE SEQUENCE.
RP
RC TISSUE=Placenta;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN NUCLEOTIDE SEQUENCE.
RP
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----
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CC -----
DR EMBL; BC073760; AAH73760.1; -; mRNA.
DR Ensembl; ENSG00000170421; Homo sapiens.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893:SrF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
SQ SEQUENCE 483 AA; 53750 MW; 09C617DC2AFBDEE3 CRC64;
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Query Match          93.9%; Score 31; DB 2; Length 483;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AEASLY 7
Db 276 AEASMY 282
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Search completed: July 5, 2006, 19:18:17
Job time : 83.375 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 18:44:12 ; Search time 64.6042 Seconds
(without alignments)
49.540 Million cell updates/sec

Title: US-10-774-928A-5

Perfect score: 33
Sequence: 1 AEAESLY 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq 8:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*
- 10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	33	100.0	7	6	Aao26385 Psoriasis
2	33	100.0	7	9	Adv04410 Leishmani
3	33	100.0	10	6	Aao26387 Psoriasis
4	33	100.0	10	9	Adv04412 Leishmani
5	33	100.0	12	8	Adi19066 Rat pepi
6	33	100.0	297	8	Adt60195 Plant pol
7	33	100.0	644	8	Adq17549 Human sof
8	33	100.0	644	9	Aea15501 Human pol
9	33	100.0	5303	4	Abb67866 Drosophil
10	31	93.9	125	4	Abg20747 Novel hum
11	31	93.9	180	8	Adn99441 Novel hum
12	31	93.9	198	8	Abm80639 Tumour-as
13	31	93.9	207	8	Adx73916 Plant ful
14	31	93.9	237	8	Adx76784 Plant ful
15	31	93.9	273	4	Abg26376 Novel hum
16	31	93.9	275	4	Abg15282 Novel hum
17	31	93.9	279	9	Aea30129 Human: cyt
18	31	93.9	279	10	Aef25706 Human: cyt
19	31	93.9	398	6	Aae38086 Human cyt
20	31	93.9	428	8	Adp29327 Human sec
21	31	93.9	429	4	Abg19547 Novel hum
22	31	93.9	429	4	Abg19546 Novel hum
23	31	93.9	431	7	Adj70823 Human hea

24	31	93.9	476	8	ADR66033	Adr66033 Human pro
25	31	93.9	476	8	ADR66931	Adr66931 Human pro
26	31	93.9	477	4	AAU06112	Aau06112 Novel hum
27	31	93.9	480	10	Aef92273	Aef92273 Human cyt
28	31	93.9	481	6	ABU52604	Abu52604 Human NOV
29	31	93.9	482	6	AAE38082	Aae38082 Human cyt
30	31	93.9	482	8	ADT51418	Adt51418 Human ker
31	31	93.9	482	8	ADT51421	Adt51421 Human ker
32	31	93.9	482	8	ADT51419	Adt51419 Human ker
33	31	93.9	482	8	ADT51422	Adt51422 Human ker
34	31	93.9	482	8	ADT51414	Adt51414 Human ker
35	31	93.9	482	8	ADT51420	Adt51420 Human ker
36	31	93.9	482	8	ADT51415	Adt51415 Human ker
37	31	93.9	482	8	ADT51416	Adt51416 Human ker
38	31	93.9	482	8	ADT51405	Adt51405 Wild-type
39	31	93.9	482	8	ADT51412	Adt51412 Human ker
40	31	93.9	482	8	ADT51413	Adt51413 Human ker
41	31	93.9	482	8	ADT51417	Adt51417 Human ker
42	31	93.9	483	5	AAU84289	Aau84289 Human end
43	31	93.9	483	6	ABR47511	Abra47511 Breast ca
44	31	93.9	483	6	ABU57621	Abu57621 Different
45	31	93.9	483	6	ADA11040	Ada11040 Human CDN

ALIGNMENTS

RESULT 1
AAO26385
ID AAO26385 standard; peptide; 7 AA.
XX
AC AAO26385;
XX
DT 30-JAN-2003 (first entry)
XX
DE Psoriasis treating immunotherapeutic peptide, SEQ ID No 5.
XX
KW Antipsoriatic; immunostimulant; gene therapy; pharmaceutical composition;
KW vaccine; immunogenic variant; immunotherapeutic agent; psoriasis;
KW gene therapy.
XX
OS Leishmania sp.
XX
PN WO200274239-A2.
XX
PD 26-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006496.
XX
PR 16-MAR-2001; 2001US-00809003.
XX
(AKIV-) AKIVA LLC.
XX
O'daly JA;
XX
WPI; 2003-018763/01.
XX
New polypeptide and immunogenic variants comprising amino acid sequences of particulate antigens, useful for the treatment and clinical remission of psoriasis.
XX
Claim 1; Page 43; 56pp; English.
XX
The invention relates to a polypeptide comprising an isolated amino acid sequence or immunogenic variants selected from any of 14 fully defined sequences of 7-16 amino acids, given in the specification. The sequences of immunotherapeutic agents and a pharmaceutical compositions comprising polynucleotides and vectors of the invention are useful for the treatment and clinical remission of psoriasis. The isolated nucleic acids are useful as probes. The sequences of the invention can be used in the treatment of disorders by gene therapy. This sequence represents one of the 14 immunotherapeutic peptides of the invention

SQ Sequence 7 AA;

Query Match 100.0%; Score 33; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
| | | | |
Db 1 AEAESLY 7

RESULT 2
ADV04410
ID ADV04410 standard; peptide; 7 AA.
XX
AC ADV04410;
XX
DT 24-FEB-2005 (first entry)
XX
DE Leishmania immunotherapeutic peptide SEQ ID NO:5.
XX
KW T-lymphocyte; immunogenicity; antigen; antipsoriatic; immunostimulant;
KW psoriasis.
XX
OS Leishmania sp.
XX
PN US2004241168-A1.
XX
PD 02-DEC-2004.
XX
PF 09-FEB-2004; 2004US-00774928.
XX
PR 16-MAR-2001; 2001US-00809003.
PR 17-OCT-2003; 2003US-00887892.
XX
PA (ODAL/) ODALY J A.
XX
PI Odaly JA;
XX
DR WPI; 2005-011563/01.
XX
PT Inhibiting selectively T-cell rolling in human, by administering compound
PT interfering with cutaneous lymphocyte antigen-E selectin interaction and
PT leukocyte function associated antigen-1 interaction.
XX
PS Claim 9; SEQ ID NO 5; 21pp; English.
XX
CC The invention relates to a novel method for selectively inhibiting T-cell
CC rolling in a human host, comprising administering a compound that
CC selectively interferes with the cutaneous lymphocyte antigen (CLA)-E
CC selectin interaction and leukocyte function associated antigen (LFA) -
CC 1/intercellular adhesion molecule (ICAM) and very late antigen
CC (VLA)/vascular cell adhesion molecule (VCAM) interactions. The compound
CC includes an immunotherapeutic agent, which comprises a purified protein
CC extract that is isolated by diethylaminoethyl Sephadex chromatography of
CC a Nonidet P-40 insoluble particulate antigen fraction derived from
CC isolated killed cells of anastigotes from one or more species of the
CC Leishmania genus, where the particulate antigen fraction is solubilized
CC with 8M urea and 0.025 M Tris(hydroxymethyl)aminomethane pH 8.3 applied
CC to diethylaminoethyl Sephadex and is eluted with a solution comprising
CC 0.1 M sodium chloride, 8 M urea and 0.025 M
CC Tris(hydroxymethyl)aminomethane pH 8.3, and the purified protein extract
CC includes polypeptides having apparent molecular weights of 73, 80 and 82
CC kDa, after total reduction and alkylation. The species is L. amazonensis,
CC L. venezuelensis, L. brasiliensis and/or L. chagasi. A compound of the
CC invention has antipsoriatic and immunostimulant activity, and inhibits T-
CC cell rolling by interfering with CLA-E selectin interaction and LFA-
CC 1/ICAM and VLA/VCAM interactions. The method is useful for selectively
CC inhibiting T-cell rolling in a human host, and for treating psoriasis.
CC The present sequence represents a Leishmania peptide used in the
CC invention.
XX

Sequence 7 AA;

Query Match 100.0%; Score 33; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
| | | | |
Db 1 AEAESLY 7

RESULT 3
AAO26387
ID AAO26387 standard; peptide; 10 AA.
XX
AC AAO26387;
XX
DT 30-JAN-2003 (first entry)
XX
DE Psoriasis treating immunotherapeutic peptide, SEQ ID NO 7.
XX
KW Antipsoriatic; immunostimulant; gene therapy; pharmaceutical composition;
KW vaccine; immunogenic variant; immunotherapeutic agent; psoriasis;
KW gene therapy.
XX
OS Leishmania sp.
XX
PN WO200274239-A2.
XX
PD 26-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006496.
XX
PR 16-MAR-2001; 2001US-00809003.
XX
PA (AKIV-) AKIVA LLC.
XX
PI O'daly JA;
XX
DR WPI; 2003-018763/01.
XX
PT New polypeptide and immunogenic variants comprising amino acid sequences
PT of particulate antigens, useful for the treatment and clinical remission
PT of psoriasis.
XX
PS Claim 1; Page 43; 56pp; English.
XX
CC The invention relates to a polypeptide comprising an isolated amino acid
CC sequence or immunogenic variants selected from any of 14 fully defined
CC sequences of 7-16 amino acids, given in the specification. The
CC immunotherapeutic agents and a pharmaceutical compositions comprising
CC polynucleotides and vectors of the invention are useful for the treatment
CC and clinical remission of psoriasis. The isolated nucleic acids are
CC useful as probes. The sequences of the invention can be used in the
CC treatment of disorders by gene therapy. This sequence represents one of
CC the 14 immunotherapeutic peptides of the invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 33; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
| | | | |
Db 1 AEAESLY 7

RESULT 4
ADV04412
ID ADV04412 standard; peptide; 10 AA.
XX
AC ADV04412;
XX

DT 24-FEB-2005 (first entry)
XX Leishmania immunotherapeutic peptide SEQ ID NO:7.
DE
XX
XX T-lymphocyte; immunogenicity; antigen; antipsoriatic; immunostimulant;
KW psoriasis.
KW
XX
XX Leishmania sp.
OS
XX
XX US2004241168-A1.
PN
XX
XX 02-DEC-2004.
PD
XX
XX 09-FEB-2004; 2004US-00774928.
PF
XX
XX 16-MAR-2001; 2001US-00809003.
PR
XX
XX 17-OCT-2003; 2003US-00687892.
PR
XX
XX (ODAL/) ODALY J A.
PA
XX
XX Odaly JA;
PI
XX
XX WPI; 2005-011563/01.
DR
XX
XX Inhibiting selectively T-cell rolling in human, by administering compound
PT interfering with cutaneous lymphocyte antigen-E selectin interaction and
PT leukocyte function associated antigen-1 interaction.
PT
XX
XX Claim 18; SEQ ID NO 7; 21pp; English.
PS
XX
XX The invention relates to a novel method for selectively inhibiting T-cell
CC rolling in a human host, comprising administering a compound that
CC selectively interferes with the cutaneous lymphocyte antigen (CLA)-E
CC selectin interaction and leukocyte function associated antigen (LFA)-
CC 1/intercellular adhesion molecule (ICAM) and very late antigen
CC (VLA)/vascular cell adhesion molecule (VCAM) interactions. The compound
CC includes an immunotherapeutic agent, which comprises a purified protein
CC extract that is isolated by diethylaminoethyl Sephadex chromatography of
CC a Nonidet P-40 insoluble particulate antigen fraction derived from
CC isolated killed cells of amastigotes from one or more species of the
CC Leishmania genus, where the particulate antigen fraction is solubilized
CC with 8M urea and 0.025 M Tris(hydroxymethyl)aminomethane pH 8.3 applied
CC to diethylaminoethyl Sephadex and is eluted with a solution comprising
CC 0.1 M sodium chloride, 8 M urea and 0.025 M
CC Tris(hydroxymethyl)aminomethane pH 8.3, and the purified protein extract
CC includes polypeptides having apparent molecular weights of 73, 80 and 82
CC kDa, after total reduction and alkylation. The species is L.amazonensis,
CC L. venezuelensis, L. brasiliensis and/or L. chagasi. A compound of the
CC invention has antipsoriatic and immunostimulant activity, and inhibits T-
CC cell rolling by interfering with CLA-E selectin interaction and LFA-
CC 1/ICAM and VLA/VCAM interactions. The method is useful for selectively
CC inhibiting T-cell rolling in a human host, and for treating psoriasis.
CC The present sequence represents a Leishmania peptide used in the
CC invention.
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 33; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AEAESLY 7
Db 1 AEAESLY 7
DE
XX
XX RESULT 5
ADI19066
ID ADI19066 standard; peptide; 12 AA.
XX
XX AC ADI19066;
XX
XX DT 15-APR-2004 (first entry)

XX Rat peptide #1 used in the exemplification of the invention.
DE
XX
XX Detrusor estrogen-regulated protein; DERP; DERP-related disorder;
KW impaired detrusor contractility; urinary retention; Alzheimer's disease;
KW cardiovascular disease; osteoporosis; smooth muscle function; nootropic;
KW neuroprotective; osteopathic; immunostimulant; therapy; rat.
XX
XX Rattus norvegicus.
OS
XX
XX US2003232374-A1.
PN
XX
XX 18-DEC-2003.
PD
XX
XX 22-MAY-2003; 2003US-00444575.
PF
XX
XX 23-MAY-2002; 2002US-0382830P.
PR
XX
XX (KUCH/) KUCHEL G A.
PA
XX
XX (ZHUQ/) ZHU Q.
PA
XX
XX Kuchel GA, Zhu Q;
PI
XX
XX WPI; 2004-052160/05.
DR
XX
XX Novel purified immunogenic detrusor estrogen-regulated polypeptide
PT fragment useful for generating antibodies and as screening reagents.
PT
XX
XX Example 11; SEQ ID NO 16; 48pp; English.
PS
XX
XX The present invention relates to a immunogenic polypeptide fragment
CC comprising ten to fifty consecutive amino acids of a fully defined
CC detrusor estrogen-regulated protein (DERP). The invention is useful for
CC diagnosing DERP-related disorder such as impaired detrusor contractility,
CC urinary retention, Alzheimer's disease, cardiovascular disease,
CC osteoporosis, or their combinations. The invention is also useful for
CC generating antibodies, as reagents in diagnostic assays, as identifiers
CC of other gene products involved in the regulation of bladder and smooth
CC muscle function, as screening reagents useful for detecting compounds
CC that are used in the regulation of bladder and smooth muscle function,
CC and as pharmaceutical agents useful for treating symptoms relating to
CC bladder and smooth muscle function. The present sequence is rat peptide
CC used in the exemplification of the invention.
XX
XX Sequence 12 AA;
SQ
Query Match 100.0%; Score 33; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AEAESLY 7
Db 3 AEAESLY 9
DE
XX
XX RESULT 6
ADT60195
ID ADT60195 standard; protein; 297 AA.
XX
XX AC ADT60195;
XX
XX DT 13-JAN-2005 (first entry)
DE
XX
XX Plant polypeptide, SEQ ID 10272.
DE
XX
XX Plant; transgenic; cold tolerance; growth rate; drought tolerance;
KW disease resistance; galactonnanan production; plant growth regulator;
KW heat tolerance; herbicide tolerance; lignin production;
KW extreme osmotic condition tolerance; pathogens resistance;
KW pest resistance; yield improvement; seed oil yield; seed protein yield.
XX
XX Viridiplantae.
OS
XX

PN US2004216190-A1.
 XX
 PD 28-OCT-2004.
 XX
 PF 18-DEC-2003; 2003US-00739930.
 XX
 PR 28-APR-2003; 2003US-00424599.
 XX
 PR 28-APR-2003; 2003US-00425115.
 XX
 PA (KOVA/) KOVALIC D K.
 XX
 PI Kovalic DK;
 XX
 DR WPI; 2004-757369/74.
 XX
 PT New recombinant DNA constructs useful in the field of biochemistry and
 PT genetics, and in particular for producing transgenic plants with improved
 PT biological characteristics.
 XX
 PS Claim 2; SEQ ID NO 10272; 14pp; English.
 XX
 CC The invention relates a recombinant DNA construct comprising a
 CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:
 CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
 CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,
 CC Arabidopsis, wheat and rape but the specification does not indicate which
 CC sequences is derived from which organism. Also included is a method of
 CC producing a plant having an improved property, comprising transforming a
 CC plant with a recombinant DNA construct comprising a promoter region
 CC functional in a plant cell operably joined to a polynucleotide encoding a
 CC polypeptide associated with the property, and growing the transformed
 CC plant. The property is selected from improving plant cold tolerance, for
 CC manipulating growth rate in plant cells by modification of the cell cycle
 CC pathway, for improving plant drought tolerance, for providing increased
 CC resistance to plant disease, for galactomannan production, for production
 CC of plant growth regulators, for improving plant heat tolerance, for
 CC improving plant tolerance to herbicides, for increasing the rate of
 CC homologous recombination in plants, for lignin production, for improving
 CC plant tolerance to extreme osmotic conditions, for improving plant
 CC tolerance to pathogens or pests, for yield improvement by modification of
 CC photosynthesis, for modifying seed oil yield and/or content, for
 CC modifying seed protein yield and/or content, for yield improvement by
 CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake
 CC and for yield improvement by providing improved plant growth and
 CC development under at least one stress condition. The polynucleotide may
 CC also encode a plant transcription factor. The methods and compositions of
 CC the present invention are useful in the field of biochemistry and
 CC genetics, in particular for producing transgenic plants with improved
 CC biological characteristics such as increased yield, improved nitrogen
 CC flow, increasing plant tolerance to cold or heat, improving plant
 CC tolerance to extreme osmotic and drought conditions, and improving plant
 CC tolerance to plant pests or pathogens. They can also be used in physical
 CC arrays of molecules, plant breeding markers, computer-based storage and
 CC analysis systems. The present sequence is one of the 5544 plant protein
 CC sequences of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20040216190.
 XX
 SQ Sequence 297 AA;
 Query Match 100.0%; Score 33; DB 8; Length 297;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEAESLY 7
 Db 226 AEAESLY 232
 |||||
 RESULT 7
 ADQ17549
 ID ADQ17549 standard; protein; 644 AA.

XX ADQ17549;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 366.
 XX
 KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004048938-A2.
 XX
 PD 10-JUN-2004.
 XX
 PF 26-NOV-2003; 2003WO-US038193.
 XX
 PR 26-NOV-2002; 2002US-0429739P.
 XX
 PA (PROT-) PROTEIN DESIGN LABS INC.
 XX
 PI Aziz N, Ginsburg WM, Zlotnik A;
 XX
 DR WPI; 2004-441208/41.
 XX
 PT Early detection of soft tissue sarcoma comprises determining expression
 PT of a gene in a first soft tissue sample and a normal soft tissue sample
 PT and comparing the gene expression, also useful in treating soft tissue
 PT sarcoma.
 XX
 PS Example 2; SEQ ID NO 366; 210pp; English.
 XX
 CC The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in both soft tissue samples, where a higher level
 CC of protein expression in the first soft tissue sample indicates the
 CC presence of soft tissue sarcoma. The method of the invention has
 CC cytostatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC protein of the invention. The current sequence is not shown within the
 CC specification per se but was submitted in CD format by the inventor.
 XX
 SQ Sequence 644 AA;
 Query Match 100.0%; Score 33; DB 8; Length 644;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEAESLY 7
 Db 367 AEAESLY 373
 |||||
 RESULT 8
 AEA15501
 ID AEA15501 standard; protein; 644 AA.
 XX
 AC AEA15501;
 XX
 DT 28-JUL-2005 (first entry)
 XX
 DE Human polypeptide #120.
 XX
 KW Diagnosis; prognosis; cancer; breast tumor; ovary tumor; stomach tumor;
 KW colon tumor; esophagus tumor; bladder tumor; non-small-cell lung cancer;
 KW cytostatic; neoplasm.
 XX
 OS Homo sapiens.
 XX

PN WO2005047534-A2.
XX
PD 26-MAY-2005.
XX
XX
PF 15-OCT-2004; 2004WO-EP011599.
XX
PR 28-OCT-2003; 2003EP-00024565.
XX
PA (FARB) BAYER HEALTHCARE AG.
XX
XX Wirtz R, Munnes M;
PI
XX
DR WPI; 2005-372393/38.
XX
DR N-PSDB; AEA15423.
XX
PT Predicting a response to cancer treatment by detecting at least 2
PT markers, which are genes or genomic nucleic acid sequences that are
PT located on one chromosomal region, which is altered in malignant
PT neoplasia.
XX
PS Claim 7; SEQ ID NO 463; 464pp; English.
XX
XX The invention relates to a method of predicting response to cancer
CC treatment comprising detection of at least 2 markers, where the markers
CC are genes and fragments or genomic nucleic acid sequences that are
CC located on one chromosomal region, which is altered in malignant
CC neoplasia. The invention also relates to a method for the prediction,
CC diagnosis or prognosis of malignant neoplasia, methods for detecting
CC deregulations in malignant neoplasia and breast cancer, a method of
CC determining the phenotype of a cell or tissue, a method for identifying
CC genomic regions which are altered on the chromosomal level and encode
CC genes that are linked by function and are differentially expressed in
CC malignant neoplasia and breast cancer, methods of screening for agents
CC which regulate the activity of a polypeptide or a polynucleotide and
CC antibodies that specifically bind to a full length or partial
CC polypeptide. The method is useful for predicting response to cancer
CC treatment. The methods and compositions are useful for predicting,
CC diagnosing, prognosing, preventing or treating malignant neoplasia
CC including breast cancer, ovarian cancer, gastric cancer, colon cancer,
CC esophageal cancer, mesenchymal cancer, bladder cancer or non-small-cell
CC lung cancer. This sequence represents a human polypeptide used in the
CC scope of the invention.
XX
SQ Sequence 644 AA;

Query Match 100.0%; Score 33; DB 9; Length 644;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
Db 367 AEAESLY 373
|||||||
RESULT 9
ABB67866
ID ABB67866 standard; protein; 5303 AA.
XX
AC ABB67866;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 30390.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
XX WO200171042-A2.
PN
XX
PD 27-SEP-2001.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
diagnostics, forensics, gene mapping, identification of mutations

PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL11969.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 30390; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 5303 AA;

Query Match 100.0%; Score 33; DB 4; Length 5303;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
Db 3378 AEAESLY 3384
|||||||
RESULT 10
ABG20747
ID ABG20747 standard; protein; 125 AA.
XX
AC ABG20747;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #20738.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
XX WO200175067-A2.
PN
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS84934.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations

CC cancer, psoriasis, diabetes, early aging, hormonal imbalance, ischemic
CC heart disease or ulcerative colitis. This sequence corresponds to a
CC protein of the invention.
XX
XX
SQ Sequence 180 AA;

Query Match 93.9%; Score 31; DB 8; Length 180;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
Db 138 AEAESMY 144
|||||:|

RESULT 12
ABM80639
ID ABM80639 standard; protein; 198 AA.
XX
AC ABM80639;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour-associated antigenic target (TAT) polypeptide PRO81266, SEQ:1661.
XX
DE Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004030615-A2.
XX
PD 15-APR-2004.
XX
PF 29-SEP-2003; 2003WO-US028547.
XX
PR 02-OCT-2002; 2002US-0414971P.
XX
PA (GETH) GENENTECH INC.
XX
PI Wu TD, Zhang Z, Zhou Y;
XX
DR WPI; 2004-347921/32.
XX
DR N-PSDB; ACN38265.
XX
PT New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
PS Claim 12; SEQ ID NO 1661; 7273pp; English.
XX

CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central

CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX
XX
SQ Sequence 198 AA;

Query Match 93.9%; Score 31; DB 8; Length 198;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
Db 98 AEAESMY 104
|||||:|

RESULT 13
ADX73916
ID ADX73916 standard; protein; 207 AA.
XX
AC ADX73916;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polypeptide seqid 43282.
XX
DE plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAK/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
DR WPI; 2004-180133/17.
XX

PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 43282; 15pp; English.
XX

CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring

CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 273 AA;

Query Match 93.9%; Score 31; DB 4; Length 273;
 Best Local Similarity 85.7%; Pred. No. 2.2e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
 |||||
 Db 264 AEAESMY 270

Search completed: July 5, 2006, 19:08:52
 Job time : 65.6042 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 20:52:16 ; Search time 37.0417 Seconds
(without alignments)
87.537 Million cell updates/sec

Title: US-10-774-928A-5

Perfect score: 33

Sequence: 1 AEAESLY 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	7	5	US-10-774-928-5
2	33	100.0	10	5	US-10-774-928-7
3	33	100.0	12	4	US-10-444-575-16
4	33	100.0	43	4	US-10-437-963-194037
5	33	100.0	202	4	US-10-437-963-162621
6	33	100.0	297	5	US-10-739-930-10272
7	33	100.0	644	5	US-10-723-860-366
8	33	100.0	5303	6	US-11-097-143-30390
9	31	93.9	125	5	US-10-450-763-51106
10	31	93.9	207	4	US-10-425-114-43282
11	31	93.9	220	4	US-10-437-963-135290
12	31	93.9	220	4	US-10-425-115-365535
13	31	93.9	237	4	US-10-425-114-46150
14	31	93.9	273	5	US-10-450-763-56735
15	31	93.9	275	5	US-10-450-763-45641
16	31	93.9	279	6	US-11-013-684-21
17	31	93.9	398	5	US-10-883-020-5
18	31	93.9	422	3	US-09-779-307-18
19	31	93.9	429	5	US-10-450-763-49905
20	31	93.9	429	5	US-10-450-763-49906
21	31	93.9	431	4	US-10-408-765A-2629
22	31	93.9	476	3	US-09-779-307-16
23	31	93.9	477	3	US-09-779-307-4
24	31	93.9	481	4	US-10-080-334-54
25	31	93.9	481	6	US-11-156-300-24
26	31	93.9	482	3	US-09-779-307-17
27	31	93.9	482	4	US-10-080-334-187

28	31	93.9	482	5	US-10-883-020-1	Sequence 1, Appli
29	31	93.9	483	3	US-09-919-497-79	Sequence 79, Appli
30	31	93.9	483	3	US-09-974-298-41	Sequence 41, Appli
31	31	93.9	483	3	US-09-981-353-158	Sequence 158, App
32	31	93.9	483	4	US-10-177-293-258	Sequence 258, App
33	31	93.9	483	4	US-10-080-334-183	Sequence 183, App
34	31	93.9	483	4	US-10-080-334-184	Sequence 184, App
35	31	93.9	483	4	US-10-080-334-185	Sequence 185, App
36	31	93.9	483	4	US-10-080-334-186	Sequence 186, App
37	31	93.9	483	4	US-10-734-564-116	Sequence 116, App
38	31	93.9	483	6	US-11-037-713-9	Sequence 9, Appli
39	31	93.9	500	5	US-10-450-763-39773	Sequence 39773, A
40	31	93.9	513	5	US-10-450-763-38492	Sequence 38492, A
41	31	93.9	521	3	US-09-976-782-8	Sequence 8, Appli
42	31	93.9	929	5	US-10-450-763-39772	Sequence 39772, A
43	31	93.9	1301	5	US-10-450-763-45996	Sequence 45996, A
44	30	90.9	55	3	US-09-864-761-41289	Sequence 41289, A
45	30	90.9	96	5	US-10-501-282-2186	Sequence 2186, Ap

ALIGNMENTS

RESULT 1

US-10-774-928-5
; Sequence 5, Application US/10774928
; Publication No. US20040241168A1
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; FILE REFERENCE: 302178
; CURRENT APPLICATION NUMBER: US/10/774,928
; CURRENT FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Leishmania
US-10-774-928-5

Query Match 100.0%; Score 33; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AEAESLY 7
Db	1	AEAESLY 7

RESULT 2

US-10-774-928-7
; Sequence 7, Application US/10774928
; Publication No. US20040241168A1
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; FILE REFERENCE: 302178
; CURRENT APPLICATION NUMBER: US/10/774,928
; CURRENT FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Leishmania
US-10-774-928-7

Query Match 100.0%; Score 33; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEAESLY 7
| | | | |
Db 1 AEAESLY 7

RESULT 3

US-10-444-575-16
; Sequence 16, Application US/10444575
; Publication No. US20030232374A1
; GENERAL INFORMATION:
; APPLICANT: University of Connecticut Health Center
; APPLICANT: Kuchel, George A
; APPLICANT: Zhu, Qing
; TITLE OF INVENTION: Compositions and Methods Relating to Detrusor Estrogen-Regulated
; FILE OF INVENTION: Protein (DERP)
; FILE REFERENCE: UCT-0035
; CURRENT APPLICATION NUMBER: US/10/444,575
; PRIOR FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: US 60/382,830
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-444-575-16

Query Match 100.0%; Score 33; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4; Length 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEAESLY 7
| | | | |
Db 3 AEAESLY 9

RESULT 4

US-10-437-963-194037
; Sequence 194037, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 194037
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_90118C.1.pap
US-10-437-963-194037

Query Match 100.0%; Score 33; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEAESLY 7
| | | | |
Db 31 AEAESLY 37

RESULT 5

US-10-437-963-162621
; Sequence 162621, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 162621
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_61696C.1.pap
US-10-437-963-162621

Query Match 100.0%; Score 33; DB 4; Length 202;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEAESLY 7
| | | | |
Db 131 AEAESLY 137

RESULT 6

US-10-739-930-10272
; Sequence 10272, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 10272
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; OTHER INFORMATION: Clone ID: TRIAE-23APR03-C3304_1.p
US-10-739-930-10272

Query Match 100.0%; Score 33; DB 5; Length 297;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEAESLY 7
| | | | |
Db 226 AEAESLY 232

RESULT 7

US-10-723-860-366
; Sequence 366, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.

; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8993
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 366
; LENGTH: 644
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-366

Query Match 100.0%; Score 33; DB 5; Length 644;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEASLY 7
Db 367 AEASLY 373

RESULT 8

US-11-097-143-30390
; Sequence 30390, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.

; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: DROSOPHILA GENES.

; CURRENT APPLICATION NUMBER: US/11/097,143
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30390
; LENGTH: 5303
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-30390

Query Match 100.0%; Score 33; DB 6; Length 5303;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEASLY 7
Db 3378 AEASLY 3384

RESULT 9

US-10-450-763-51106

; Sequence 51106, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 51106
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: DOMAIN
; LOCATION: (94)..(125)
; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL00226C, p-value=9.400e-19, raw score of 13.23
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (65)..(125)
; OTHER INFORMATION: Intermediate filament proteins domain identified by PFam,
; OTHER INFORMATION: accession name filament, E-value=1.8e-21, PFam score of 84.5
US-10-450-763-51106

Query Match 93.9%; Score 31; DB 5; Length 125;
Best Local Similarity 85.7%; Pred. No. 81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEASLY 7
Db 115 AEASLY 121

RESULT 10

US-10-425-114-43282
; Sequence 43282, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 43282
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700077413_FLI.pep
US-10-425-114-43282

Query Match 93.9%; Score 31; DB 4; Length 207;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEASLY 7
Db 136 AEASLY 142

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RESULT 11
US-10-437-963-135290
; Sequence 135290, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 135290
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_36980C.1.pep
US-10-437-963-135290

Query Match          93.9%; Score 31; DB 4; Length 220;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
DB 149 AEAESMY 155

RESULT 12
US-10-425-115-365535
; Sequence 365535, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 365535
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_96532C.1.pep
US-10-425-115-365535

Query Match          93.9%; Score 31; DB 4; Length 220;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
DB 149 AEAESMY 155

RESULT 13
US-10-425-114-46150
; Sequence 46150, Application US/10425114
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; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 46150
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 701161793_FLI.pep
US-10-425-114-46150

Query Match          93.9%; Score 31; DB 4; Length 237;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
DB 194 AEAESMY 200

RESULT 14
US-10-450-763-56735
; Sequence 56735, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56735
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (177)..(225)
; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL00226B, p-values=3.348e-35, raw score of 23.86
US-10-450-763-56735

Query Match          93.9%; Score 31; DB 5; Length 273;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
DB 264 AEAESMY 270
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RESULT 15
US-10-450-763-45641
; Sequence 45641, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 45641
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (179)..(227)
; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL00226B, p-value=3.348e-35, raw score of 23.86
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (87)..(273)
; OTHER INFORMATION: Intermediate filament proteins domain identified by Pfam,
; OTHER INFORMATION: accession name filament, E-values=3.2e-89, Pfam score of 309.8
US-10-450-763-45641

Query Match 93.9%; Score 31; DB 5; Length 275;
Best Local Similarity 85.7%; Pred. NO. 1.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
| | | | | | |
Db 266 AEAESNY 272

Search completed: July 5, 2006, 20:57:19
Job time : 37.0417 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 20:53:13 ; Search time 3.20833 Seconds
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58.543 Million cell updates/sec

Title: US-10-774-928A-5

Perfect score: 33
Sequence: 1 AEAESLY 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 112942

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pap.*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	221	6	US-10-449-902-30681 Sequence 30681, A
2	31	93.9	220	6	US-10-449-902-30877 Sequence 30877, A
3	31	93.9	220	6	US-10-449-902-33167 Sequence 33167, A
4	31	93.9	483	7	US-11-105-233-180 Sequence 180, App
5	30	90.9	282	6	US-10-449-902-54246 Sequence 54246, A
6	30	90.9	474	6	US-10-449-902-31122 Sequence 31122, A
7	30	90.9	520	7	US-11-293-697-3712 Sequence 3712, App
8	30	90.9	527	7	US-10-449-902-54681 Sequence 54681, A
9	30	90.9	637	7	US-11-293-697-2455 Sequence 2455, App
10	30	90.9	754	6	US-10-449-902-41136 Sequence 41136, A
11	29	87.9	514	6	US-10-449-902-52901 Sequence 52901, A
12	29	87.9	514	6	US-10-449-902-53911 Sequence 53911, A
13	28	84.8	915	6	US-10-953-349-35135 Sequence 35135, A
14	28	84.8	297	6	US-10-449-902-44464 Sequence 44464, A
15	27	81.8	214	6	US-10-953-349-2848 Sequence 2848, App
16	27	81.8	346	6	US-10-449-902-40486 Sequence 40486, A
17	27	81.8	428	6	US-10-935-291B-4 Sequence 4, Appli
18	27	81.8	530	7	US-11-174-307B-4746 Sequence 4746, App
19	26	78.8	155	7	US-11-293-697-3730 Sequence 3730, App
20	26	78.8	223	6	US-10-449-902-43747 Sequence 43747, A
21	26	78.8	258	6	US-10-953-349-3597 Sequence 3597, App
22	26	78.8	259	6	US-10-953-349-3596 Sequence 3596, App
23	26	78.8	264	6	US-10-953-349-3595 Sequence 3595, App
24	26	78.8	296	6	US-10-471-571A-2010 Sequence 2010, App
25	26	78.8	348	6	US-10-449-902-35774 Sequence 35774, A

ALIGNMENTS

RESULT 1

US-10-449-902-30681
; Sequence 30681, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 30681
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-30681

Query Match 100.0%; Score 33; DB 6; Length 221;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AEAESLY 7
DB 150 AEAESLY 156

RESULT 2

US-10-449-902-30877
; Sequence 30877, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269

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; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30877
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-30877

Query Match      93.9%; Score 31; DB 6; Length 220;
Best Local Similarity 85.7%; Pred. No. 4.3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 AEAESLY 7
DB      149 AEAESMY 155

RESULT 3
US-10-449-902-33167
; Sequence 33167, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33167
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-33167

Query Match      93.9%; Score 31; DB 6; Length 220;
Best Local Similarity 85.7%; Pred. No. 4.3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 AEAESLY 7
DB      149 AEAESMY 155

RESULT 4
US-11-105-233-180
; Sequence 180, Application US/11105233
; Publication No. US20060134653A1
; GENERAL INFORMATION:
; APPLICANT: Thiagalingam et al
; TITLE OF INVENTION: Differential Expression of Genes in MSI
; FILE REFERENCE: 1657/2001
; CURRENT APPLICATION NUMBER: US/11/105,233
; CURRENT FILING DATE: 2005-04-13
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 180
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-233-180

Query Match      93.9%; Score 31; DB 7; Length 483;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 AEAESLY 7
DB      276 AEAESMY 282

RESULT 5
US-10-449-902-54246
; Sequence 54246, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54246
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-54246

Query Match      90.9%; Score 30; DB 6; Length 282;
Best Local Similarity 85.7%; Pred. No. 9.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 AEAESLY 7
DB      26 AEAESLY 32

RESULT 6
US-10-449-902-31122
; Sequence 31122, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31122
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-31122

Query Match      90.9%; Score 30; DB 6; Length 474;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 AEAESLY 7
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Db 314 AEAESVY 320
|||||:-|

RESULT 7

US-11-293-697-3712
; Sequence 3712, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3712
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3712

Query Match 90.9%; Score 30; DB 7; Length 520;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
|||||:-|

Db 298 AEAELY 304
|||||:-|

RESULT 8

US-10-449-902-54681
; Sequence 54681, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54681
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-54681

Query Match 90.9%; Score 30; DB 6; Length 527;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
|||||:-|

Db 367 AEAESVY 373
|||||:-|

RESULT 9

US-11-293-697-2455
; Sequence 2455, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE

; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2455
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-2455

Query Match 90.9%; Score 30; DB 7; Length 637;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
|||||:-|

Db 414 AEAETLY 420
|||||:-|

RESULT 10

US-10-449-902-41136
; Sequence 41136, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41136
; LENGTH: 754
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-41136

Query Match 90.9%; Score 30; DB 6; Length 754;
Best Local Similarity 85.7%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
|||||:-|

Db 464 AEAQSLY 470
|||||:-|

RESULT 11

US-10-449-902-52901
; Sequence 52901, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52901
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-52901

Query Match 87.9%; Score 29; DB 6; Length 514;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AEAESLY 7
|||
Db 335 AEAESFY 341

RESULT 12
US-10-449-902-53911
; Sequence 53911, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53911
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-53911

Query Match 87.9%; Score 29; DB 6; Length 514;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AEAESLY 7
|||
Db 335 AEAESFY 341

RESULT 13
US-10-953-349-35135
; Sequence 35135, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35135
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-35135

Query Match 84.8%; Score 28; DB 6; Length 95;
Best Local Similarity 85.7%; Pred. No. 8.7;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AEAESLY 7
|||
Db 24 AEESLY 30

RESULT 14
US-10-449-902-44464
; Sequence 44464, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44464
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-44464

Query Match 84.8%; Score 28; DB 6; Length 217;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AEAESLY 7
|||
Db 146 AEESLY 152

RESULT 15
US-10-953-349-2848
; Sequence 2848, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2848
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-2848

Query Match 81.8%; Score 27; DB 6; Length 214;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AEAESLY 7
|||
Db 145 AEESLY 151

Search completed: July 5, 2006, 20:57:47
Job time : 3.20833 secs

GenCore version 5.1.9
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OM protein - protein search, using 'sw model

Run on: July 5, 2006, 19:24:38 ; Search time 12.3958 Seconds
(without alignments)
49.429 Million cell updates/sec

Title: US-10-774-928A-5

Perfect score: 33
Sequence: 1 AEAESLY 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE COMB pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1 pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	7	2	US-09-809-003A-5
2	33	100.0	10	2	US-09-809-003A-7
3	33	100.0	637	2	US-09-949-016-8152
4	33	100.0	643	2	US-09-538-092-844
5	31	93.9	443	2	US-09-949-016-10582
6	31	93.9	482	2	US-09-538-092-858
7	31	93.9	483	2	US-09-919-497-79
8	31	93.9	502	2	US-09-949-016-11033
9	30	90.9	243	1	US-08-597-236-3
10	30	90.9	243	1	US-08-746-682A-3
11	30	90.9	398	2	US-10-104-047-3388
12	30	90.9	608	2	US-10-094-749-2446
13	30	90.9	619	2	US-10-094-749-1964
14	30	90.9	619	2	US-10-094-749-2525
15	29	87.9	286	2	US-09-252-991A-22234
16	29	87.9	542	2	US-09-302-540-15640
17	29	87.9	735	2	US-09-902-540-13533
18	29	87.9	925	2	US-09-328-352-5244
19	28	84.8	106	2	US-09-248-796A-26131
20	28	84.8	213	1	US-08-531-525-11
21	28	84.8	213	1	US-08-718-270A-11
22	28	84.8	213	2	US-09-134-000C-3952
23	28	84.8	887	2	US-09-540-236-2911
24	28	84.8	1890	2	US-09-502-540-15442
25	27	81.8	107	2	US-09-543-681A-6074
26	27	81.8	171	2	US-09-248-796A-17720

27	81.8	193	2	US-09-543-681A-4479	Sequence 4479, Ap
28	81.8	235	2	US-09-620-405B-487	Sequence 487, App
29	81.8	235	2	US-09-604-287A-487	Sequence 487, App
30	81.8	235	2	US-09-834-759-487	Sequence 487, App
31	81.8	235	2	US-10-076-622-487	Sequence 487, App
32	81.8	235	2	US-10-124-805-487	Sequence 487, App
33	81.8	274	2	US-09-949-016-9095	Sequence 9095, Ap
34	81.8	310	2	US-09-540-236-2984	Sequence 2984, Ap
35	81.8	323	2	US-09-543-681A-6957	Sequence 6957, Ap
36	81.8	384	2	US-09-902-540-10867	Sequence 10867, A
37	81.8	399	1	US-08-096-623A-20	Sequence 20, Appli
38	81.8	422	5	PCT-US91-01360-2	Sequence 2, Appli
39	81.8	428	2	US-10-179-784-4	Sequence 4, Appli
40	81.8	493	2	US-09-949-016-6203	Sequence 6203, Ap
41	81.8	505	2	US-09-620-405B-478	Sequence 478, App
42	81.8	505	2	US-09-620-405B-485	Sequence 485, App
43	81.8	505	2	US-09-604-287A-478	Sequence 478, App
44	81.8	505	2	US-09-604-287A-485	Sequence 485, App
45	81.8	505	2	US-09-834-759-478	Sequence 478, App

ALIGNMENTS

RESULT 1

US-09-809-003A-5
; Sequence 5, Application US/098090003A

; Patent No. 6673351

; GENERAL INFORMATION:

; APPLICANT: O'Daly, Jose

; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission

; FILE REFERENCE: Psoriasis

; FILE REFERENCE: 302178

; CURRENT APPLICATION NUMBER: US/09/809,003A

; CURRENT FILING DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Leishmania

US-09-809-003A-5

Query Match 100.0%; Score 33; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AEAESLY	7
DB	1	AEAESLY	7

RESULT 2

US-09-809-003A-7
; Sequence 7, Application US/098090003A

; Patent No. 6673351

; GENERAL INFORMATION:

; APPLICANT: O'Daly, Jose

; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission

; FILE REFERENCE: Psoriasis

; FILE REFERENCE: 302178

; CURRENT APPLICATION NUMBER: US/09/809,003A

; CURRENT FILING DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 7

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Leishmania

US-09-809-003A-7

Query Match 100.0%; Score 33; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.42;

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
Db 1 AEAESLY 7

RESULT 3
US-09-949-016-8152
; Sequence 8152, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8152
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8152

Query Match 100.0%; Score 33; DB 2; Length 637;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
Db 367 AEAESLY 373

RESULT 4
US-09-538-092-844
; Sequence 844, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurPatSeqFormatter Version 0.9
; SEQ ID NO 844
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P04264
US-09-538-092-844

Query Match 100.0%; Score 33; DB 2; Length 643;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
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Db 366 AEAESLY 372

RESULT 5
US-09-949-016-10582
; Sequence 10582, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10582
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10582

Query Match 93.9%; Score 31; DB 2; Length 443;
Best Local Similarity 85.7%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
Db 236 AEAESMY 242

RESULT 6
US-09-538-092-858
; Sequence 858, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurPatSeqFormatter Version 0.9
; SEQ ID NO 858
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P05787
US-09-538-092-858

Query Match 93.9%; Score 31; DB 2; Length 482;
Best Local Similarity 85.7%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
Db 275 AEAESMY 281
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```
RESULT 7
US-09-919-497-79
; Sequence 79, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-79

Query Match          93.9%; Score 31; DB 2; Length 483;
Best Local Similarity 85.7%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
DB 276 AEAESMY 282

RESULT 8
US-09-949-016-11033
; Sequence 11033, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11033
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11033

Query Match          93.9%; Score 31; DB 2; Length 502;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
DB 295 AEAESMY 301

RESULT 9
US-08-597-236-3
; Sequence 3, Application US/08597236
; Patent No. 5733765
; GENERAL INFORMATION:
; APPLICANT: STINGELE, Francesca
; APPLICANT: MOLLET, Beat
; TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
; EXOPOLYSACCHARIDES
```

```
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americans
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/597,236
; FILING DATE:
; CLASSIFICATION: 426
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95201669.9
; FILING DATE: 20-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fanucci A., Allan
; REGISTRATION NUMBER: 30256
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-597-236-3

Query Match          90.9%; Score 30; DB 1; Length 243;
Best Local Similarity 85.7%; Pred. No. 63;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
DB 64 AEAESLY 70

RESULT 10
US-08-746-682A-3
; Sequence 3, Application US/08746682A
; Patent No. 5786184
; GENERAL INFORMATION:
; APPLICANT: STINGELE, Francesca
; APPLICANT: MOLLET, Beat
; TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
; EXOPOLYSACCHARIDES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americans
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,682A
; FILING DATE: 14-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/597,236
; FILING DATE: 20-JUN-1995
; APPLICATION NUMBER: EP 95201669.9
; FILING DATE: 20-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fanucci A., Allan
```

; REGISTRATION NUMBER: 30256
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-746-682A-3

Query Match 90.9%; Score 30; DB 1; Length 243;
Best Local Similarity 85.7%; Pred. No. 63;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEAESLY 7
||||:|
Db 64 AEAEALY 70

RESULT 11

US-10-104-047-3388
; Sequence 3388, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25

; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3388
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-104-047-3388

Query Match 90.9%; Score 30; DB 2; Length 398;
Best Local Similarity 85.7%; Pred. No. 11e-02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEAESLY 7
||||:|
Db 199 AEAEALY 205

RESULT 12

US-10-094-749-2446
; Sequence 2446, Application US/10094749
; Patent No. 6979557
; GENERAL INFORMATION:

; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO

; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749

; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2446
; LENGTH: 608
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2446

Query Match 90.9%; Score 30; DB 2; Length 608;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEAESLY 7
||||:|
Db 412 AEAEALY 418

RESULT 13

US-10-094-749-1964
; Sequence 1964, Application US/10094749
; Patent No. 6979557
; GENERAL INFORMATION:

; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI

; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO

; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24

; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1964
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-1964

Query Match 90.9%; Score 30; DB 2; Length 619;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEAESLY 7
||||:|
Db 396 AEAEALY 402

RESULT 14

US-10-094-749-2525
; Sequence 2525, Application US/10094749

Patent No. 6979557
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKI, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2525
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2525

Query Match 90.9%; Score 30; DB 2; Length 619;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
Db 396 AEAETLY 402

RESULT 15
US-09-252-991A-23234
; Sequence 23234, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23234
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23234

Query Match 87.9%; Score 29; DB 2; Length 286;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AEAESLY 7
|||||

Db 88 AEAEXLY 94

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Job time: 12.3958 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 19:09:18 ; Search time 14.5631 Seconds
(without alignments)
79.283 Million cell updates/sec

Title: US-10-774-928A-6
Perfect score: 69
Sequence: 1 NYSPPYNTDDL 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: Piri.*
2: Piri.*
3: Piri.*
4: Piri.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	100.0	622	2 I37984	keratin 9, type I,
2	53	76.8	442	2 A95196	sugar ABC transpor
3	53	76.8	442	2 F98062	hypothetical prote
4	50	72.5	359	2 B26135	keratin, 52K type
5	50	72.5	420	2 A37343	keratin 13, type I
6	50	72.5	458	1 KRH03	keratin 13, type I
7	50	72.5	472	1 KRH0E	keratin 14, type I
8	50	72.5	473	2 JC4313	keratin 16, type I
9	50	72.5	526	1 KRBOVI	keratin, 54K type I
10	50	72.5	561	2 A31994	keratin 10, type I
11	50	72.5	593	1 KRH00	keratin 10, type I
12	47	68.1	368	2 A28825	keratin, type I no
13	46	66.7	569	1 KRMS51	keratin, 59K type
14	46	66.7	570	2 S07330	keratin, epidermal
15	44	63.8	1167	2 B71924	cag island protein
16	43	62.3	400	1 KRH09	keratin 19, type I
17	43	62.3	513	1 S43941	protein kinase DUN
18	43	62.3	702	2 C84111	hypothetical prote
19	43	62.3	1247	2 E71616	hypothetical prote
20	43	62.3	1536	2 S59841	4-alpha-glucanotra
21	43	62.3	1577	2 T30858	glucosyltransferas
22	42	60.9	371	2 A64481	hypothetical prote
23	42	60.9	432	2 S30433	keratin 17, type I
24	42	60.9	437	2 A55682	keratin 13, type I
25	42	60.9	437	4 A33652	probable keratin 1
26	41	59.4	352	2 E70249	hypothetical prote
27	41	59.4	399	2 A25470	cytochrome P-450
28	40	58.0	371	2 F90486	dehydrogenase, pro
29	40	58.0	433	2 S01631	keratin, type I, e

ALIGNMENTS

RESULT 1

I37984

N;Alternate names: cytoskeletal - human

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence, revision 02-Jul-1996 #text change 09-Jul-2004

C;Accession: I37984; S40307; S77921; S41161; B35494; I37943

R;Reis, A.; Hennies, H.C.; Langbein, L.; Digweed, M.; Mischke, D.; Drechsler, M.; Schrock, Nature Genet. 6, 174-179, 1994

A;Title: Keratin 9 gene mutations in epidermolytic palmoplantar keratoderma (EPPK).

A;Reference number: I37984; MUID:94214498; PMID:7512862

A;Accession: I37984

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: DNA

A;Residues: 1-622 <RES>

R;Langbein, L.; Heid, H.W.; Moll, I.; Franke, W.W. Differentiation 55, 57-71, 1993

A;Title: Molecular characterization of the body site-specific human epidermal cytochrome

A;Reference number: I37943; MUID:94131202; PMID:7507869

A;Accession: S40307

A;Molecule type: mRNA

A;Residues: 1-622 <LAN>

A;Cross-references: UNIPARC:UPI000012DAE1; EMBL:Z29074; NID:9435475; PIDN:CAA82315.1; PI

A;Accession: S77921

A;Molecule type: protein

A;Residues: 29-53;62-104;167-188;199-233;241-249;295-362;374-430;450-480;579-604 <LAF>

A;Cross-references: UNIPARC:UPI00001774A9; UNIPARC:UPI00001774AA; UNIPARC:UPI00001774AB;

4B0; UNIPARC:UPI00001774B1

R;Langbein, L.

submitted to the EMBL Data Library, December 1993

A;Reference number: S41161

A;Accession: S41161

A;Molecule type: mRNA

A;Residues: 1-11, 'SR', 13-622 <LAW>

A;Cross-references: UNIPARC:UPI000016ABA2; EMBL:Z29074; NID:9435475; PIDN:CAA82315.1; PI

R;Rosen, E.M.; Meromsky, L.; Romero, R.; Setter, E.; Goldberg, I.

Biochem. Biophys. Res. Commun. 168, 1082-1088, 1990

A;Title: Human placenta contains an epithelial scatter protein.

A;Reference number: A35494; MUID:90267446; PMID:2140676

A;Accession: B35494

A;Molecule type: protein

A;Residues: 'X', 450-465 <ROS>

A;Cross-references: UNIPARC:UPI00001774B2

C;Genetics:

A;Gene: GDB:KRT9; EPPK

A;Cross-references: GDB:303970; OMIM:144200

A;Map position: 17q12-17q21

A;Introns: 213/3; 241/2; 293/3; 347/3; 389/3; 464/2

A;Note: defects in this gene may cause epidermolytic palmoplantar keratoderma

C;Superfamily: cytoskeletal keratin

C;Keywords: coiled coil; intermediate filament

L1 protein - human
conserved hypochet
probable membrane
hypothetical prote
tipC protein - sli
hypothetical prote
probable transcrip
periplasmic chaper
hypothetical prote
probable transcrip
keratin 3, type I,
rhophry-associated
keratin, 47.6K typ
keratin, 48K type
keratin 3, type I,
complement factor

F:1-153/Domain: head #status predicted <HEA>
F:154-459/Domain: helical rod #status predicted <ROD>
F:460-622/Domain: tail #status predicted <TAI>

Query Match 100.0%; Score 69; DB 2; Length 622;
Best Local Similarity 100.0%; Pred. No. 0.00074;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYSPPYNTIDDL 12
|||:|||||
Db 199 NYSPPYNTIDDL 210

RESULT 2
A95196
sugar ABC transporter, sugar-binding protein SPL683 [imported] - Streptococcus pneumoniae
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: A95196
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidrich, J.;
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a Virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: A95196
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-442 <KUR>
A:Cross-references: UNIPROT:Q97PB6; UNIPARC:Q8DN08; UNIPARC:UPI0000051948; GB:AE005672;
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SPL683

Query Match 76.8%; Score 53; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSPYNTID 10
|||:|||||
Db 390 YSPYNTID 398

RESULT 3
F98062
hypothetical protein ABC-SBP [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: F98062
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
y, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: F98062
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-442 <KUR>
A:Cross-references: UNIPROT:Q97PB6; UNIPARC:Q8DN08; UNIPARC:UPI0000051948; GB:AE007317;
C:Genetics:
A:Gene: ABC-SBP

Query Match 76.8%; Score 53; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSPYNTID 10
|||:|||||
Db 390 YSPYNTID 398

RESULT 4
B26135

keratin, 52K type I epidermal (clone pkSCC 52) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: B26135
R:Knapp, B.; Rentrop, M.; Schweizer, J.; Winter, H.
J. Biol. Chem. 262, 938-945, 1987

A;Title: Three cDNA sequences of mouse type I keratins. Cellular localization of the mRNA
A:Reference number: A92654; MUID:87109202; PMID:2433272

A:Accession: B26135
A:Molecule type: mRNA
A:Residues: 1-359 <KNA>

A:Cross-references: UNIPROT:Q61781; UNIPARC:UPI0000020FF9; GB:M13806; NID:g198628; PIDN:1
C:Superfamily: cytoskeletal keratin

Query Match 72.5%; Score 50; DB 2; Length 359;
Best Local Similarity 66.7%; Pred. No. 0.73;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYSPPYNTIDDL 12
:||||:||||
Db 42 DYSPYFKTIEDL 53

RESULT 5
A37343

keratin 13, type I, cytoskeletal, short splice form - human
N:Alternate names: cytokeratin 13
C:Species: Homo sapiens (man)
C>Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 09-Jul-2004
C:Accession: A37343

R:Kuruc, N.; Leube, R.E.; Moll, I.; Bader, B.L.; Franke, W.W.
Differentiation 42, 111-123, 1989
A;Title: Synthesis of cytokeratin 13, a component characteristic of internal stratified

A:Reference number: A37343; MUID:90228645; PMID:2483837
A:Accession: A37343
A:Molecule type: mRNA

A:Residues: 1-420 <KUR>
A:Cross-references: UNIPROT:PI3646; UNIPARC:UPI0000160DOC; GB:X52426; NID:g30376; PIDN:1

C:Genetics:
A:Gene: GDB:KRT13

A:Cross-references: GDB:120740; OMIM:148065
A:Map position: 17q21-17q22

C:Superfamily: cytoskeletal keratin
C:Keywords: alternative splicing; coiled coil; intermediate filament

F:1-96/Domain: head <HEA>
F:97-412/Domain: helical rod #status predicted <ROD>

F:413-420/Domain: tail <TAI>

Query Match 72.5%; Score 50; DB 2; Length 420;
Best Local Similarity 66.7%; Pred. No. 0.86;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYSPPYNTIDDL 12
:||||:||||
Db 151 DYSPYKTIIEEL 162

RESULT 6
KRH03

keratin 13, type I, cytoskeletal, long splice form - human
N:Alternate names: cytokeratin 13

C:Species: Homo sapiens (man)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C:Accession: S06088; B37343; A33403
R:Mischke, D.; Wächter, E.; Hochstrasser, K.; Wild, A.G.; Schulz, P.
Nucleic Acids Res. 17, 7984, 1989

A;Title: The N-, but not the C-terminal domains of human keratins 13 and 15 are closely

A:Reference number: S06088; MUID:90016882; PMID:2477803
A:Accession: S06088

A:Molecule type: mRNA

A;Residues: 1-458 <MIS1>
A;Cross-references: UNIPROT:P13646; UNIPARC:UPI0000016AB96; EMBL:X14640; NID:g34032; PIDN
A;Accession: A33216
A;Molecule type: protein
A;Residues: 291-299 <MIS2>
A;Cross-references: UNIPARC:UPI00000173D50
R;Kuruc, N.; Leube, R.E.; Moll, I.; Bader, B.L.; Franke, W.W.
Differentiation 42, 111-123, 1989
A;Title: Synthesis of cytokeratin 13, a component characteristic of internal stratified
A;Reference number: A37343; MUID:90228645; PMID:2483837
A;Accession: B37343
A;Molecule type: mRNA
A;Residues: 1-57.'G'.59-458 <KUR>
A;Cross-references: UNIPARC:UPI0000012DAE6; GB:X52426
R;Schulz, P.; Wächter, E.; Hochstrasser, K.; Wild, A.G.; Mischke, D.
Biochem. Biophys. Res. Commun. 162, 1522-1527, 1989
A;Title: Sequence of a human keratin 13 specific cDNA encompassing coil 1B through the 3
A;Reference number: A33403; MUID:89350978; PMID:2475110
A;Accession: A33403
A;Molecule type: mRNA
A;Residues: 158-458 <SCH>
A;Cross-references: UNIPARC:UPI00000173D51
C;Genetics:
A;Gene: GDB:KRT13
A;Cross-references: GDB:120740; OMIM:148065
A;Map position: 17q21-17q22
C;Superfamily: cytoskeletal keratin
C;Keywords: alternative splicing; coiled coil; intermediate filament
F;1-96/Domain: head <HEA>
F;97-412/Domain: helical rod #status predicted <ROD>
F;413-458/Domain: tail <TAI>

Query Match 72.5%; Score 50; DB 1; Length 458;
Best Local Similarity 66.7%; Pred. No. 0.94;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NYSPPYNTIDDL 12
Db 151 DYSPPYKTIEL 162

RESULT 7
KRHUE
keratin 14, type I, cytoskeletal - human
N;Alternate names: 50K type I keratin; cytokeratin 14; epidermal type I keratin
C;Species: Homo sapiens (man)
C;Date: 13-Jun-1983 #sequence revision 08-Feb-1996 #text_change 31-Dec-2004
C;Accession: A26763; A90858; A90829; I39329; A02939
R;Marchuk, D.; McCrohon, S.; Fuchs, E.
Proc. Natl. Acad. Sci. U.S.A. 82, 1609-1613, 1985
A;Title: Complete sequence of a gene encoding a human type I keratin: sequences homolog
A;Reference number: A26763; MUID:85166180; PMID:2580298
A;Accession: A26763
A;Molecule type: DNA
A;Residues: 1-472 <MAR1>
A;Cross-references: UNIPROT:P02533; UNIPROT:Q13092; UNIPARC:UPI0000016A8A1; GB:J00124; NI
R;Marchuk, D.; McCrohon, S.; Fuchs, E.
Cell 39, 491-498, 1984
A;Title: Remarkable conservation of structure among intermediate filament genes.
A;Reference number: A90858; MUID:85074457; PMID:6210150
A;Accession: A90858
A;Molecule type: DNA
A;Residues: 2-472 <MAR2>
A;Cross-references: UNIPARC:UPI00000173D4B; GB:J00124; NID:g186704; PIDN:AAB59562.1; PID:
A;Note: Initiator Met not shown
R;Hanukoglu, I.; Fuchs, E.
Cell 31, 243-252, 1982
A;Title: The cDNA sequence of a human epidermal keratin: divergence of sequence but cons
A;Reference number: A90829; MUID:83129327; PMID:6186381
A;Accession: A90829
A;Molecule type: mRNA
A;Residues: 64-93.'T'.95-472 <HAN>
A;Cross-references: UNIPARC:UPI00000173D4C; GB:J00124; NID:g186704

R;Albers, K.; Fuchs, E.
J. Cell Biol. 105, 791-806, 1987
A;Title: The expression of mutant epidermal keratin cDNAs transfected in simple epitheli
A;Reference number: I39329; MUID:87308384; PMID:2442174
A;Accession: I39329
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 326-348.'V'.350-467.'DGSSSSASCQFFGLM' <ALB>
A;Cross-references: UNIPARC:UPI000007119B; GB:X28646; NID:g177138; PIDN:AAA96689.1; PID:
C;Comment: The mammalian cytokeratins are a heterogeneous group of intermediate filament
segments with beta conformation, and amino and carboxyl ends with diverse length and se
C;Comment: The helical core plays a role in the polymerization of two polypeptide chains
nal specificity to each chain and is responsible for the end-to-end linkage of about 10
C;Comment: Each end domain consists of a set of subdomains distributed with bilateral sy
ggesting functional significance. Because they are easily removed by proteolysis, these
C;Comment: The rod domain is flanked by V1 and V2 subdomains that are highly variable in
subdomains are strongly basic and are also variable in sequence.
C;Comment: The cytoskeletal and microfibrillar keratins are classified into two types, t
atin IF protein subunit appears to be a heterotetramer of two type I and two type II pro
C;Genetics:
A;Gene: GDB:KRT14; EBS4; EBS3
A;Cross-references: GDB:132145; OMIM:148066
A;Map position: 17q12-17q21
A;Introns: 175/3; 203/2; 255/3; 309/3; 351/3; 425/2; 441/1
A;Note: defects in this gene may result in epidermolysis bullosa simplex, Dowling-Meara
C;Complex: heterotetramer of two type I and two type II proteins, usually keratin 5 (see
C;Keywords: coiled coil; heterotetramer; intermediate filament
F;2-472/Product: keratin, 50K type I cytoskeletal #status predicted <MAT>
F;2-115/Domain: head <HED>
F;2-115/Region: E1 and V1 subdomains
F;116-426/Domain: rod <ROD>
F;116-150/Region: coil 1A
F;151-161/Region: linker 1
F;162-262/Region: coil 1B
F;263-278/Region: linker 12
F;279-297/Region: coil 2A
F;298-305/Region: linker 2
F;306-426/Region: coil 2B
F;364/Region: stutter
F;427-472/Domain: tail <END>
F;427-472/Region: V2 and E2 subdomains

Query Match 72.5%; Score 50; DB 1; Length 472;
Best Local Similarity 66.7%; Pred. No. 0.97;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NYSPPYNTIDDL 12
Db 161 DYSPPYKTIEL 172

RESULT 8
JC4313
keratin 16, type I, cytoskeletal - human
N;Alternate names: 46K keratin type I; cytokeratin 16
C;Species: Homo sapiens (man)
C;Date: 06-Dec-1995 #sequence revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4313; A24843; I58129
R;Paladini, R.D.; Takahashi, K.; Gant, T.M.; Coulombe, P.A.
Biochem. Biophys. Res. Commun. 215, 517-523, 1995
A;Title: cDNA cloning and bacterial expression of the human type I keratin 16.
A;Reference number: JC4313; MUID:96011809; PMID:7487986
A;Accession: JC4313
A;Molecule type: mRNA
A;Residues: 1-473 <PAL>
A;Cross-references: UNIPROT:P08779; UNIPARC:UPI0000016B4A5; GB:S79867; NID:g1195530; PIDN
A;Experimental source: epidermal keratinocytes
R;Raychaudhuri, A.; Marchuk, D.; Lindhurst, M.; Fuchs, E.
Mol. Cell. Biol. 6, 539-548, 1986
A;Title: Three tightly linked genes encoding human type I keratins: conservation of sequ
A;Reference number: A24843; MUID:87064338; PMID:2431270
A;Accession: A24843

A;Residues: 452-593 <KOR1>
A;Cross-references: UNIPARC:UPI0000173D52; PIDN: AAB21315.1; PID: g244509
A;Note: Sequence extracted from NCBI backbone (NCBIP:79427)
A;Accession: B38182
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 452-463 'P', 465-507 'Y', 523-593 <KOR2>
A;Cross-references: UNIPARC:UPI0000173D53; PIDN: AAB21314.1; PID: g244508
A;Note: Sequence extracted from NCBI backbone (NCBIP:79431)
R;Kachenko, A.V.; Buchman, V.I.; Bliskovsky, V.V.; Shvets, Y.P.; Kisselev, L.L.
Gene 116, 245-251, 1992
A;Title: Exons I and VII of the gene (Ker10) encoding human keratin 10 undergo structural changes during differentiation
A;Reference number: PC1102; MUID: 92339897; PMID: 1378806
A;Accession: PC1102
A;Molecule type: mRNA
A;Residues: 'G', 198-407, 'Q', 409-450, 'G', 452-486, 491-524, 534-593 <TKA>
A;Cross-references: UNIPARC:UPI000016AB8B; GB: M77663; NID: g186628; PIDN: AAA59199.1; PID: 56-579, 'P', 581-593 <DAR1>
A;Experimental source: embryonic skin, clone HK51
R;Darmon, M.Y.; Semat, A.; Darmon, M.C.; Vasseur, M.
Mol. Biol. Rep. 12, 277-283, 1987
A;Title: Sequence of a cDNA encoding human keratin No 10 selected according to structural homology with keratin No 1
A;Reference number: S14666; MUID: 98122104; PMID: 2448602
A;Accession: S14666
A;Molecule type: mRNA
A;Residues: 130-278 'YV', 281-311, 'I', 313-339, 'V', 341-373, 'R', 375-407, 'Q', 409-459, 'RS', 465-579, 'P', 581-593 <DAR1>
A;Cross-references: UNIPARC:UPI0000173D54; EMBL: M19156; NID: g186769
A;Note: The sequence from Fig. 3 is inconsistent with the nucleotide sequence from Fig. 3 submitted to the EMBL Data Library, May 1988
R;Darmon, M.Y.; Semat, A.; Darmon, M.C.; Vasseur, M.
A;Reference number: S14667
A;Accession: S14667
A;Molecule type: mRNA
A;Residues: 130-278, 'YV', 281-311, 'I', 313-339, 'V', 341-373, 'R', 375-407, 'Q', 409-459, 'RS', 465-593 <DAR2>
A;Cross-references: UNIPARC:UPI0000173D55; EMBL: M19156; NID: g186769; PIDN: AAA59468.1; PID: 56-593 <DAR2>
A;Note: The translated sequence in GenBank entry HUMKRT10A, release 111.0, differs from C;Genetics:
A;Gene: GDB: KRT10; KPP
A;Cross-references: GDB: 118828; OMIM: 148080
A;Map position: 17q12-17q21
A;Introns: 209/3; 237/2; 289/3; 343/3; 385/3; 458/2; 592/3
A;Note: this gene encodes variants with considerable length polymorphism
A;Note: mutations in this gene can cause epidermolytic hyperkeratosis and keratosis palm
C;Complex: heterotetramer of two type I and two type II proteins, usually keratin 1 (see C;Superfamily: cytoskeletal keratin
C;Keywords: coiled coil; heterotetramer; intermediate filament; polymorphism
F;1-145/Domain: head <HEA>
F;146-456/Domain: helical rod #status predicted <ROD>
F;457-593/Domain: tail <TAI>

Query Match 72.5%; Score 50; DB 1; Length 593;
Best Local Similarity 75.0%; Pred. No. 1.2;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYSPPYNTIDDL 12
Db 195 DYSKYKXTIDDL 206

RESULT 12
A28825
keratin, type I nonepidermal - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A28825
R;LaFlamme, S.E.; Jamrich, M.; Richter, K.; Sargent, T.D.; Dawid, I.B.
Genes Dev. 2, 853-862, 1988
A;Title: Xenopus endo B is a keratin preferentially expressed in the embryonic notochord
A;Reference number: A28825; MUID: 89092007; PMID: 2463213
A;Accession: A28825
A;Molecule type: mRNA
A;Residues: 1-368 <LAF>

A;Cross-references: UNIPROT: P08802; UNIPARC: UPI000012DAEC; GB: Y00230; NID: g64863; PIDN: C;Genetics:
A;Start codon: GGT
C;Superfamily: cytoskeletal keratin
C;Keywords: coiled coil

Query Match 68.1%; Score 47; DB 2; Length 368;
Best Local Similarity 66.7%; Pred. No. 2.4;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYSPPYNTIDDL 12
Db 63 DWSPPYNTIEDL 74

RESULT 13
KRMSE1
keratin, 59K type I cytoskeletal - mouse
N;Alternate names: 59-kDa type I keratin
C;Species: Mus musculus (house mouse)
C;Date: 15-Nov-1984 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
R;Krieg, T.M.; Schafer, C.K.; Filpula, D.; Flaherty, P.; Steinert, P.M.; Roop, J. Biol. Chem. 260, 5867-5870, 1985
A;Title: Organization of a type I keratin gene. Evidence for evolution of intermediate filaments from a single ancestral gene.
A;Reference number: A02940; MUID: 85207552; PMID: 2581944
A;Accession: A02940
A;Molecule type: DNA
A;Residues: 1-569 <KRI>
A;Cross-references: UNIPROT: P02535; UNIPARC: UPI000027415; GB: L00193; GB: K00391; NID: g191944
A;Note: Initiator Met not shown
C;Comment: The authors translated the codon GAG for residue 41 as Gly
C;Comment: Fourier analysis has identified a 7-residue repeating pattern (heptad) between forms a stable alpha-helical coiled coil but is interrupted by three short regions with the sequence at or near the beginning of heptad repeats. Several of these sites are conserved in the amino and carboxyl ends are rich in glycine, serine, and aromatic residues.
C;Genetics: 206/3; 234/2; 286/3; 340/3; 382/3; 455/2; 568/2
A;Introns: 206/3; 234/2; 286/3; 340/3; 382/3; 455/2; 568/2
C;Superfamily: cytoskeletal keratin
C;Keywords: coiled coil; intermediate filament
F;1-143/Domain: head <HED>
F;1-143/Region: E1 and V1 subdomains
F;144-457/Domain: rod <ROD>
F;144-178/Region: coil 1A
F;179-192/Region: linker 1
F;193-293/Region: coil 1B
F;294-309/Region: linker 12
F;310-328/Region: coil 2A
F;329-336/Region: linker 2
F;337-457/Region: coil 2B
F;395/Region: stutter
F;458-569/Domain: tail <END>
F;458-569/Region: V2 and E2 subdomains

Query Match 66.7%; Score 46; DB 1; Length 569;
Best Local Similarity 66.7%; Pred. No. 5.8;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYSPPYNTIDDL 12
Db 192 DYSKYKXTIEDL 203

RESULT 14
S07330
keratin, epidermal - mouse
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S07330
R;Steinert, P.M.; Rice, R.H.; Roop, D.R.; Trus, B.L.; Steven, A.C.
Nature 302, 794-800, 1983
A;Title: Complete amino acid sequence of a mouse epidermal keratin subunit and implications for the structure of the intermediate filament.

A;Reference number: S07330; MUID:83192464; PMID:6188955
A;Accession: S07330
A;Molecule type: mRNA
A;Residues: 1-570 <STE>
A;Cross-references: UNIPROT:P02535; UNIPARC:UPI000016CE76; EMBL:V00830; NID:952786; PIDN
A;Note: the authors translated the codon TTC for residue 25 as Ser, TTC for residue 29 as
C;Superfamily: cytoskeletal keratin
C;Keywords: coiled coil; intermediate filament

Query Match 66.7%; Score 46; DB 2; Length 570;
Best Local Similarity 66.7%; Pred. No. 5.8;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYSPPYNTIDDL 12
Db 192 DYSKYKTIEDL 203

RESULT 15
B71924
cag island protein, cytotoxicity associated immunodominant antigen - Helicobacter pylori
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: B71924
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: B71924
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1167 <ARN>
A;Cross-references: UNIPROT:Q92LT1; UNIPARC:UPI0000126DD7; GB:AE001483; GB:AE001439; NID
A;Experimental source: strain J99
C;Genetics:
A;Gene: caga

Query Match 63.8%; Score 44; DB 2; Length 1167;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NYSPPYNTIDDL 12
Db 948 NHEPIYATIDDL 959

Search completed: July 5, 2006, 19:20:31
Job time : 15.5631 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 18:28:56 ; Search time 122.796 Seconds
(without alignments)
90.395 Million cell updates/sec

Title: US-10-774-928A-6

Perfect score: 69

Sequence: 1 NYSPPYNTIDDL 12

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	100.0	623	1 K1C9 HUMAN	P35527 homo sapien
2	61	88.4	13	2 Q9UC27 HUMAN	Q9UC27 homo sapien
3	60	87.0	431	2 Q566F9 XENLA	Q566F9 xenopus lae
4	60	87.0	431	2 Q6GLQ7 XENLA	Q6GLQ7 xenopus lae
5	55	79.7	786	2 O18740 CANFA	O18740 canis famil
6	53	76.8	61	2 Q879M7 STRP3	Q879M7 streptococc
7	53	76.8	172	2 Q3DHY3 STRAG	Q3DHY3 streptococc
8	53	76.8	219	2 Q3DI09 STRAG	Q3DI09 streptococc
9	53	76.8	438	2 Q3D3U6 STRAG	Q3D3U6 streptococc
10	53	76.8	438	2 Q3DBH3 STRAG	Q3DBH3 streptococc
11	53	76.8	438	2 Q3DFK5 STRAG	Q3DFK5 streptococc
12	53	76.8	438	2 Q3DL75 STRAG	Q3DL75 streptococc
13	53	76.8	438	2 Q3DSY5 STRAG	Q3DSY5 streptococc
14	53	76.8	438	2 Q3K3Z3 STRAL	Q3K3Z3 streptococc
15	53	76.8	438	2 Q8E2F4 STRA5	Q8E2F4 streptococc
16	53	76.8	438	2 Q8E7W2 STRA3	Q8E7W2 streptococc
17	53	76.8	439	2 Q48VD5 STRPM	Q48VD5 streptococc
18	53	76.8	439	2 Q5XDY4 STRP6	Q5XDY4 streptococc
19	53	76.8	439	2 Q7CNL8 STRP8	Q7CNL8 streptococc
20	53	76.8	439	2 Q9A1I9 STRP1	Q9A1I9 streptococc
21	53	76.8	442	2 Q8DN08 STRR6	Q8DN08 streptococc
22	53	76.8	442	2 Q97PE6 STRPN	Q97PE6 streptococc
23	51	73.9	618	2 Q8CIS9 RAT	Q8CIS9 rattus norv
24	50	72.5	85	2 Q2TAZ7 HUMAN	Q2TAZ7 homo sapien
25	50	72.5	403	2 Q5NZP1 AZOSE	Q5NZP1 azoarcus sp
26	50	72.5	449	2 Q2M1G8 MOUSE	Q2M1G8 mus musculu
27	50	72.5	452	2 Q6SEK1 MOUSE	Q6SEK1 mus musculu
28	50	72.5	452	2 Q6IFU7 RAT	Q6IFU7 rattus norv
29	50	72.5	452	2 Q6IFX2 MOUSE	Q6IFX2 mus musculu
30	50	72.5	458	1 K1C13 HUMAN	P13646 homo sapien
31	50	72.5	467	1 K1C14_CHICK	Q6P21 gallus gall

32	50	72.5	468	1 K1C16 MOUSE	Q9Z2K1 mus musculu
33	50	72.5	469	2 Q3SYP5 MOUSE	Q3SYP5 mus musculu
34	50	72.5	470	2 Q3ZAW8 MOUSE	Q3ZAW8 mus musculu
35	50	72.5	471	1 K1C14 HUMAN	P02533 homo sapien
36	50	72.5	472	1 K1C16 HUMAN	P08779 homo sapien
37	50	72.5	473	2 Q9EOD7 MOUSE	Q9EOD7 mus musculu
38	50	72.5	474	2 Q9EOD6 MOUSE	Q9EOD6 mus musculu
39	50	72.5	484	1 K1C14 MOUSE	Q61781 mus musculu
40	50	72.5	485	1 K1C14 RAT	Q61FV1 rattus norv
41	50	72.5	526	1 K1C10 BOVIN	P06394 bos taurus
42	50	72.5	561	2 Q14664 HUMAN	Q14664 homo sapien
43	50	72.5	584	2 Q8N175 HUMAN	Q8N175 homo sapien
44	50	72.5	593	1 K1C10 HUMAN	P13645 homo sapien
45	49	71.0	127	2 Q5AH45 CANAL	Q5AH45 candida alb

ALIGNMENTS

RESULT 1

K1C9_HUMAN
ID K1C9_HUMAN STANDARD; PRT; 623 AA.
AC P35527; O00109; Q14665;
DT 01-JUN-1994, integrated into UniprotKB/Swiss-Prot.
DT 08-NOV-2005, sequence version 2.
DT 07-FEB-2006, entry version 50.
DE Keratin, type I cytoskeletal 9 (Cytokeratin-9) (CK-9) (Keratin-9) (K9).
GN Name=KRT9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND PARTIAL PROTEIN SEQUENCE.
RC TISSUE=Foot sole tissue;
RX MEDLINE=94131202; PubMed=7507869;
RA Langbein L., Heid H.W., Moll I., Franke W.W.;
RT "Molecular characterization of the body site-specific human epidermal cytoke-
RT cytoke-
RT cytoke-
RT cytoke-
RL Differentiation 55:57-72(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS EPPK LYS-161; GLN-163
RP AND TRP-163.
RX MEDLINE=94214498; PubMed=7512862;
RA Reis A., Hennies H.-C., Langbein L., Digweed M., Mischke D.,
RA Dreschler M., Schroek E., Royer-Pokora B., Franke W.W., Sperling K.,
RA Kuester W.;
RT "Keratin 9 gene mutations in epidermolytic palmoplantar keratoderma (EPPK).";
RL Nat. Genet. 6:174-179(1994).
RN [3]
RP PROTEIN SEQUENCE OF 14-29, AND MASS SPECTROMETRY.
RC TISSUE=Cervix carcinoma;
RA Bienvenut W.V.;
RL Unpublished observations (AUG-2005).
RN [4]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 147-372, AND VARIANT EPPK GLN-163.
RX MEDLINE=96228052; PubMed=8647270; DOI=10.1016/0014-5793(96)00393-6;
RA Kobayashi S., Tanaka T., Matsuoyoshi N., Inamura S.;
RT "Keratin 9 point mutation in the pedigree of epidermolytic hereditary
RT palmoplantar keratoderma perturbs keratin intermediate filament
RT network formation.";
RL FEBS Lett. 386:149-155(1996).
RN [5]
RP PROTEIN SEQUENCE OF 450-466.
RX MEDLINE=90267446; PubMed=2140676;
RA Rosen E.M., Meromsky L., Romero R., Setter E., Goldberg I.;
RT "Human placenta contains an epithelial scatter protein.";
RL Biochem. Biophys. Res. Commun. 168:1082-1088(1990).
RN [6]

RP VARIANTS EPPK VAL-157 AND PRO-172.
RX MEDLINE=94274199; PubMed=7516304; DOI=10.1007/BF00201564;
RA Hennies H.-C., Zehender D., Kunze J., Kuester W., Reis A.;
RT "Keratin 9 gene mutational heterogeneity in patients with
RL epidermolytic palmoplantar keratoderma."; Hum. Genet. 93:649-654 (1994).
RN [7]
RP VARIANT EPPK SER-161.
RX MEDLINE=95015968; PubMed=753529; DOI=10.1111/1523-1747.ep12395570;
RA Bonifas J.M., Matsumura K., Chen M.A., Berth-Jones J.,
RX Hutchinson P.E., Zloczower M., Fritsch P.O., Epstein E.H. Jr.;
RA "Mutations of keratin 9 in two families with palmoplantar
RX epidermolytic hyperkeratosis."; J. Invest. Dermatol. 103:474-477 (1994).
RN [8]
RP VARIANT EPPK TYR-161.
RX MEDLINE=94184355; PubMed=7511021;
RA Torched D., Blanchet-Bardon C., Serova O., Langbein L., Narod S.,
RA Janin N., Goguel A.F., Bernheim A., Franke W.W., Lenoir G.M.,
RA Feunteun J.;
RX "Epidermolytic palmoplantar keratoderma cosegregates with a keratin 9
RX mutation in a pedigree with breast and ovarian cancer."; Nat. Genet. 6:106-110 (1994).
RN [9]
RP VARIANTS EPPK TRP-163 AND SER-168.
RX MEDLINE=95164983; PubMed=7532199; DOI=10.1111/1523-1747.ep12666018;
RA Rothnagel J.A., Wojcik S., Liefer K.M., Dominey A.M., Huber M.,
RA Hohl D., Roop D.R.;
RX "Mutations in the IA domain of keratin 9 in patients with
RX epidermolytic palmoplantar keratoderma."; J. Invest. Dermatol. 104:430-433 (1995).
RN [10]
RP VARIANT EPPK VAL-160.
RX MEDLINE=97348961; PubMed=9204965; DOI=10.1111/1523-1747.ep1276751;
RA Endo H., Hatamochi A., Shinkai H.;
RX "A novel mutation of a leucine residue in coil 1A of keratin 9 in
RX epidermolytic palmoplantar keratoderma."; J. Invest. Dermatol. 109:113-115 (1997).
RN [11]
RP VARIANTS EPPK THR-157, VAL-157 AND GLN-163.
RX MEDLINE=99072662; PubMed=9856842;
RA DOI=10.1046/j.1523-1747.1998.00445.x;
RA Covello S.P., Irvine A.D., McKenna K.E., Munro C.S., Nevin N.C.,
RA Smith F.J.D., Utito J., McLean W.H.I.;
RX "Mutations in keratin K9 in kindreds with epidermolytic palmoplantar
RX keratoderma and epidemiology in Northern Ireland."; J. Invest. Dermatol. 111:1207-1209 (1998).
CC -I- FUNCTION: May serve an important special function either in the
CC mature palmar and plantar skin tissue or in the morphogenic
CC program of the formation of these tissues.
CC -I- SUBUNIT: Heterotrimer of two type I and two type II keratins.
CC -I- TISSUE SPECIFICITY: Expressed in the terminally differentiated
CC epidermis of palms and soles.
CC -I- DISEASE: Defects in KRT9 are a cause of epidermolytic palmoplantar
CC keratoderma (EPPK) (MIM:144200); also abbreviated EPPK. EPPK is
CC an autosomal dominant disease characterized by diffuse thickening
CC of the epidermis on the entire surface of palms and soles sharply
CC bordered with erythematous margins.
CC -I- MISCELLANEOUS: There are two types of cytoskeletal and
CC microfibrillar keratin, I (acidic) and II (neutral to basic) (40-
CC 55 and 56-70 kDa, respectively).
CC -I- SIMILARITY: Belongs to the intermediate filament family.
CC -I- CAUTION: Was originally (Ref.4) thought to be a 60 kDa chain of
CC placental scatter protein.
CC -I- DATABASE: NAME=Human Intermediate Filament Mutation Database;
CC WWW="http://www.interfil.org".
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; Z29074; CAA82315.1; -; mRNA.
CC EMBL; S69510; AAC60619.1; -; mRNA.
CC EMBL; X75015; CAA52924.1; -; Genomic DNA.

DR EMBL; AB001594; BAA19418.1; -; mRNA.
DR PIR; I37984; I37984.
DR HSSP; P08670; IKG7.
DR Interact; P35527; -.
DR Ensembl; ENSG00000171403; Homo sapiens.
DR RefSeq; HGNC:6447; KRT9.
DR MIM; 144200; phenotype.
DR MIM; 607606; gene.
DR GO; GO:0005208; F:structural constituent of cytoskeleton; TAS.
DR GO; GO:0008544; P:epidermis development; TAS.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin I.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PROSITE; PS00226; IF, 1.
KW Coiled coil; Direct protein sequencing; Disease mutation;
KW Intermediate filament; Keratin.
FT CHAIN 1 623 Keratin, type I cytoskeletal 9.
FT /FTID=PRO_0000063640.
FT REGION 1 152 Head.
FT REGION 153 461 Rod.
FT REGION 153 188 Coil 1A.
FT REGION 189 207 Linker 1.
FT REGION 208 239 Coil 1B.
FT REGION 300 322 Linker 12.
FT REGION 323 461 Coil 2.
FT REGION 462 623 Tail.
FT COMBIAS 15 26 Poly-Gly.
FT VARIANT 157 157 M -> T (in EPPK).
FT VARIANT 157 157 /FTID=VAR_010499.
FT VARIANT 160 160 M -> V (in EPPK).
FT VARIANT 160 160 /FTID=VAR_010500.
FT VARIANT 161 161 L -> V (in EPPK).
FT VARIANT 161 161 /FTID=VAR_010501.
FT VARIANT 161 161 N -> K (in EPPK).
FT VARIANT 161 161 /FTID=VAR_003822.
FT VARIANT 161 161 N -> S (in EPPK).
FT VARIANT 161 161 /FTID=VAR_010502.
FT VARIANT 161 161 N -> Y (in EPPK).
FT VARIANT 163 163 /FTID=VAR_010503.
FT VARIANT 163 163 R -> Q (in EPPK).
FT VARIANT 163 163 /FTID=VAR_003823.
FT VARIANT 163 163 R -> W (in EPPK).
FT VARIANT 168 168 /FTID=VAR_003824.
FT VARIANT 172 172 L -> S (in EPPK).
FT VARIANT 172 172 /FTID=VAR_003825.
FT VARIANT 172 172 Q -> P (in EPPK).
FT CONFLICT 12 13 /FTID=VAR_010504.
FT SEQUENCE 623 AA; 62129 MW; DE1D5A462FF96D10 CRC64; SR -> T (in Ref. 1; AAC60619 and 2).
SQ
Query Match 100.0%; Score 69; DB 1; Length 623;
Best Local Similarity 100.0%; Pred. No. 0.024; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0;
QY 1 NYSPYNTIDDL 12
DB 200 NYSPYNTIDDL 211
RESULT 2
ID Q9UC27 HUMAN PRELIMINARY; PRT; 13 AA.
AC Q9UC27;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE 94 kDa epidermal cyokeratin-like protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;


```

RN  PROTEIN SEQUENCE.
RP  MEDLINE=95226590; PubMed=7536047;
RA  Boue F., Duquenne C., Lassealle B., Lefevre A., Finaz C.;
RT  "FLB1, a human protein of epididymal origin that is involved in the
RL  sperm-oocyte recognition process.";
RL  Biol. Reprod. 52:267-278 (1995).
CC  -----
CC  Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC  -----
SQ  SEQUENCE 13 AA; 1610 MW; 000A683B81B7A45B CRC64;

Query Match      88.4%; Score 61; DB 2; Length 13;
Best Local Similarity 91.7%; Pred. No. 0.0079;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 NYSPPYNTIDDL 12
Db  |||||:|||||
    1 NYSPPYNTIDDL 12

RESULT 3
ID  Q566F9_XENLA PRELIMINARY; PRT; 431 AA.
AC  Q566F9;
DT  10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT  10-MAY-2005, sequence version 1.
DT  07-FEB-2006, entry version 4.
DE  MGC84388 protein.
GN  Name=MGC84388;
OS  Xenopus laevis (African clawed frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC  Xenopodinae; Xenopus; Xenopus.
OX  NCBI_TaxID=8355;
[1]
RN  NUCLEOTIDE SEQUENCE.
RP  TISSUE=Brain;
RX  MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA  Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA  Richardson P.;
RT  "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT  initiative.";
RL  Dev. Dyn. 225:384-391 (2002).
[2]
RN  NUCLEOTIDE SEQUENCE.
RP  TISSUE=Brain;
RX  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalón D.K., Grimwood J., Schmutz J., Myers R.M.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Abramson R.D., Mullahy S.J.,
RA  Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Bosak S.A., Casavant T.L., Scheetz T.E.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA  Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA  Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA  Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[3]
RN  NUCLEOTIDE SEQUENCE.
RP  TISSUE=Brain;
RA  Klein S., Gerhard D.S.;
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RL  Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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CC  -----
DR  EMBL; BC093567; AAH93567.1; -; mRNA.
DR  GO; GO:0005198; F:structural molecule activity; IEA.
DR  InterPro; IPR001664; IF.
DR  InterPro; IPR002957; Keratin_I.
DR  Pfam; PF00038; Filament; 1.
DR  PRINTS; PR01248; TYPE1KERATIN.
DR  PROSITE; PS00226; IF; UNKNOWN 1.
SQ  SEQUENCE 431 AA; 47704 MW; 13EB6E9019731326 CRC64;

Query Match      87.0%; Score 60; DB 2; Length 431;
Best Local Similarity 83.3%; Pred. No. 0.45;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  1 NYSPPYNTIDDL 12
Db  |||||:|||||
    131 NYSPPYNTIDEL 142

RESULT 4
ID  Q6GLQ7_XENLA PRELIMINARY; PRT; 431 AA.
AC  Q6GLQ7;
DT  19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT  19-JUL-2004, sequence version 1.
DT  07-FEB-2006, entry version 15.
DE  MGC84388 protein.
GN  Name=MGC84388;
OS  Xenopus laevis (African clawed frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC  Xenopodinae; Xenopus; Xenopus.
OX  NCBI_TaxID=8355;
[1]
RN  NUCLEOTIDE SEQUENCE.
RP  TISSUE=Brain;
RX  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA  Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA  Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA  Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN  NUCLEOTIDE SEQUENCE.
RP  TISSUE=Brain;
RX  MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA  Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA  Richardson P.;
RT  "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT  initiative.";
RL  Dev. Dyn. 225:384-391 (2002).
[3]
RN  NUCLEOTIDE SEQUENCE.
RP  TISSUE=Brain;
```

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RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----
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CC -----
DR EMBL; BC074402; AH74402.1; -; mRNA.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PROSITE; PS00226; IF; UNKNOWN_1.
KW Intermediate filament.
SQ SEQUENCE 431 AA; 47723 MW; 0032E596D1B243C8 CRC64;

Query Match 87.0%; Score 60; DB 2; Length 431;
Best Local Similarity 83.3%; Pred. No. 0.45;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYSPPYNTIDDL 12
Db 131 NYSPPYSTIDEL 142

RESULT 5
O18740 CANFA PRELIMINARY; PRT; 786 AA.
ID O18740
AC O18740
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Keratin.
GN Name=KRT9;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
[1]_TaxID=9615;
RN NUCLEOTIDE SEQUENCE.
RP Lacharme P., Hitté C., Jouquand S., Priat C., Galibert F.;
RT "Identification and analysis of the dog keratin 9 (KRT9) gene.";
RL Anim. Genet. 9:173-178(1998).
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CC -----
DR EMBL; AF000949; AAC26971.1; -; Genomic_DNA.
DR HSSP; P08670; IGK7.
DR Ensembl; ENSCAF00000015952; Canis familiaris.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002952; Eggshell.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01228; EGGSHELL.
DR PRINTS; PR01248; TYPE1KERATIN.
SQ SEQUENCE 786 AA; 76354 MW; 272AB5425DD09535 CRC64;

Query Match 79.7%; Score 55; DB 2; Length 786;
Best Local Similarity 75.0%; Pred. No. 5.3;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYSPPYNTIDDL 12
Db 184 DYSPPYDTIDEL 195

RESULT 6
O879M7_STRP3

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ID O879M7_STRP3 PRELIMINARY; PRT; 61 AA.
AC O879M7; Q7CFH2;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Putative sugar transporter sugar binding lipoprotein.
GN OrderedLocustNames=SPe0186, SPyM3_0181,
OS Streptococcus pyogenes serotype M3.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=301448;
[1]_TaxID=301448;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=SSI-1 / Serotype M3;
RC MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
RX Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
RA Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
RA Hayashi H., Hattori M., Hamada S.;
RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
RT large-scale genomic rearrangement in invasive strains and new insights
RT into phage evolution.";
RL Genome Res. 13:1042-1055(2003).
[2]_Genome Res. 13:1042-1055(2003).
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=MGAS315 / Serotype M3;
RC MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
RX Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Perkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
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CC -----
DR EMBL; BA000034; BAC63281.1; -; Genomic_DNA.
DR EMBL; AE014140; AAM78788.1; -; Genomic_DNA.
DR GO; GO:0005351; F:sugar porter activity; IEA.
KW Complete proteome; Lipoprotein; Sugar transport.
SQ SEQUENCE 61 AA; 7153 MW; A82311231A615BB7 CRC64;

Query Match 76.8%; Score 53; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSPYNTID 10
Db 11 YSPYNTID 19

RESULT 7
Q3DHV3_STRAG PRELIMINARY; PRT; 172 AA.
ID Q3DHV3_STRAG PRELIMINARY; PRT; 172 AA.
AC Q3DHV3;
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 22-NOV-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Sugar ABC transporter, sugar-binding protein (Fragment).
GN Name=ABC; ORFNames=SAL_0058;
OS Streptococcus agalactiae 515.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=342614;
[1]_TaxID=342614;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=515;
RC PubMed=16172379; DOI=10.1073/pnas.0506758102;
RX Tettelin H., Maignani V., Cieleszczak M.J., Donati C., Medini D.,
RA Ward N.L., Angluoli S.V., Crabtree J., Jones A.L., Durkin A.S.,
RA deBoy R.T., Davidse T.M., Mora M., Scarselli M., Margarit y Ros I.,

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RA Peterson J.D., Hauser C.R., Sundaram J.P., Nelson W.C., Madupu R.,
RA Brinkac L.M., Dodson R.J., Rosovitz M.J., Sullivan S.A.,
RA Daugherty S.C., Haft D.H., Selengut J., Gwinn M.L., Zhou L., Zafar N.,
RA Khouri H., Radune D., Dimitrov G., Watkins K., O'Connor K.J.,
RA Smith S., Utterback T.R., White O., Rubens C.E., Grandi G.,
RA Madoff L.C., Kasper D.L., Telford J.L., Wessels M.R., Rappuoli R.,
RA Fraser C.M.;
RA "Genome analysis of multiple pathogenic isolates of Streptococcus
RT agalactiae: implications for the microbial 'pan-genome'.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:13950-13955(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL; AAJ01000204; EAO70053.1; -; Genomic_DNA.
FT NON TER 172
SQ SEQUENCE 172 AA; 19717 MW; AA3ED19930171D02 CRC64;

Query Match 76.8%; Score 53; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YSPYNTID 10
Db 143 YSPYNTID 151

RESULT 8
Q3D109_STRAG PRELIMINARY; PRT; 219 AA.
ID Q3D109_STRAG PRELIMINARY; PRT; 219 AA.
AC Q3D109;
RA Tettelin H., Maignani V., Cieslewicz M.J., Donati C., Medini D.,
RA Ward N.L., Angiuoli S.V., Crabtree J., Jones A.L., Durkin A.S.,
RA DeBoy R.T., Davidson T.M., Mora M., Scarselli M., Margarit y Ros I.,
RA Peterson J.D., Hauser C.R., Sundaram J.P., Nelson W.C., Madupu R.,
RA Brinkac L.M., Dodson R.J., Rosovitz M.J., Sullivan S.A.,
RA Daugherty S.C., Haft D.H., Selengut J., Gwinn M.L., Zhou L., Zafar N.,
RA Khouri H., Radune D., Dimitrov G., Watkins K., O'Connor K.J.,
RA Smith S., Utterback T.R., White O., Rubens C.E., Grandi G.,
RA Madoff L.C., Kasper D.L., Telford J.L., Wessels M.R., Rappuoli R.,
RA Fraser C.M.;
RA "Genome analysis of multiple pathogenic isolates of Streptococcus
RT agalactiae: implications for the microbial 'pan-genome'.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:13950-13955(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAJ01000187; EAO70079.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 219 AA; 24808 MW; 0326049A3A49847 CRC64;

Query Match 76.8%; Score 53; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 2.9;
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YSPYNTID 10
Db 168 YSPYNTID 176

RESULT 9
Q3D306_STRAG PRELIMINARY; PRT; 438 AA.
ID Q3D306_STRAG PRELIMINARY; PRT; 438 AA.
AC Q3D306;
RA Tettelin H., Maignani V., Cieslewicz M.J., Donati C., Medini D.,
RA Ward N.L., Angiuoli S.V., Crabtree J., Jones A.L., Durkin A.S.,
RA DeBoy R.T., Davidson T.M., Mora M., Scarselli M., Margarit y Ros I.,
RA Peterson J.D., Hauser C.R., Sundaram J.P., Nelson W.C., Madupu R.,
RA Brinkac L.M., Dodson R.J., Rosovitz M.J., Sullivan S.A.,
RA Daugherty S.C., Haft D.H., Selengut J., Gwinn M.L., Zhou L., Zafar N.,
RA Khouri H., Radune D., Dimitrov G., Watkins K., O'Connor K.J.,
RA Smith S., Utterback T.R., White O., Rubens C.E., Grandi G.,
RA Madoff L.C., Kasper D.L., Telford J.L., Wessels M.R., Rappuoli R.,
RA Fraser C.M.;
RA "Genome analysis of multiple pathogenic isolates of Streptococcus
RT agalactiae: implications for the microbial 'pan-genome'.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:13950-13955(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAJ01000005; EAO78911.1; -; Genomic_DNA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
SQ SEQUENCE 438 AA; 48904 MW; 71B5BCC655254106 CRC64;

Query Match 76.8%; Score 53; DB 2; Length 438;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YSPYNTID 10
Db 387 YSPYNTID 395

RESULT 10
Q3D8H3_STRAG PRELIMINARY; PRT; 438 AA.
ID Q3D8H3_STRAG PRELIMINARY; PRT; 438 AA.
AC Q3D8H3;
RA Tettelin H., Maignani V., Cieslewicz M.J., Donati C., Medini D.,
RA Ward N.L., Angiuoli S.V., Crabtree J., Jones A.L., Durkin A.S.,
RA DeBoy R.T., Davidson T.M., Mora M., Scarselli M., Margarit y Ros I.,
RA Peterson J.D., Hauser C.R., Sundaram J.P., Nelson W.C., Madupu R.,
RA Brinkac L.M., Dodson R.J., Rosovitz M.J., Sullivan S.A.,
RA Daugherty S.C., Haft D.H., Selengut J., Gwinn M.L., Zhou L., Zafar N.,
RA Khouri H., Radune D., Dimitrov G., Watkins K., O'Connor K.J.,
RA Smith S., Utterback T.R., White O., Rubens C.E., Grandi G.,
RA Madoff L.C., Kasper D.L., Telford J.L., Wessels M.R., Rappuoli R.,
RA Fraser C.M.;
RA "Genome analysis of multiple pathogenic isolates of Streptococcus
RT agalactiae: implications for the microbial 'pan-genome'.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:13950-13955(2005).
CC -!- CAUTION: The sequence shown here is derived from an
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CC preliminary data.
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CC -----
DR EMBL; AAJ01000187; EAO70079.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 219 AA; 24808 MW; 0326049A3A49847 CRC64;
```

```
RC STRAIN=COH1;
RX PubMed=16172379; DOI=10.1073/pnas.0506758102;
RA Tettelin H., Maignani V., Cieslewicz M.J., Donati C., Medini D.,
RA Ward N.L., Angiuoli S.V., Crabtree J., Jones A.L., Durkin A.S.,
RA DeBoy R.T., Daviden T.M., Mora M., Scarselli M., Margarit y Ros I.,
RA Peterson J.D., Hauser C.R., Sundaram J.P., Nelson W.C., Madupu R.,
RA Brinkac L.M., Dodson R.J., Rosovitz M.J., Sullivan S.A.,
RA Daugherty S.C., Haft D.H., Selengut J., Gwinn M.L., Zhou L., Zafar N.,
RA Khouri H., Radune D., Dimitrov G., Watkins K., O'Connor K.J.,
RA Smith S., Uterback T.R., White O., Rubens C.E., Grandi G.,
RA Madoff L.C., Kasper D.L., Telford J.L., Wessels M.R., Rappuoli R.,
RA Fraser C.M.;
RA "Genome analysis of multiple pathogenic isolates of Streptococcus
RT agalactiae: implications for the microbial 'pan-genome'. ";
RL Proc. Natl. Acad. Sci. U.S.A. 102:13950-13955(2005).
CC -!- CAUTION: The sequence shown here is derived from an
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CC -----
DR EMBL; AAJ01000025; EAO75793.1; -; Genomic DNA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
SQ SEQUENCE 438 AA; 48858 MW; FEB4395F0DAF1171 CRC64;

Query Match 76.8%; Score 53; DB 2; Length 438;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSPYNTID 10
Db |||||||
387 YSPYNTID 395

RESULT 11
Q3DFK5_STRAG PRELIMINARY; PRT; 438 AA.
AC Q3DFK5;
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 4.
DE Sugar ABC transporter, sugar-binding protein.
GN ORFNames=SAM_0020;
OS Streptococcus agalactiae CJB11.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=342617;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16172379; DOI=10.1073/pnas.0506758102;
RA Tettelin H., Maignani V., Cieslewicz M.J., Donati C., Medini D.,
RA Ward N.L., Angiuoli S.V., Crabtree J., Jones A.L., Durkin A.S.,
RA DeBoy R.T., Daviden T.M., Mora M., Scarselli M., Margarit y Ros I.,
RA Peterson J.D., Hauser C.R., Sundaram J.P., Nelson W.C., Madupu R.,
RA Brinkac L.M., Dodson R.J., Rosovitz M.J., Sullivan S.A.,
RA Daugherty S.C., Haft D.H., Selengut J., Gwinn M.L., Zhou L., Zafar N.,
RA Khouri H., Radune D., Dimitrov G., Watkins K., O'Connor K.J.,
RA Smith S., Uterback T.R., White O., Rubens C.E., Grandi G.,
RA Madoff L.C., Kasper D.L., Telford J.L., Wessels M.R., Rappuoli R.,
RA Fraser C.M.;
RA "Genome analysis of multiple pathogenic isolates of Streptococcus
RT agalactiae: implications for the microbial 'pan-genome'. ";
RL Proc. Natl. Acad. Sci. U.S.A. 102:13950-13955(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAJ01000011; EAO73713.1; -; Genomic DNA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
SQ SEQUENCE 438 AA; 48858 MW; FEB4395F0DAF1171 CRC64;

Query Match 76.8%; Score 53; DB 2; Length 438;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSPYNTID 10
Db |||||||
387 YSPYNTID 395

RESULT 12
Q3DL75_STRAG PRELIMINARY; PRT; 438 AA.
AC Q3DL75;
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 4.
DE Sugar ABC transporter, sugar-binding protein.
GN ORFNames=SAL_0039;
OS Streptococcus agalactiae 515.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=342614;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16172379; DOI=10.1073/pnas.0506758102;
RA Tettelin H., Maignani V., Cieslewicz M.J., Donati C., Medini D.,
RA Ward N.L., Angiuoli S.V., Crabtree J., Jones A.L., Durkin A.S.,
RA DeBoy R.T., Daviden T.M., Mora M., Scarselli M., Margarit y Ros I.,
RA Peterson J.D., Hauser C.R., Sundaram J.P., Nelson W.C., Madupu R.,
RA Brinkac L.M., Dodson R.J., Rosovitz M.J., Sullivan S.A.,
RA Daugherty S.C., Haft D.H., Selengut J., Gwinn M.L., Zhou L., Zafar N.,
RA Khouri H., Radune D., Dimitrov G., Watkins K., O'Connor K.J.,
RA Smith S., Uterback T.R., White O., Rubens C.E., Grandi G.,
RA Madoff L.C., Kasper D.L., Telford J.L., Wessels M.R., Rappuoli R.,
RA Fraser C.M.;
RA "Genome analysis of multiple pathogenic isolates of Streptococcus
RT agalactiae: implications for the microbial 'pan-genome'. ";
RL Proc. Natl. Acad. Sci. U.S.A. 102:13950-13955(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAJ01000029; EAO71192.1; -; Genomic DNA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
SQ SEQUENCE 438 AA; 48858 MW; FEB4395F0DAF1171 CRC64;

Query Match 76.8%; Score 53; DB 2; Length 438;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSPYNTID 10
Db |||||||
387 YSPYNTID 395

RESULT 13
Q3DSY5_STRAG PRELIMINARY; PRT; 438 AA.
AC Q3DSY5;
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Bacterial extracellular solute-binding protein domain protein.
DE
```

```
GN ORFNames=SAJ_0091;
OS Streptococcus agalactiae 18RS21.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=342613;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=18RS21;
RX PubMed=16172379; DOI=10.1073/pnas.0506758102;
RA Tettelin H., Maignani V., Cieslewicz M.J., Donati C., Medini D.,
RA Ward N.L., Angiuoli S.V., Crabtree J., Jones A.L., Durkin A.S.,
RA DeBoy R.T., Davidson T.M., Mora M., Scarselli M., Margarit y Ros I.,
RA Peterson J.D., Hauser C.R., Sundaram J.P., Nelson W.C., Madupu R.,
RA Brinkac L.M., Dodson R.J., Rosovitz M.J., Sullivan S.A.,
RA Daugherty S.C., Haft D.H., Selengut J., Gwinn M.L., Zhou L., Zafar N.,
RA Khouri H., Radune D., Dimitrov G., Watkins K., O'Connor K.J.,
RA Smith S., Utterback T.R., White O., Rubens C.E., Grandi G.,
RA Madoff L.C., Kasper D.L., Telford J.L., Wessels M.R., Rappuoli R.,
RA Fraser C.M.;
RT "Genome analysis of multiple pathogenic isolates of Streptococcus
RT agalactiae: implications for the microbial 'pan-genome'.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:13950-13955(2005).
CC -!- CAUTION: The sequence shown here is derived from an
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CC -----
DR EMBL; AJ001000037; EA062652.1; -; Genomic DNA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
SQ SEQUENCE 438 AA; 48902 MW; 480FAD6B0A0F30B5 CRC64;

Query Match 76.8%; Score 53; DB 2; Length 438;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YSPYNTID 10
Db 387 YSPYNTID 395

RESULT 14
Q3K323 STRA1 PRELIMINARY; PRT; 438 AA.
AC Q3K323;
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 4.
DE Carbohydrate uptake 1 (CUT1) family ABC transporter, carbohydrate-
DE binding protein.
GN Streptococcus agalactiae serotype Ia.
OS Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=355315;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=A909 / ATCC 27591 / Serotype Ia;
RX PubMed=16172379; DOI=10.1073/pnas.0506758102;
RA Tettelin H., Maignani V., Cieslewicz M.J., Donati C., Medini D.,
RA Ward N.L., Angiuoli S.V., Crabtree J., Jones A.L., Durkin A.S.,
RA DeBoy R.T., Davidson T.M., Mora M., Scarselli M., Margarit y Ros I.,
RA Peterson J.D., Hauser C.R., Sundaram J.P., Nelson W.C., Madupu R.,
RA Brinkac L.M., Dodson R.J., Rosovitz M.J., Sullivan S.A.,
RA Daugherty S.C., Haft D.H., Selengut J., Gwinn M.L., Zhou L., Zafar N.,
RA Khouri H., Radune D., Dimitrov G., Watkins K., O'Connor K.J.,
RA Smith S., Utterback T.R., White O., Rubens C.E., Grandi G.,
RA Madoff L.C., Kasper D.L., Telford J.L., Wessels M.R., Rappuoli R.,
RA Fraser C.M.;
RT "Genome analysis of multiple pathogenic isolates of Streptococcus
RT agalactiae: implications for the microbial 'pan-genome'.";

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RL Proc. Natl. Acad. Sci. U.S.A. 102:13950-13955(2005).
CC -----
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CC -----
DR EMBL; CP000114; ABA45153.1; -; Genomic DNA.
DR TIGR; SAK 0067; -;
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006059; SBP_bac_1.
DR Pfam; PF01547; SBP_bac_1; 1.
KW Complete proteome.
SQ SEQUENCE 438 AA; 48904 MW; 71B5BCC655254106 CRC64;

Query Match 76.8%; Score 53; DB 2; Length 438;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YSPYNTID 10
Db 387 YSPYNTID 395

RESULT 15
Q8E2F4 STRA5 PRELIMINARY; PRT; 438 AA.
ID Q8E2F4 STRA5 PRELIMINARY; PRT; 438 AA.
AC Q8E2F4;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Sugar ABC transporter, sugar-binding protein.
DE OrderedLocusNames=SAG0034.
GN Streptococcus agalactiae serotype V.
OS Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=2603 V/R / ATCC BAA-611 / Serotype V;
RX MEDLINE=2222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
RA Tettelin H., Maignani V., Cieslewicz M.J., Eisen J.A., Peterson S.N.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
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CC -----
DR EMBL; AE014193; AAM98942.1; -; Genomic DNA.
DR HSP; P02928; ILAX.
DR TIGR; SAG0034; -;
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006059; SBP_bac_1.
DR Pfam; PF01547; SBP_bac_1; 1.
KW Complete proteome.
SQ SEQUENCE 438 AA; 48858 MW; FEB4395F0DAF1171 CRC64;

Query Match 76.8%; Score 53; DB 2; Length 438;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YSPYNTID 10
Db 387 YSPYNTID 395
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Search completed: July 5, 2006, 19:01:34
Job time : 123.896 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 18:28:26 ; Search time 104.272 Seconds

(without alignments)
52.618 Million cell updates/sec

Title: US-10-774-928A-6

Perfect score: 69

Sequence: 1 NYSPTYNTIDDL 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.8.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*
- 10: Geneseq2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	100.0	12	6 AAO26386	Aao26386 Psoriasis
2	69	100.0	12	9 ADV04411	Adv04411 Leishmani
3	69	100.0	13	4 AAU68343	Aau68343 Human Bre
4	69	100.0	27	10 AEE36578	Aee36578 Human ser
5	69	100.0	622	8 ADS88365	Ads88365 Human pro
6	69	100.0	622	9 AEA15476	Aea15476 Human pol
7	69	100.0	622	9 AEB13340	Aeb13340 Mutant ke
8	65	94.2	600	7 ADF55631	Adf55631 Protein (
9	53	76.8	420	2 AAWS5075	Aaw55075 Streptoco
10	53	76.8	420	5 ABP54569	Abp54569 S. pneumo
11	53	76.8	420	7 ADC45107	Adc45107 S. pneumo
12	53	76.8	438	3 AAY91342	Aay91342 Group B S
13	53	76.8	438	5 ABP25884	Abp25884 Streptoco
14	53	76.8	438	5 ABP29681	Abp29681 Streptoco
15	53	76.8	438	8 ADV89335	Adv89335 Streptoco
16	53	76.8	438	8 ADV82758	Adv82758 Streptoco
17	53	76.8	438	5 ADV80588	Adv80588 Streptoco
18	53	76.8	439	5 ABP25885	Abp25885 Streptoco
19	53	76.8	442	6 ABU02156	Abu02156 S. pneumo
20	53	76.8	442	8 ADA46665	Ada46665 Streptoco
21	53	76.8	443	3 AAY81621	Aay81621 Streptoco
22	53	76.8	458	8 ADR94508	Adr94508 Novel S.
23	53	76.8	458	9 AEA58378	Aea58378 Streptoco

24	50	72.5	166	8 ABO60156	AbO60156 Human gen
25	50	72.5	200	8 ADR98843	Adr98843 Lung spec
26	50	72.5	221	4 ABG23687	Abg23687 Novel hum
27	50	72.5	260	8 ADR98840	Adr98840 Lung spec
28	50	72.5	351	8 ADR98908	Adr98908 Lung spec
29	50	72.5	355	7 ADB64789	Adb64789 Human pro
30	50	72.5	378	8 ADR98947	Adr98947 Lung spec
31	50	72.5	388	8 ADR98903	Adr98903 Lung spec
32	50	72.5	392	8 ADR98906	Adr98906 Lung spec
33	50	72.5	414	8 ADR98904	Adr98904 Lung spec
34	50	72.5	420	8 ABM81872	Abm81872 Tumour-as
35	50	72.5	420	9 AEA15473	Aea15473 Human pol
36	50	72.5	425	8 ADR98902	Adr98902 Lung spec
37	50	72.5	446	8 ADR98907	Adr98907 Lung spec
38	50	72.5	452	8 ADR98901	Adr98901 Lung spec
39	50	72.5	458	7 ADR75392	Adr75392 Prostate
40	50	72.5	469	8 ADJ76198	Adj76198 Marker ge
41	50	72.5	469	8 ADS85099	Ads85099 Mouse ato
42	50	72.5	470	8 ADJ75405	Adj75405 Marker ge
43	50	72.5	470	8 ADN04448	Adn04448 Antipsori
44	50	72.5	472	8 ADN98876	Adn98876 Novel hum
45	50	72.5	472	8 ADR98900	Adr98900 Lung spec

ALIGNMENTS

RESULT 1
AAO26386
ID AAO26386 standard; peptide; 12 AA.
XX
AC AAO26386;
XX
DT 30-JAN-2003 (first entry)
XX
DE Psoriasis treating immunotherapeutic peptide, SEQ ID No 6.
XX
KW Antipsoriatic; immunostimulant; gene therapy; pharmaceutical composition;
KW vaccine; immunogenic variant; immunotherapeutic agent; psoriasis;
KW gene therapy.
XX
OS Leishmania sp.
XX
PN WO200274239-A2.
XX
PD 26-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006496.
XX
PR 16-MAR-2001; 2001US-00809003.
XX
(AKIV-) AKIVA LLC.
PI O'daly JA;
XX
DR WPI; 2003-018763/01.
XX
PT New polypeptide and immunogenic variants comprising amino acid sequences of particulate antigens, useful for the treatment and clinical remission of psoriasis.
XX
PS Claim 1; Page 43; 56pp; English.
XX
CC The invention relates to a polypeptide comprising an isolated amino acid sequence or immunogenic variants selected from any of 14 fully defined sequences of 7-16 amino acids, given in the specification. The sequences of immunotherapeutic agents and a pharmaceutical compositions comprising polynucleotides and vectors of the invention are useful for the treatment and clinical remission of psoriasis. The isolated nucleic acids are useful as probes. The sequences of the invention can be used in the treatment of disorders by gene therapy. This sequence represents one of the 14 immunotherapeutic peptides of the invention

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SQ Sequence 12 AA;
Query Match 100.0%; Score 69; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYSPPYNTIDDL 12
   |||||
DB 1 NYSPPYNTIDDL 12

RESULT 2
ADV04411
ID ADV04411 standard; peptide; 12 AA.
XX
AC ADV04411;
XX
DT 24-FEB-2005 (first entry)
XX
DE Leishmania immunotherapeutic peptide SEQ ID NO:6.
XX
KW T-lymphocyte; immunogenicity; antigen; antipsoriatic; immunostimulant;
KW psoriasis.
XX
OS Leishmania sp.
XX
PN US2004241168-A1.
XX
PD 02-DEC-2004.
XX
PF 09-FEB-2004; 2004US-00774928.
XX
PR 16-MAR-2001; 2001US-00809003.
PR 17-OCT-2003; 2003US-00687892.
XX
PA (ODAL/) ODALY J A.
PI Odaly JA;
XX
WPI; 2005-011563/01.
XX
Inhibiting selectively T-cell rolling in human, by administering compound
PT interfering with cutaneous lymphocyte antigen-E selectin interaction and
PT leukocyte function associated antigen-1 interaction.
XX
Claim 9; SEQ ID NO 6; 21pp; English.
XX
The invention relates to a novel method for selectively inhibiting T-cell
CC rolling in a human host, comprising administering a compound that
CC selectively interferes with the cutaneous lymphocyte antigen (CLA)-E
CC selectin interaction and leukocyte function associated antigen (LFA)-
CC 1/intercellular adhesion molecule (ICAM) and very late antigen
CC (VLA)/vascular cell adhesion molecule (VCAM) interactions. The compound
CC includes an immunotherapeutic agent, which comprises a purified protein
CC extract that is isolated by diethylaminoethyl Sephadex chromatography of
CC a Nonidet P-40 insoluble particulate antigen fraction derived from
CC isolated killed cells of amastigotes from one or more species of the
CC Leishmania genus, where the particulate antigen fraction is solubilized
CC with 8M urea and 0.025 M Tris(hydroxymethyl)aminomethane pH 8.3 applied
CC to diethylaminoethyl Sephadex and is eluted with a solution comprising
CC 0.1 M sodium chloride, 8 M urea and 0.025 M
CC Tris(hydroxymethyl)aminomethane pH 8.3, and the purified protein extract
CC includes polypeptides having apparent molecular weights of 73, 80 and 82
CC kDa, after total reduction and alkylation. The species is L. amazonensis,
CC L. venezuelensis, L. brasiliensis and/or L. chagasi. A compound of the
CC invention has antipsoriatic and immunostimulant activity, and inhibits T-
CC cell rolling by interfering with CLA-E selectin interaction and LFA-
CC 1/ICAM and VLA/VCAM interactions. The method is useful for selectively
CC inhibiting T-cell rolling in a human host, and for treating psoriasis.
CC The present sequence represents a Leishmania peptide used in the
CC invention.
XX
Sequence 12 AA;
Query Match 100.0%; Score 69; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYSPPYNTIDDL 12
   |||||
DB 1 NYSPPYNTIDDL 12

RESULT 3
AAU68343
ID AAU68343 standard; peptide; 13 AA.
XX
AC AAU68343;
XX
DT 16-JAN-2002 (first entry)
XX
DE Human Breast cancer-associated protein isoform, BPI-342 peptide.
XX
KW Human; Breast cancer-associated protein isoform; breast cancer;
KW immunogen; cytostatic; BPI; tryptic digest peptide.
XX
OS Homo sapiens.
XX
PN WO200171357-A2.
XX
PD 27-SEP-2001.
XX
PF 20-MAR-2001; 2001WO-GB001219.
XX
PR 20-MAR-2000; 2000GB-00006695.
PR 24-MAR-2000; 2000GB-00007265.
XX
PA (OXFO-) OXFORD GLYSCSCIENCES UK LTD.
XX
PI Herath HMAc, O'hare MJ, Page MJ, Parekh RB, Waterfield MD;
XX WPI; 2001-611532/70.
XX
Identifying proteins for clinical screening, diagnosis and prognosis of
PT breast cancer, comprises detecting Breast Cancer-Associated Protein
PT Isoforms (BPIs) using two-dimensional electrophoresis.
XX
Claim 9; Page 50; 197pp; English.
XX
The invention relates to diagnosing, determining the stage or severity,
CC or identifying the risk of a subject developing cancer (especially breast
CC cancer), or monitoring the effect of therapy on a subject with cancer,
CC comprising analysing a test sample using two-dimensional electrophoresis
CC and detecting Breast Cancer-Associated Protein Isoforms (BPIs). The
CC methods disclosed are used for the diagnosis and prognosis of breast
CC cancer, for determining the severity of breast cancer, and for
CC identifying a subject at risk of developing breast cancer, and monitoring
CC the effect of therapy administered to a subject. Antibodies raised
CC against the binding domain of a BPI, the binding domain of a BPI, a
CC nucleic acid encoding a BPI, or a nucleic acid that inhibits the function
CC of a BPI can be incorporated into a pharmaceutical composition for
CC treating or preventing breast cancer. The methods use sensitive and
CC specific biomarkers provide early diagnosis of breast cancer, and the
CC compositions are more potent, specific, and has a more rapid effect with
CC fewer side effects than other prior art methods. The present sequence is
CC a tryptic digest peptide from a BPI of the invention
XX
Sequence 13 AA;
Query Match 100.0%; Score 69; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYSPPYNTIDDL 12
   |||||
DB 1 NYSPPYNTIDDL 12
```


RESULT 4
ID AEE36578 standard; peptide; 27 AA.
XX AEE36578;
XX AC
XX XX
DT 09-FEB-2006 (first entry)
XX DE
DE Human serum N-linked glycopeptide SEQ ID NO: 682.
XX
XX Bioinformatics; blood; serum; plasma protein; protein detection;
KW mass spectroscopy; proteomics; glycosylation; diagnosis; cancer;
KW cystic acid; diabetes; antidiabetic; inflammation; antinflammatory;
KW rheumatoid arthritis; antiarthritic; antirheumatic; psychiatric disorder;
KW neuroleptic; neurological disease; infection; antimicrobial.
XX
XX Homo sapiens.
XX WO2005114221-A2.
PN
XX
PD 01-DEC-2005.
XX
PF 20-MAY-2005; 2005WO-US017842.
XX
PR 21-MAY-2004; 2004US-0573593P.
XX
XX (SYST-) INST SYSTEMS BIOLOGY.
PA
PI Aebersold RH, Zhang H;
XX
XX WPI; 2006-020173/02.
DR
PT Identifying glycopolypeptides in a serum or plasma sample, by identifying
PT released sample glycopeptide fragments that correspond to standard
PT peptides.
XX
PS Claim 1; SEQ ID NO 682; 193pp; English.
XX
CC The invention relates to identifying glycopolypeptides in a serum or
CC plasma sample comprising immobilizing derivatized sample
CC glycopolypeptides to a solid support, releasing the sample glycopeptide
CC fragments from the solid support, adding to the released sample
CC glycopeptide fragments standard peptides, and identifying released sample
CC glycopeptide fragments that correspond to standard peptides added by mass
CC spectroscopy. Also included are a method for identifying one or more
CC diagnostic markers for a disease, a composition comprising peptides
CC containing the glycosylation sites (AEE35897-AEE39378, where the peptides
CC each correspond to peptide fragments derived by cleavage of polypeptides
CC using the same cleavage reagent) and a kit comprising peptides containing
CC the glycosylation sites (AEE35897-AEE39378). The methods are useful for
CC identifying glycopolypeptides in a serum or plasma sample. The methods
CC can be used for blood serum profiling for the detection of prognostic and
CC diagnostic protein markers. It can also be used to identify and/or
CC validate drug targets and to evaluate drug efficacy, drug dosing, and/or
CC drug toxicity. The methods can also be used for the detection of changes
CC in the state of glycosylation of proteins based on the concurrent
CC application of protein abundance measurement of protein glycosylation on
CC the same sample. The method allows fast throughput and simplicity. It can
CC be readily adapted for high throughput analysis of samples, which can be
CC particularly advantageous for the analysis of clinical specimens. The
CC method can also be automated to facilitate the processing of multiple
CC samples. The present sequence is a human glycopeptide comprising an N-
CC linked glycosylation site, suitable for use as a reference peptide in the
CC method of the invention.
XX
SQ Sequence 27 AA;

Query Match 100.0%; Score 69; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 9.7e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYSPYNTIDDL 12
DB |||||
2 NYSPYNTIDDL 13
RESULT 5
ADS88365
ID ADS88365 standard; protein; 622 AA.
XX
AC ADS88365;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human protein of a TNF-alpha signalling pathway protein complex Seq 220.
XX
KW protein complex; tumour necrosis factor-alpha signalling pathway;
KW TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
KW inflammatory bowel disease; infectious disease; septic shock;
KW bacterial infection; neurological disease; stroke-induced inflammation;
KW neurodegenerative disease; cancer; antiinflammatory; antiarthritic;
KW antirheumatic; cytostatic; antibacterial; gene therapy; human.
XX
OS Homo sapiens.
XX
XX WO2004035783-A2.
PN
XX
PD 29-APR-2004.
XX
XX 24-SEP-2003; 2003WO-EP050655.
PF
XX 26-SEP-2002; 2002EP-00021809.
PR
XX 10-FEB-2003; 2003EP-00100274.
PR
XX (CELL-) CELLZOME AG.
PA
XX Bouwmeester T, Huhse B, Bauch A, Ruffner H, Bauer A, Kuester B;
PI Superti-Furga G, Kruse U;
XX
XX WPI; 2004-348460/32.
DR
XX
XX New protein complex comprising at least one first and second protein of
PT the Tumor Necrosis Factor-alpha(TNF-alpha)-signalling pathway, useful for
PT diagnosing or treating inflammation, neurological diseases, infectious
PT diseases or cancer.
XX
PS Example; SEQ ID NO 220; 1980pp; English.
XX
CC This invention relates to novel protein complexes of the tumour necrosis
CC factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to
CC methods for preparing these complexes comprising at least two component
CC proteins, as well as screening methods to identify modulators of the
CC pathway, which include antibodies, agonists and antagonists thereof. The
CC present invention describes a protein complex and kit that are useful for
CC diagnosing, prognosing or treating chronic inflammatory diseases such as
CC rheumatoid arthritis and inflammatory bowel disease; infectious diseases
CC such as septic shock and bacterial infections; neurological diseases such
CC as stroke-induced inflammation in neurons; neurodegenerative diseases and
CC cancer. Accordingly, these complexes can be used for the development of
CC pharmaceutical compositions that exhibit antiinflammatory, antiarthritic,
CC antirheumatic, cytostatic and antibacterial activities and can be used
CC for gene therapy purposes. In particular, the invention further provides
CC siRNA-oligonucleotides useful for inhibiting protein expression for in
CC vitro or cell culture assays. This polypeptide is a human protein that
CC can be used in combination with other proteins provided in the
CC specification to form novel complexes of the TNF-alpha signalling pathway
CC of the invention.
XX
SQ Sequence 622 AA;

Query Match 100.0%; Score 69; DB 8; Length 622;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYSPPYNTIDDL 12
 Db 199 NYSPPYNTIDDL 210

RESULT 6
 AEA15476
 ID AEA15476 standard; protein; 622 AA.
 AC AEA15476;
 XX
 DT 28-JUL-2005 (first entry)
 DE Human polypeptide #95.
 XX
 KW Diagnosis; prognosis; cancer; breast tumor; ovary tumor; stomach tumor;
 KW colon tumor; esophagus tumor; bladder tumor; non-small-cell lung cancer;
 KW cytostatic; neoplasm.
 XX
 OS Homo sapiens.
 XX
 PN WO2005047534-A2.
 XX
 PD 26-MAY-2005.
 XX
 PF 15-OCT-2004; 2004WO-EP011599.
 XX
 PR 28-OCT-2003; 2003EP-00024565.
 XX
 PA (FARB) BAYER HEALTHCARE AG.
 XX
 PI Wirtz R, Munnes M;
 DR WPI; 2005-372393/38.
 DR N-PSDB; AEA15398.
 XX

Predicting a response to cancer treatment by detecting at least 2 markers, which are genes or genomic nucleic acid sequences that are located on one chromosomal region, which is altered in malignant neoplasia.

Claim 7; SEQ ID NO 438; 464pp; English.

The invention relates to a method of predicting response to cancer treatment comprising detection of at least 2 markers, where the markers are genes and fragments or genomic nucleic acid sequences that are located on one chromosomal region, which is altered in malignant neoplasia. The invention also relates to a method for the prediction, diagnosis or prognosis of malignant neoplasia, methods for detecting deregulations in malignant neoplasia and breast cancer, a method of determining the phenotype of a cell or tissue, a method for identifying genomic regions which are altered on the chromosomal level and encode genes that are linked by function and are differentially expressed in malignant neoplasia and breast cancer, methods of screening for agents which regulate the activity of a polypeptide or a polynucleotide and antibodies that specifically bind to a full length or partial polypeptide. The method is useful for predicting response to cancer treatment. The methods and compositions are useful for predicting, diagnosing, prognosing, preventing or treating malignant neoplasia including breast cancer, ovarian cancer, gastric cancer, colon cancer, esophageal cancer, mesenchymal cancer, bladder cancer or non-small-cell lung cancer. This sequence represents a human polypeptide used in the scope of the invention.

Query Match 100.0%; Score 69; DB 9; Length 622;
 Best Local Similarity 100.0%; Pred. No. 0.0041;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYSPPYNTIDDL 12
 Db 199 NYSPPYNTIDDL 210

RESULT 7
 AEB13340
 ID AEB13340 standard; protein; 622 AA.
 XX
 AC AEB13340;
 XX
 DT 08-SEP-2005 (first entry)
 DE Mutant keratin-9 SEQ ID NO 5.
 XX
 KW antigen; tumor-associated antigen; diagnostic; therapeutic; tumor marker;
 KW squamous cell carcinoma;
 KW autoantibody-mediated identification of antigens; AMIDA; cytostatic;
 KW neoplasm; cancer; skin tumor; ear, nose, throat disease; mutant;
 KW keratin-9.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO2005061537-A2.
 XX
 PD 07-JUL-2005.
 XX
 PF 22-DEC-2004; 2004WO-EP014634.
 XX
 PR 22-DEC-2003; 2003DE-01060456.
 XX
 PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
 PA (VAEC-) VAECGENE BIOTECH GMBH.
 XX
 PI Gires O, Zeidler R, Muenz M, Schaffrik M;
 DR WPI; 2005-479443/48.
 XX

Antigen for skin tumors in the nose and throat, uses at least one protein from a selected sequence or their variants with a hybridized isolated nucleic acid encoding the transcribed product.

Claim 1; SEQ ID NO 5; 54pp; German.

This invention describes the detection of novel antigens associated with squamous cell carcinomas using autoantibody-mediated identification of antigens (AMIDA). The invention also describes methods for producing antigen-presenting cells and T cells that are specific for the antigens described. The antigens can be used in a diagnostic formulation or as a pharmaceutical product for therapy or as a vaccine, for diagnosis and therapy of squamous cell tumors and skin tumors associated with the ear, nose and throat (ENT). The tumor antigen is an improved diagnostic marker for tumor identification, and is also an effective therapeutic agent.

This sequence represents the tumor-associated antigen corresponding to a mutant keratin-9.

Sequence 622 AA;

Query Match 100.0%; Score 69; DB 9; Length 622;
 Best Local Similarity 100.0%; Pred. No. 0.0041;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYSPPYNTIDDL 12
 Db 199 NYSPPYNTIDDL 210

RESULT 8
 ADF55631
 ID ADF55631 standard; protein; 600 AA.
 XX
 AC ADF55631;
 XX
 DT 12-FEB-2004 (first entry)
 XX

DE Protein (SEQ ID 1) related to oyster pearl keratin protein.
 XX
 KW pearl protein composite; PPC; mother of pearl manufacture; jewellery;
 KW nanotechnology; oyster; keratin.
 XX
 OS Unidentified.
 XX
 PN JP2003012696-A.
 XX
 PD 15-JAN-2003.
 XX
 PF 03-JUL-2001; 2001JP-00202033.
 XX
 PR 03-JUL-2001; 2001JP-00202033.
 XX
 PA (MATSU) MATSUSHIRO A.
 XX
 DR WPI; 2003-451748/43.
 XX
 XX Pearl protein composite useful in manufacture of mother of pearl,
 PT comprises at least two protein components having preset molecular weight
 PT as determined by sodium dodecyl sulfate gel electrophoresis.
 XX
 PS Example 4; SEQ ID NO 1; 25pp; Japanese.
 XX
 CC The invention relates to a novel pearl protein composite (PPC) comprising
 CC at least two protein components as determined by sodium dodecyl sulphate
 CC (SDS) gel electrophoresis. The composite of the invention may be useful
 CC for the manufacture of mother of pearl for jewellery and also in
 CC nanotechnology. The pearl protein composite (PPC) is effectively utilised
 CC in manufacture of artificial pearls. The current sequence is that of the
 CC protein (SEQ ID 1) of the invention which is related to oyster pearl
 CC keratin protein and is homologous to a human keratin.
 XX
 SQ Sequence 600 AA;
 Query Match 94.2%; Score 65; DB 7; Length 600;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYSPYNTID 11
 DB 199 NYSPYNTID 209
 RESULT 9
 AAW5075
 ID AAW5075 standard; protein; 420 AA.
 XX
 AC AAW5075;
 XX
 DT 02-OCT-1998 (first entry)
 XX
 DE Streptococcus pneumoniae SP0016 protein.
 XX
 KW Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;
 KW detection; pneumonia; otitis media; meningitis.
 XX
 OS Streptococcus pneumoniae.
 XX
 PN WO9818930-A2.
 XX
 PD 07-MAY-1998.
 XX
 PF 30-OCT-1997; 97WO-US019422.
 XX
 PR 31-OCT-1996; 96US-0029960P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Kunsch CA, Choi GH, Johnson LS, Hromockyj A;
 XX WPI; 1998-272224/24.
 DR

DR N-PSDB; AAV27336.
 XX
 PT Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae
 PT - or their epitope-containing fragments, useful in protective or
 PT therapeutic vaccines, and for diagnosis.
 XX
 PS Claim 11; Page 54; 118pp; English.
 XX
 CC The present sequence represents a protein from Streptococcus pneumoniae.
 CC The nucleic acid sequence encoding the Streptococcus pneumoniae protein
 CC can be useful in vaccines for inducing protective antibodies against
 CC Streptococcus pneumoniae, for treatment or prevention of infection e.g.
 CC pneumonia, otitis media or meningitis. Probes based on the nucleic acid
 CC are used to detect Streptococcus infection (by usual hybridisation or
 CC amplification methods), also for isolating Streptococcus genes or their
 CC allelic variants. The protein can be used similarly to detect specific
 CC antibodies in standard immunoassays, especially for diagnosing or
 CC monitoring infections. Antibodies which bind the protein are used to
 CC detect corresponding antigens, to purify the protein and for passive
 CC immunisation (optionally coupled to a toxin). Vaccines are administered,
 CC e.g. by injection, orally or through the skin, typically at 0.01-1000
 CC (especially 10-300) mu g/ml per dose
 XX
 SQ Sequence 420 AA;
 Query Match 76.8%; Score 53; DB 2; Length 420;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 YSPYNTID 10
 DB 368 YSPYNTID 376
 RESULT 10
 ABP54569
 ID ABP54569 standard; protein; 420 AA.
 XX
 AC ABP54569;
 XX
 DT 04-SEP-2002 (first entry)
 XX
 DE S. pneumoniae SP016 protein sequence SEQ ID NO:26.
 XX
 KW Streptococcus pneumoniae; epitope; vaccine; antigenic protein;
 KW antibacterial; Streptococcal infection; detection.
 XX
 OS Streptococcus pneumoniae.
 XX
 PN US2002061545-A1.
 XX
 PD 23-MAY-2002.
 XX
 PF 22-JAN-2001; 2001US-00765272.
 XX
 PR 30-OCT-1997; 97US-00961083.
 XX
 PA (CHOI/) CHOI G H.
 PA (KUNS/) KUNSCH C A.
 PA (BARA/) BARASH S C.
 PA (DILL/) DILLON P J.
 PA (DOUG/) DOUGHERTY B.
 PA (FANN/) FANNON M R.
 PA (ROSE/) ROSEN C A.
 XX
 PI Choi GH, Kunsch CA, Barash SC, Dillon PJ, Dougherty B, Fannon MR;
 PI Rosen CA;
 XX
 DR WPI; 2002-479261/51.
 DR N-PSDB; ABQ84804.
 XX
 XX New Streptococcus pneumoniae antigens, useful for detecting Streptococcus
 PT and for preventing or attenuating disease caused by Streptococcus

PT infection.
PS Claim 11; Page 23; 70pp; English.
XX ABQ84792 to ABQ84904 represents nucleic acids which encode the
CC Streptococcus pneumoniae antigens given in ABP54557 to ABP54669. The S.
CC pneumoniae antigens have antibacterial activity and can be used in
CC vaccines. The S. pneumoniae antigens can also be used to prevent or
CC attenuate a Streptococcal infection in an animal. The polynucleotides
CC encoding the S. pneumoniae antigens can be used to detect Streptococcus
CC nucleic acids. ABQ84905 to ABQ85130 represent primers used in the cloning
CC of S. pneumoniae ORFs (open reading frames) which are used in an example
CC from the present invention
XX
SQ Sequence 420 AA;

Query Match 76.8%; Score 53; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YSPYNTID 10
Db 368 YSPYNTID 376
|||||

RESULT 11
ADC45107
ID ADC45107 standard; protein; 420 AA.
XX
AC ADC45107;
XX
XX 18-DEC-2003 (first entry)
XX
XX S. pneumoniae antigenic protein SP016.
DE
XX Antigen; bacterial infection; vaccine; pneumonia; antibacterial.
KW
XX Streptococcus pneumoniae.
OS
XX US6573082-B1.
PN
XX
XX 03-JUN-2003.
PD
XX
XX 28-MAR-2000; 2000US-00536784.
PF
XX 31-OCT-1996; 96US-0029960P.
PR
XX 30-OCT-1997; 97US-00961083.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Choi GH, Kunsch CA, Barash SC, Dillon PJ, Dougherty B, Fannon MR;
PI Rosen CA;
XX
XX WPI; 2003-764574/72.
DR N-PSDB; ADC45106.
XX
XX Novel polynucleotide encoding Streptococcus pneumoniae polypeptides
PT useful for producing vaccines for prevention or attenuation of infection
PT by Streptococcus pneumoniae.
XX
XX Example 1; SEQ ID NO 26; 58pp; English.
PS
XX The invention relates to an isolated polynucleotide consisting of a
CC Streptococcus pneumoniae nucleic acid (appearing as ADC45122 and encoding
CC SP028) one of 113 disclosed nucleic acids encoding 113 S. pneumoniae
CC antigens. Also included are making a recombinant vector by inserting the
CC nucleic acid into a vector, an isolated polynucleotide consisting of at
CC least 50 or 100 contiguous nucleotides of the SP028 nucleic acid, and a
CC recombinant host cell comprising the SP028 polynucleotide. The nucleic
CC acids are useful as DNA vaccine against Streptococcus pneumoniae
CC infection (e.g. pneumonia). Nucleic acids derived from the S. pneumoniae
CC antigen nucleic acids are useful as probes for use in diagnostic methods
CC for detecting S. pneumoniae gene expression. The present sequence

CC represents an S. pneumoniae antigenic protein.
XX
SQ Sequence 420 AA;

Query Match 76.8%; Score 53; DB 7; Length 420;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YSPYNTID 10
Db 368 YSPYNTID 376
|||||

RESULT 12
AAY91342
ID AAY91342 standard; protein; 438 AA.
XX
AC AAY91342;
XX
XX 30-MAY-2000 (first entry)
XX
XX Group B Streptococcus protein sequence SEQ ID NO:75.
DE
XX Group B Streptococcus; Streptococcus agalactiae; protein antigen;
KW vaccine; screening; immunogen; detection; diagnosis; infection; antibody;
KW antibody; antibacterial.
XX
OS Streptococcus agalactiae.
XX
XX WO200006736-A2.
PN
XX 10-FEB-2000.
PD
XX 27-JUL-1999; 99WO-GB002444.
PF
XX 27-JUL-1998; 98GB-00016335.
PR
XX 19-MAR-1999; 99US-0125163P.
XX
XX (MICR-) MICROBIAL TECHNIKS LTD.
PA
XX
XX Le Page RWF, Wells JM, Hanniffy SB;
PI WPI; 2000-195299/17.
DR
XX New Group B Streptococcus protein, useful as vaccine, for diagnosis of
PT Streptococcal infections and for screening of antibodies or affibodies.
PT
XX Claim 1; Fig 1; 123pp; English.
PS
XX AAA05803 to AAA05872 encode proteins, polypeptides and peptides (given in
CC AAY91275 to AAY91343) isolated from Group B Streptococcus (GBS), also
CC known as Streptococcus agalactiae. The GBS polynucleotides and
CC polypeptides have antibacterial activity. Immunogenic compositions
CC comprising GBS polynucleotides or polypeptides can be used as vaccines
CC and for the treatment or prophylaxis of GBS infection. The
CC polynucleotides and polypeptides can also be used in the detection of GBS
CC and for screening DNA encoding bacterial cell envelope associated or
CC secreted antigens in gram positive bacteria. AAA05873 to AAA05941
CC represent primers used in the exemplification of the present invention
XX
SQ Sequence 438 AA;

Query Match 76.8%; Score 53; DB 3; Length 438;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YSPYNTID 10
Db 387 YSPYNTID 395
|||||

RESULT 13
ABP25884

ID ABP25884 standard; protein; 438 AA.
XX AC ABP25884;
XX DT 02-JUL-2002 (first entry)
XX DE Streptococcus polypeptide SEQ ID NO 944.
XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
XX KW group A streptococcus; Streptococcus pyogenes; antibacterial;
XX KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX OS Streptococcus agalactiae.
XX PN WO200234771-A2.
XX PD 02-MAY-2002.
XX PF 29-OCT-2001; 2001WO-GB004789.
XX PR 27-OCT-2000; 2000GB-00026333.
XX PR 24-NOV-2000; 2000GB-00028727.
XX PR 07-MAR-2001; 2001GB-00005640.
XX PA (CHIR-) CHIRON SPA.
XX PA (GENO-) INST GENOMIC RES.
XX PI Telford J, Masignani V, Margarit Y Rosi, Grandi G, Fraser C;
XX PI Tettelin H;
XX DR WPI; 2002-352536/38.
XX DR N-PSDB; ABN66515.
XX PT New Streptococcus protein for the treatment or prevention of infection or
XX PT disease caused by Streptococcus bacteria, such as meningitis, and for
XX PT detecting a compound that binds to the protein.
XX PS Claim 1; Page 3248; 4525pp; English.
XX CC The invention relates to a protein (ABP25413-ABP30895) from group B
XX CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
XX CC (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in
XX CC the specification. The proteins have antibacterial and antiinflammatory
XX CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
XX CC antibodies that bind (I) are used in the manufacture of medicaments for
XX CC the treatment or prevention of infection or disease caused by
XX CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
XX CC Nucleic acids encoding (I) are used to detect Streptococcus in a
XX CC biological sample. (I) is used to determine whether a compound binds to
XX CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
XX CC Streptococcus that is prevented or treated may be meningitis. Nucleic
XX CC acid encoding (I) may be used to recombinantly produce (I) and may be
XX CC used in gene therapy. Antibodies to (I) are used for affinity
XX CC chromatography, immunoassays, and distinguishing/identifying
XX CC Streptococcus proteins
XX SQ Sequence 438 AA;
Query Match 76.8%; Score 53; DB 5; Length 438;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 YSPYNTID 10
Db 387 YSPYNTID 395
RESULT 14
ABP29681
ID ABP29681 standard; protein; 438 AA.
XX AC ABP29681;
XX DT 24-FEB-2005 (first entry)
XX

XX DT 02-JUL-2002 (first entry)
XX DE Streptococcus polypeptide SEQ ID NO 8538.
XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
XX KW group A streptococcus; Streptococcus pyogenes; antibacterial;
XX KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX OS Streptococcus agalactiae.
XX PN WO200234771-A2.
XX PD 02-MAY-2002.
XX PF 29-OCT-2001; 2001WO-GB004789.
XX PR 27-OCT-2000; 2000GB-00026333.
XX PR 24-NOV-2000; 2000GB-00028727.
XX PR 07-MAR-2001; 2001GB-00005640.
XX PA (CHIR-) CHIRON SPA.
XX PA (GENO-) INST GENOMIC RES.
XX PI Telford J, Masignani V, Margarit Y Rosi, Grandi G, Fraser C;
XX PI Tettelin H;
XX DR WPI; 2002-352536/38.
XX DR N-PSDB; ABN70312.
XX PT New Streptococcus protein for the treatment or prevention of infection or
XX PT disease caused by Streptococcus bacteria, such as meningitis, and for
XX PT detecting a compound that binds to the protein.
XX PS Claim 1; Page 3964; 4525pp; English.
XX CC The invention relates to a protein (ABP25413-ABP30895) from group B
XX CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
XX CC (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in
XX CC the specification. The proteins have antibacterial and antiinflammatory
XX CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
XX CC antibodies that bind (I) are used in the manufacture of medicaments for
XX CC the treatment or prevention of infection or disease caused by
XX CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
XX CC Nucleic acids encoding (I) are used to detect Streptococcus in a
XX CC biological sample. (I) is used to determine whether a compound binds to
XX CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
XX CC Streptococcus that is prevented or treated may be meningitis. Nucleic
XX CC acid encoding (I) may be used to recombinantly produce (I) and may be
XX CC used in gene therapy. Antibodies to (I) are used for affinity
XX CC chromatography, immunoassays, and distinguishing/identifying
XX CC Streptococcus proteins
XX SQ Sequence 438 AA;
Query Match 76.8%; Score 53; DB 5; Length 438;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 YSPYNTID 10
Db 387 YSPYNTID 395
RESULT 15
ADV89335
ID ADV89335 standard; protein; 438 AA.
XX AC ADV89335;
XX DT 24-FEB-2005 (first entry)
XX

DE Streptococcus agalactiae protein sequence, SEQ ID 1729.
 XX Antibacterial; Vaccine; bacterial infection.
 KW Streptococcus agalactiae.
 OS FR2824074-A1.
 XX 31-OCT-2002.
 PD 26-APR-2001; 2001FR-00005642.
 XX 26-APR-2001; 2001FR-00005642.
 PF (INSP) INST PASTEUR.
 PR (CNRS) CNRS CENT NAT RECH SCI.
 XX Glaser P, Rusniok C, Chevalier F, Frangeul L, Lalioui L;
 PI Zouine M, Couve E, Buchrieser C, Poyart C, Trieu CP, Kunst F;
 XX WPI; 2004-101891/11.
 DR Genomic nucleotide sequences encoding polypeptides of Streptococcus
 XX agalactiae for the development of vaccines, diagnostic tools, DNA chips
 PT and identification of therapeutic targets.
 XX Claim 6; SEQ ID NO 1729; 2687pp; French.
 PS The present invention relates to novel Streptococcus agalactiae
 XX nucleotide sequences (I; ADV87607-ADV87745) and novel polypeptides (II;
 CC ADV87746-ADV89950). The nucleotide sequences encode polypeptides of S.
 CC agalactiae involved in the synthesis of amino acids, cell membranes,
 CC intermediate (central) metabolism, energetic metabolism, fatty acid and
 CC phospholipid metabolism, nucleotide metabolism including purines,
 CC pyrimidines and/or nucleosides, regulatory functions, replication,
 CC transcription, translation, protein transport, adaptation to atypical
 CC conditions, sensitivity to medicines and/or analogues, functions related
 CC to transposons, biosynthesis of cofactors, prosthetic groups and
 CC transporters, cell membrane proteins and cellular machinery. (I) are
 CC useful for the detection and/or amplification of nucleic acids.
 CC Pharmaceutical composition comprising (I) or (II) are useful for
 CC treatment of a bacterial S. agalactiae infection. Note: WO200292818A2 is
 CC equivalent for the present basic patent FR2824074A1. WO200292818A2
 CC contains 6617 sequence whereas the present patent only contains 2344
 XX sequences.
 SQ Sequence 438 AA;

Query Match 76.8%; Score 53; DB 8; Length 438;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSPYNTID 10
 DB 387 YSPYNTID 395
 |||||

Search completed: July 5, 2006, 18:43:55
 Job time : 106.272 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 5, 2006, 20:38:52 ; Search time 87.8447 Seconds
(without alignments)
63.277 Million cell updates

Title: US-10-774-928A-6
Perfect score: 69
Sequence: 1 NYSPPYNTIDDL 12

Scoring table: BLOSUM62
Gapop 10.0 , Gape

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published Applications_AA_Main:
1: /EMC_Celerra_SIDS3/ptodata/2/
2: /EMC_Celerra_SIDS3/ptodata/2/
3: /EMC_Celerra_SIDS3/ptodata/2/
4: /EMC_Celerra_SIDS3/ptodata/2/
5: /EMC_Celerra_SIDS3/ptodata/2/
6: /EMC_Celerra_SIDS3/ptodata/2/
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	69	100.0	12	5	US-10-774-928-6	Sequence 6, Appli
2	69	100.0	13	3	US-09-988-493-239	Sequence 239, App
3	53	76.8	420	3	US-09-765-272-26	Sequence 26, Appl
4	53	76.8	420	6	US-11-106-649-26	Sequence 137, Appl
5	53	76.8	438	3	US-09-769-736-137	Sequence 26, Appl
6	53	76.8	438	6	US-11-123-241-137	Sequence 137, App
7	53	76.8	439	5	US-10-474-792-96	Sequence 96, Appl
8	53	76.8	442	3	US-09-769-787-121	Sequence 121, App
9	53	76.8	442	5	US-10-472-928-3466	Sequence 3466, Ap
10	53	76.8	442	5	US-10-873-528-121	Sequence 121, App
11	53	76.8	458	5	US-10-617-320-3143	Sequence 3143, Ap
12	50	72.5	101	4	US-10-425-115-308578	Sequence 308578, A
13	50	72.5	166	4	US-10-029-386-33790	Sequence 33790, A
14	50	72.5	221	5	US-10-450-763-54046	Sequence 54046, A
15	50	72.5	355	4	US-10-104-047-2943	Sequence 2943, Ap
16	50	72.5	355	6	US-11-072-512-2943	Sequence 2943, Ap
17	50	72.5	458	4	US-10-205-823-216	Sequence 216, App
18	50	72.5	458	6	US-11-051-454-216	Sequence 216, App
19	50	72.5	469	5	US-10-631-467-1450	Sequence 1450, Ap
20	50	72.5	470	5	US-10-631-467-657	Sequence 657, App
21	50	72.5	472	6	US-11-037-713-35	Sequence 35, Appl
22	50	72.5	558	5	US-10-450-763-54047	Sequence 54047, A
23	50	72.5	567	5	US-10-450-763-54049	Sequence 54049, A
24	50	72.5	593	4	US-10-435-696-50	Sequence 50, Appl
25	50	72.5	618	3	US-09-925-300-1381	Sequence 1381, Ap
26	50	72.5	887	5	US-10-450-763-54043	Sequence 54043, A
27	50	72.5	1113	5	US-10-450-763-37061	Sequence 37061, A

28	45	65-2	324	5	US-10-501-282-172	Sequence 172, App
29	45	65-2	352	5	US-10-501-282-174	Sequence 174, App
30	45	65-2	381	5	US-10-501-282-176	Sequence 176, App
31	45	65-2	392	5	US-10-501-282-177	Sequence 178, App
32	44	63-8	1167	4	US-10-335-977-8633	Sequence 8633, App
33	44	63-8	1167	6	US-11-052-554A-121	Sequence 121, App
34	44	63-8	1178	4	US-10-335-977-8634	Sequence 8634, App
35	44	63-8	1183	4	US-10-335-977-8635	Sequence 8635, App
36	43	62-3	13	3	US-09-988-493-48	Sequence 48, Appl
37	43	62-3	49	4	US-10-767-701-50836	Sequence 50836, A
38	43	62-3	142	3	US-09-738-973-213	Sequence 213, App
39	43	62-3	142	3	US-09-854-133-213	Sequence 213, App
40	43	62-3	142	4	US-10-144-649A-213	Sequence 213, App
41	43	62-3	143	3	US-09-925-301-1456	Sequence 1456, App
42	43	62-3	157	5	US-10-450-763-40381	Sequence 40381, A
43	43	62-3	247	4	US-10-104-047-3859	Sequence 3859, App
44	43	62-3	247	6	US-11-073-512-3859	Sequence 3859, App
45	43	62-3	354	5	US-10-732-931-15525	Sequence 15525, A

ALIGNMENTS

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RESULT 1
US-10-774-928-6
; Sequence 6, Application US/10774928
; Publication No. US20040241168A1
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Meth
; FILE REFERENCE: 302178
; CURRENT APPLICATION NUMBER: US/10/774,928
; CURRENT FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Leishmania
US-10-774-928-6

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Query Match	100.0%;	Score 69;	DB 5;	Length 12;
Best Local Similarity	100.0%;	Pred. No. 0.00022;		
Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 NYSPYNTIDDL 12
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Db 1 NYSPYNTIDDL 12

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RESULT 2
US-09-988-493-239
/ Sequence 239, Application US/09988493
/ Publication No. US20030064419A1
/ GENERAL INFORMATION:
/ APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
/ APPLICANT: O'Hare, Michael John
/ APPLICANT: Page, Martin John
/ APPLICANT: Parekh, Rajesh Bhikhu
/ APPLICANT: Waterfield, Michael Derek
/ TITLE OF INVENTION: Proteins, Genes, and Their Use for
/ TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer
/ FILE REFERENCE: 2543-1-024
/ CURRENT APPLICATION NUMBER: US/09/988,493
/ CURRENT FILING DATE: 2002-05-21
/ PRIOR APPLICATION NUMBER: PCT/GB01/01219
/ PRIOR FILING DATE: 2001-03-20
/ PRIOR APPLICATION NUMBER: GB 0006695.1
/ PRIOR FILING DATE: 2000-03-20
/ PRIOR APPLICATION NUMBER: GB 0007265.2
/ PRIOR FILING DATE: 2000-02-24
/ NUMBER OF SEQ ID NOS: 308

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 239
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapien
US-09-988-493-239

Query Match          100.0%; Score 69; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYSPTYNTIDDL 12
    |||||
Db 1 NYSPTYNTIDDL 12

RESULT 3
US-09-765-272-26
; Sequence 26, Application US/09765272
; Patent No. US20020061545A1
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-765-272-26

Query Match          76.8%; Score 53; DB 3; Length 420;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YSPYNTID 10
    |||||
Db 368 YSPYNTID 376

RESULT 4
US-11-106-649-26
; Sequence 26, Application US/11106649
; Publication No. US20050181439A1
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; GENERAL INFORMATION:
; APPLICANT: Choi et al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; FILE REFERENCE: PB340P2C3D1
; CURRENT APPLICATION NUMBER: US/11/106,649
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 09/765,271
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 09/536,784
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 08/961,083
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,960
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 454
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-11-106-649-26

Query Match          76.8%; Score 53; DB 6; Length 420;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YSPYNTID 10
    |||||
Db 368 YSPYNTID 376

RESULT 5
US-09-769-736-137
; Sequence 137, Application US/09769736
; Publication No. US20030138775A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Le Page, Richard WF
; APPLICANT: Wells, Jeremy M
; APPLICANT: Hanniffy, Sean B
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21089wo
; CURRENT APPLICATION NUMBER: US/09/769,736
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: GB 9816335.5
; PRIOR FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: US 60/125163
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 137
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-09-769-736-137

Query Match          76.8%; Score 53; DB 3; Length 438;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YSPYNTID 10
    |||||
Db 387 YSPYNTID 395

RESULT 6
US-11-123-241-137
; Sequence 137, Application US/11123241
; Publication No. US20060078565A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Le Page, Richard WF
; APPLICANT: Wells, Jeremy M
```



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; APPLICANT: Hanniffy, Sean B
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21083wo
; CURRENT APPLICATION NUMBER: US/11/123,241
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: US/09/769,736
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: GB 9816335.5
; PRIOR FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: US 60/125163
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 137
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-11-123-241-137

Query Match          76.8%; Score 53; DB 6; Length 438;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSPYNTID 10
DB 387 YSPYNTID 395

RESULT 7
US-10-474-792-96
; Sequence 96, Application US/10474792
; Publication No. US20040236072A1
; GENERAL INFORMATION:
; APPLICANT: Olmsted, Stephen
; APPLICANT: Zagursky, Robert
; APPLICANT: Nickbarg, Elliot
; APPLICANT: Winter, Laurie
; TITLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
; FILE REFERENCE: AM 100399
; CURRENT APPLICATION NUMBER: US/10/474,792
; CURRENT FILING DATE: 2003-10-14
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 96
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-474-792-96

Query Match          76.8%; Score 53; DB 5; Length 439;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSPYNTID 10
DB 389 YSPYNTID 397

RESULT 8
US-09-769-787-121
; Sequence 121, Application US/09769787
; Publication No. US20030091577A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/09/769,787
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; SEQ ID NO 121

; APPLICANT: Chiron SpA
; TITLE OF INVENTION: THE INSTITUTE FOR GENOMIC RESEARCH
; FILE REFERENCE: P026926WO
; CURRENT APPLICATION NUMBER: US/10/472,928
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: GB-0107658.7
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4979
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 3466
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; OTHER INFORMATION: sugar ABC transporter, sugar-binding protein
; OTHER INFORMATION: Cellular location: lipoprotein
; OTHER INFORMATION: Similar to strain R6 sequence 15903570 (0.E+01)
US-10-472-928-3466

Query Match          76.8%; Score 53; DB 5; Length 442;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSPYNTID 10
DB 390 YSPYNTID 398

RESULT 9
US-10-472-928-3466
; Sequence 1466, Application US/10472928
; Publication No. US20050020813A1
; GENERAL INFORMATION:
; APPLICANT: Chiron SpA
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026926WO
; CURRENT APPLICATION NUMBER: US/10/472,928
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: GB-0107658.7
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4979
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 3466
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; OTHER INFORMATION: sugar ABC transporter, sugar-binding protein
; OTHER INFORMATION: Cellular location: lipoprotein
; OTHER INFORMATION: Similar to strain R6 sequence 15903570 (0.E+01)
US-10-472-928-3466

Query Match          76.8%; Score 53; DB 3; Length 442;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSPYNTID 10
DB 390 YSPYNTID 398

RESULT 10
US-10-873-528-121
; Sequence 121, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 121
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; LENGTH: 442
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-121

Query Match      76.8%; Score 53; DB 5; Length 442;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSPYNTID 10
Db 390 YSPYNTID 398

RESULT 11
US-10-617-320-3143
; Sequence 3143, Application US/10617320
; Publication No. US20050136404A1
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/617,320
; FILING DATE: 10-Jul-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3143:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...458
; SEQUENCE DESCRIPTION: SEQ ID NO: 3143:
US-10-617-320-3143

Query Match      76.8%; Score 53; DB 5; Length 458;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSPYNTID 10
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|||||
Db 406 YSPYNTID 414

RESULT 12
US-10-425-115-308578
; Sequence 308578, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 308578
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_44492C.1.pep
US-10-425-115-308578

Query Match      72.5%; Score 50; DB 4; Length 101;
Best Local Similarity 66.7%; Pred. No. 2.4;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYSPYNTIDDL 12
Db 45 DYSPYFKTIEDL 56

RESULT 13
US-10-029-386-33790
; Sequence 33790, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33790
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL353997.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.98
; OTHER INFORMATION: SWISSPROT HIT: P08779, EVALUATION 3.00e-27
US-10-029-386-33790

Query Match      72.5%; Score 50; DB 4; Length 166;
Best Local Similarity 66.7%; Pred. No. 4;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYSPYNTIDDL 12
Db 152 DYSPYFKTIEDL 163

RESULT 14
US-10-450-763-54046
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; Sequence 54046, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 54046
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (128)..(143)
; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX.
; OTHER INFORMATION: accession number BL00226A, p-value=1.857e-15, raw score of 12.77
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (128)..(221)
; OTHER INFORMATION: Intermediate filament proteins domain identified by Pfam,
; OTHER INFORMATION: accession name filament, E-value=1.4e-49, Pfam score of 178.1
US-10-450-763-54046

Query Match 72.5%; Score 50; DB 5; Length 221;
Best Local Similarity 66.7%; Pred. No. 5.4;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYSPYNTIDDL 12
:||||:|
Db 175 DYSPYKTIEDL 186

RESULT 15
US-10-104-047-2943
; Sequence 2943, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2943
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2943

Query Match 72.5%; Score 50; DB 4; Length 355;
Best Local Similarity 66.7%; Pred. No. 8.9;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYSPYNTIDDL 12
:||||:|
Db 139 DYSPYKTIEDL 150

Search completed: July 5, 2006, 20:52:00
Job time : 87.8447 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 20:39:32 ; Search time 6.87379 Seconds
(without alignments)
46.842 Million cell updates/sec

Title: US-10-774-928A-6
Perfect score: 69
Sequence: 1 NYSPTYNTIDDL 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 112942

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	100.0	27	7	US-11-134-871-682
2	43	62.3	400	7	US-11-105-233-182
3	39	56.5	23	7	US-11-134-871-701
4	39	56.5	23	7	US-11-134-871-3401
5	39	56.5	540	6	US-10-449-902-51440
6	38	55.1	212	6	US-10-449-902-36492
7	38	55.1	212	6	US-10-449-902-51948
8	37	53.6	159	6	US-10-953-349-14759
9	37	53.6	315	6	US-10-953-349-28574
10	37	53.6	360	6	US-10-953-349-28573
11	37	53.6	394	6	US-10-953-349-28572
12	37	53.6	399	6	US-10-449-902-31745
13	37	53.6	399	6	US-10-449-902-55264
14	37	53.6	1051	6	US-10-449-902-55175
15	37	53.6	1466	6	US-10-985-570-1
16	37	53.6	1466	7	US-11-105-233-44
17	37	53.6	1466	7	US-11-105-233-167
18	36	52.2	25	7	US-11-134-871-2867
19	36	52.2	261	6	US-10-471-571A-496
20	36	52.2	424	7	US-11-105-233-183
21	36	52.2	599	6	US-10-471-571A-484
22	36	52.2	809	6	US-10-449-902-42942
23	35.5	51.4	315	6	US-10-953-349-9204
24	35.5	51.4	400	6	US-10-953-349-9203
25	35.5	51.4	401	6	US-10-953-349-9202

Sequence 52, Appl
Sequence 2032, Ap
Sequence 30011, A
Sequence 42693, A
Sequence 30010, A
Sequence 2031, Ap
Sequence 324, App
Sequence 2030, Ap
Sequence 5594, Ap
Sequence 12, Appl
Sequence 61, Appl
Sequence 4, Appl
Sequence 8, Appl
Sequence 6, Appl
Sequence 47769, A
Sequence 10, Appl
Sequence 40557, A
Sequence 52546, A
Sequence 55424, A
Sequence 29415, A

26 35 50.7 243 7 US-11-347-766-52
27 35 50.7 260 6 US-10-953-349-2032
28 35 50.7 272 6 US-10-953-349-30011
29 35 50.7 273 6 US-10-449-902-42693
30 35 50.7 320 6 US-10-953-349-30010
31 35 50.7 352 6 US-10-953-349-2031
32 35 50.7 375 6 US-10-471-571A-324
33 35 50.7 382 6 US-10-953-349-2030
34 35 50.7 411 6 US-10-471-571A-5594
35 35 50.7 433 7 US-11-315-766-12
36 35 50.7 489 7 US-11-251-208-61
37 35 50.7 530 7 US-11-315-766-4
38 35 50.7 533 7 US-11-315-766-8
39 35 50.7 533 7 US-11-315-766-6
40 35 50.7 618 6 US-10-449-902-47769
41 35 50.7 626 6 US-10-542-516-10
42 35 50.7 641 6 US-10-449-902-40557
43 35 50.7 656 6 US-10-449-902-52546
44 35 50.7 1033 6 US-10-449-902-55424
45 34 49.3 172 6 US-10-953-349-29415

ALIGNMENTS

RESULT 1
US-11-134-871-682
; Sequence 682, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Abersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Quatification of Serum Glycoproteins
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 682
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-682

Query Match 100.0%; Score 69; DB 7; Length 27;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYSPTYNTIDDL 12
Db 2 NYSPTYNTIDDL 13

RESULT 2
US-11-105-233-182
; Sequence 182, Application US/11105233
; Publication No. US20060134653A1
; GENERAL INFORMATION:
; APPLICANT: Thiagalingam et al
; TITLE OF INVENTION: Differential Expression of Genes in MSI
; TITLE OF INVENTION: Tumors
; FILE REFERENCE: 1657/2001
; CURRENT APPLICATION NUMBER: US/11/105,233
; CURRENT FILING DATE: 2005-04-13
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-105-233-182

Query Match 62.3%; Score 43; DB 7; Length 400;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NYSPTYNTIDDL 12
Db 126 DYSHYTTIQDL 137

RESULT 3

US-11-134-871-701
; Sequence 701, Application US/111134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Quantification of Serum Glycoproteins
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; PRIOR FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 701
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-701

Query Match 56.5%; Score 39; DB 7; Length 23;
Best Local Similarity 60.0%; Pred. No. 0.93;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SPYNTIDDL 12
Db 2 SPYNTSDEI 11

RESULT 4

US-11-134-871-3401
; Sequence 3401, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Quantification of Serum Glycoproteins
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; PRIOR FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3401
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-3401

Query Match 56.5%; Score 39; DB 7; Length 23;
Best Local Similarity 60.0%; Pred. No. 0.93;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SPYNTIDDL 12
Db 2 SPYNTSDEI 11

RESULT 5

US-10-449-902-51440
; Sequence 51440, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51440
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-51440

Query Match 56.5%; Score 39; DB 6; Length 540;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 YYNTIDDL 12
Db 420 YYNTIEDM 427

RESULT 6

US-10-449-902-36492
; Sequence 36492, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36492
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-36492

Query Match 55.1%; Score 38; DB 6; Length 212;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NYSPTYNTID 10
Db 106 NKSPYHEIVD 115

RESULT 7

US-10-449-902-51948
; Sequence 51948, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:

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; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51948
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-51948

Query Match      55.1%; Score 38; DB 6; Length 212;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 NYSPPYNTID 10
Db      106 NKSPYHETVD 115

RESULT 8
US-10-953-349-14759
; Sequence 14759, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14759
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-14759

Query Match      53.6%; Score 37; DB 6; Length 159;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      1 NYSPPYNTIDDL 12
Db      5 NRKIYNTMDEI 16

RESULT 9
US-10-953-349-28574
; Sequence 28574, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28574
; LENGTH: 315
; TYPE: PRT
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; ORGANISM: Triticum aestivum
US-10-953-349-28574

Query Match      53.6%; Score 37; DB 6; Length 315;
Best Local Similarity 70.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 YSPYNTID 11
Db      263 YSVYNTTRSD 272

RESULT 10
US-10-953-349-28573
; Sequence 28573, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28573
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-28573

Query Match      53.6%; Score 37; DB 6; Length 360;
Best Local Similarity 70.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 YSPYNTID 11
Db      308 YSVYNTTRSD 317

RESULT 11
US-10-953-349-28572
; Sequence 28572, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28572
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-28572

Query Match      53.6%; Score 37; DB 6; Length 394;
Best Local Similarity 70.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 YSPYNTID 11
Db      342 YSVYNTTRSD 351

RESULT 12
US-10-449-902-31745
; Sequence 31745, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
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; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31745
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-31745

Query Match      53.6%; Score 37; DB 6; Length 399;
Best Local Similarity 70.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 YSPYYNTIDD 11
DB      347 YSVYNTIRSD 356

RESULT 13
US-10-449-902-55264
; Sequence 55264, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55264
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-55264

Query Match      53.6%; Score 37; DB 6; Length 399;
Best Local Similarity 70.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 YSPYYNTIDD 11
DB      347 YSVYNTIRSD 356

RESULT 14
US-10-449-902-55175
; Sequence 55175, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
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; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55175
; LENGTH: 1051
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-55175

Query Match      53.6%; Score 37; DB 6; Length 1051;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 SPYYNTIDDL 12
DB      601 TPIQNTIDDL 610

RESULT 15
US-10-985-570-1
; Sequence 1, Application US/10985570
; Publication No. US20060100138A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, David R.
; APPLICANT: Polarek, James W.
; APPLICANT: Yang, Chunlin
; TITLE OF INVENTION: IMPLANTABLE COLLAGEN COMPOSITIONS
; FILE REFERENCE: FP0305 US
; CURRENT APPLICATION NUMBER: US/10/985,570
; CURRENT FILING DATE: 2004-11-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-985-570-1

Query Match      53.6%; Score 37; DB 6; Length 1466;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 NYSPYYNTID 10
DB      150 NYSPQYDSYD 159

Search completed: July 5, 2006, 20:53:04
Job time : 7.87379 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 5, 2006, 19:18:42 ; Search time 27.0291 Seconds
(without alignments)
38.861 Million cell updates/sec

Title: US-10-774-928A-6
Perfect score: 69
Sequence: 1 NYSPPYNTIDDL 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	100.0	12	US-09-809-003A-6	Sequence 6, Appli
2	53	76.8	420	US-08-961-083-26	Sequence 26, Appl
3	53	76.8	420	US-09-536-784-26	Sequence 26, Appl
4	53	76.8	420	US-09-765-271-26	Sequence 26, Appl
5	53	76.8	420	US-09-765-272A-26	Sequence 26, Appl
6	53	76.8	442	US-09-583-110-3180	Sequence 3180, Ap
7	53	76.8	442	US-09-769-787-121	Sequence 121, App
8	53	76.8	458	US-09-107-433-3143	Sequence 3143, Ap
9	50	72.5	355	US-10-104-047-2943	Sequence 2943, Ap
10	50	72.5	435	US-09-949-016-8415	Sequence 8415, Ap
11	50	72.5	435	US-09-949-016-8792	Sequence 8792, Ap
12	50	72.5	471	US-09-538-092-837	Sequence 837, App
13	50	72.5	593	US-09-538-092-919	Sequence 919, App
14	49	71.0	151	US-09-248-796A-23537	Sequence 23537, A
15	49	71.0	152	US-09-248-796A-27566	Sequence 27566, A
16	46	66.7	242	US-09-949-016-20477	Sequence 20477, A
17	44	63.8	31	US-07-934-656A-13	Sequence 13, Appl
18	43	62.3	142	US-09-370-838-213	Sequence 213, App
19	43	62.3	142	US-09-854-133-213	Sequence 213, App
20	43	62.3	247	US-10-104-047-3859	Sequence 3859, Ap
21	43	62.3	400	US-07-730-953-2	Sequence 2, Appli
22	43	62.3	442	US-09-949-016-8625	Sequence 8625, Ap
23	43	62.3	1577	US-08-793-824-2	Sequence 2, Appli
24	42	60.9	432	US-08-705-660-18	Sequence 18, Appl
25	42	60.9	432	US-08-989-045-18	Sequence 18, Appl
26	42	60.9	432	US-09-919-172-9	Sequence 9, Appli

27	42	60.9	432	2	US-09-315-355A-18	Sequence 18, Appl
28	41	59.4	185	2	US-09-949-016-9796	Sequence 9796, Ap
29	41	59.4	323	2	US-09-830-230A-644	Sequence 644, App
30	41	59.4	358	2	US-09-830-230A-643	Sequence 643, App
31	40.5	58.7	420	2	US-09-248-796A-17357	Sequence 17357, A
32	40	58.0	31	1	US-07-934-656A-10	Sequence 10, Appl
33	40	58.0	31	1	US-07-934-656A-14	Sequence 14, Appl
34	40	58.0	255	2	US-09-107-433-4006	Sequence 4006, Ap
35	40	58.0	401	2	US-09-248-796A-15983	Sequence 15983, A
36	40	58.0	433	2	US-09-248-796A-20493	Sequence 20493, A
37	40	58.0	501	2	US-09-583-110-3372	Sequence 3372, Ap
38	39	56.5	113	2	US-09-583-110-4936	Sequence 4936, Ap
39	39	56.5	121	2	US-09-107-433-4803	Sequence 4803, Ap
40	39	56.5	124	7	5514582-38	Patent No. 5514582
41	39	56.5	265	1	US-08-177-109A-57	Sequence 57, Appl
42	39	56.5	265	1	US-08-687-706-57	Sequence 16, Appl
43	39	56.5	314	3	US-10-128-713A-16	Sequence 16, Appl
44	39	56.5	364	2	US-09-328-352-6641	Sequence 6641, Ap
45	39	56.5	520	2	US-09-292-858B-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-809-003A-6
; Sequence 6, Application US/09809003A
; Patent No. 6673351
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; FILE OF INVENTION: Psoriasis
; FILE REFERENCE: 302178
; CURRENT APPLICATION NUMBER: US/09/809,003A
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Leishmania
US-09-809-003A-6

Query Match 100.0%; Score 69; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.2e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYSPPYNTIDDL 12
DB 1 NYSPPYNTIDDL 12

RESULT 2
US-08-961-083-26
; Sequence 26, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-961-083-26

Query Match 76.8%; Score 53; DB 2; Length 420;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSPYNTID 10
Db 368 YSPYNTID 376

RESULT 3
US-09-536-784-26
; Sequence 26, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,271
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/536,784
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-536-784-26
Query Match 76.8%; Score 53; DB 2; Length 420;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSPYNTID 10
Db 368 YSPYNTID 376

RESULT 5
US-09-765-272A-26
; Sequence 26, Application US/09765272A
; Patent No. 6929930
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines
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;; Vaccines
;;
;; NUMBER OF SEQUENCES: 454
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;; COMPUTER: Dell Latitude C610
;; OPERATING SYSTEM: Windows 2000
;; SOFTWARE: ASCII Text
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/765,272A
;; FILING DATE: 22-Jan-2001
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/961,083
;; FILING DATE: OCT-30-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lin J. Hymel
;; REGISTRATION NUMBER: 45,414
;; REFERENCE/DOCKET NUMBER: PB340P2C2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (301) 610-5790
;; TELEFAX: (301) 309-8439
;; INFORMATION FOR SEQ ID NO: 26:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 420 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-765-272A-26

Query Match 76.8%; Score 53; DB 2; Length 420;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSPYNTID 10
Db 368 YSPYNTID 376

RESULT 6
US-09-583-110-3180
; Sequence 3180, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 3180
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3180

Query Match 76.8%; Score 53; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 1.2;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSPYNTID 10
Db 390 YSPYNTID 398

RESULT 7
US-09-769-787-121
; Sequence 121, Application US/09769787
; Patent No. 6936252
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/09/769,787
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 121
; TYPE: PRT
; LENGTH: 442
; ORGANISM: Streptococcus pneumoniae
US-09-769-787-121

Query Match 76.8%; Score 53; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSPYNTID 10
Db 390 YSPYNTID 398

RESULT 8
US-09-107-433-3143
; Sequence 3143, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489

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; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3143:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...458
; SEQUENCE DESCRIPTION: SEQ ID NO: 3143:
US-09-107-433-3143

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Best Local Similarity 100.0%; Pred. No. 1.2; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 2 YSPYNTID 10
Db 406 YSPYNTID 414

RESULT 9
US-10-104-047-2943
; Sequence 2943, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2943
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2943

Query Match 72.5%; Score 50; DB 2; Length 355;
Best Local Similarity 66.7%; Pred. No. 2.8;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NYSPTYNTIDDL 12
Db 139 DYSPYKTIIEEL 150

RESULT 10
US-09-949-016-8415
; Sequence 8415, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; SOFTWARE: CuratPatSeqFormatter Version 0.9
; SEQ ID NO 837
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Homo sapiens

; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3143:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8415

Query Match 72.5%; Score 50; DB 2; Length 435;
Best Local Similarity 66.7%; Pred. No. 3.4;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NYSPTYNTIDDL 12
Db 166 DYSPYKTIIEEL 177

RESULT 11
US-09-949-016-8792
; Sequence 8792, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8792
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8792

Query Match 72.5%; Score 50; DB 2; Length 435;
Best Local Similarity 66.7%; Pred. No. 3.4;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NYSPTYNTIDDL 12
Db 166 DYSPYKTIIEEL 177

RESULT 12
US-09-538-092-837
; Sequence 837, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratPatSeqFormatter Version 0.9
; SEQ ID NO 837
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Homo sapiens
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P02533
US-09-538-092-837

Query Match 72.5%; Score 50; DB 2; Length 471;
Best Local Similarity 66.7%; Pred. No. 3.8;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYSPPYNTIDDL 12
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Db 160 DYSPYKTIIDL 171

RESULT 13

US-09-538-092-919
Sequence 919, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Glot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CurapatSeqformatter Version 0.9
SEQ ID NO 919
LENGTH: 593
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P13645
US-09-538-092-919

Query Match 72.5%; Score 50; DB 2; Length 593;
Best Local Similarity 75.0%; Pred. No. 4.8;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYSPPYNTIDDL 12
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Db 195 DYSPYKTIIDL 206

RESULT 14

US-09-248-796A-23537
Sequence 23537, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 23537
LENGTH: 151
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-23537

Query Match 71.0%; Score 49; DB 2; Length 151;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYSPPYNTIDDL 12
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Db 113 NYSYYNSLDEL 124

RESULT 15

US-09-248-796A-27566
Sequence 27566, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 27566
LENGTH: 152
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-27566

Query Match 71.0%; Score 49; DB 2; Length 152;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYSPPYNTIDDL 12
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Db 117 NYSYYNSLDEL 128

Search completed: July 5, 2006, 19:24:27
Job time : 27.0291 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 5, 2006, 19:09:18 ; Search time 12.1359 Seconds
(without alignments)
79.283 Million cell updates/sec

Title: US-10-774-928A-7

Perfect score: 47

Sequence: 1 AEAEELYQSK 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 80:*

2: PIR1:*

3: PIR2:*

4: PIR3:*

5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	643	1 KRHU2	keratin 1, type II
2	44	93.6	553	2 I59009	epidermal keratin
3	41	87.2	390	2 A60093	cytokeatin, type I
4	41	87.2	534	2 I37942	keratin 4, type II
5	41	87.2	629	2 A29666	keratin, 65K type
6	40	85.1	581	1 KRMS2	keratin, type II C
7	39	83.0	483	2 A34720	keratin 8, type II
8	38	80.9	384	2 I61769	keratin 6d, type I
9	38	80.9	564	1 KRHUBA	keratin 6a, type I
10	38	80.9	564	1 KRHUBB	keratin 6b, type I
11	38	80.9	564	2 I61770	keratin 6e, type I
12	38	80.9	564	2 I61768	keratin 6c, type I
13	38	80.9	564	2 I61771	keratin 6f, type I
14	38	80.9	638	2 I53169	keratin-like prote
15	37	78.7	257	2 I38025	cytokeatin 2 - hu
16	37	78.7	346	2 S34165	keratin, type II -
17	37	78.7	480	2 A56694	keratin, type II
18	37	78.7	491	2 S05408	keratin, type II,
19	37	78.7	503	2 S29094	keratin, type II,
20	37	78.7	508	1 KRSHU2	keratin type II, m
21	37	78.7	513	2 S08381	hemolysin I secret
22	37	78.7	707	2 D43599	keratin, 58K type
23	36	76.6	310	2 S43855	keratin, 53K type
24	36	76.6	370	2 A25004	keratin 8, type II
25	36	76.6	487	2 J70407	keratin 8, type II
26	36	76.6	489	2 S05474	cytokeatin EndoA
27	36	76.6	490	2 JS0658	intermediate filam
28	35	74.5	458	2 S09228	keratin, type II -
29	35	74.5	461	2 A43782	keratin, type II -

ALIGNMENTS

RESULT 1

KRHU2

keratin 1, type II, cytoskeletal - human

N;Alternate names: 67K type II epidermal keratin; cytokeratin 1

C;Species: Homo sapiens (man)

C;Date: 04-Dec-1986 #sequence_revision 22-Oct-1999 #text_change 10-Dec-1999

C;Accession: A22940; A02950; A43342

R;Johnson, L.D.; Idler, W.W.; Zhou, X.M.; Roop, D.R.; Steinert, P.M.

Proc. Natl. Acad. Sci. U.S.A. 82, 1896-1900, 1985

A;Reference number: A22940; MUID:85166239; PMID:2580302

A;Accession: A22940

A;Molecule type: DNA

A;Residues: 1-643 <JOH>

A;Cross-references: UNIPARC:UPI0000173D59; GB:M11845; GB:M11846; N

R;Steinert, P.M.; Parry, D.A.D.; Idler, W.W.; Johnson, L.D.; Steven, A.C.; Roop, D.R.

J. Biol. Chem. 260, 7142-7149, 1985

A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67,000

late filament subunits.

A;Reference number: A92535; MUID:85207740; PMID:2581964

A;Accession: A02950

A;Molecule type: mRNA

A;Residues: 151-183, 'K', 185-199, 'N', 201-204, 'K', 206-236, 'S', 238-239, 'R', 241-356, 'Y', 358-

, 'S', 638-643 <STE>

A;Cross-references: UNIPARC:UPI000016ABD0; GB:M10938; NID:g186787; PIDN:AAA36153.1; PID:

A;Experimental source: tissue neonatal foreskin

A;Note: the authors translated the codon CUG for residue 476 as Met

R;Chipev, C.C.; Korge, B.P.; Markova, N.; Bale, S.J.; DiGiovanna, J.J.; Compton, J.G.; S

Cell 70, 821-828, 1992

A;Title: A leucine---proline mutation in the H1 subdomain of keratin 1 causes epidermol

A;Reference number: A43342; MUID:92386601; PMID:1381288

A;Accession: A43342

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 144-146, 'P', 148-159, 'P', 161-183, 'K', 185-186 <CHI>

A;Cross-references: UNIPARC:UPI0000173D59; GB:M11215; GB:M11845; GB:M11846; N

A;Note: sequence extracted from NCBI backbone (NCBIP:112784)

C;Comment: The cytoskeletal and microfibrillar keratins are classified into two types, t

atin IF protein subunit appears to be a heterotetramer of two type I and two type II pro

C;Comment: Keratin 1 is expressed in terminally differentiating epidermis.

C;Genetics:

A;Gene: GDB:KRT1

A;Cross-references: GDB:128198; OMIM:139350

A;Map position: 12q11-12q13

A;Note: defects in this gene may result in epidermolytic hyperkeratosis

C;Complex: heterotetramer of two type I, usually keratin 10 (see PIR:KRU00), and two typ

C;Superfamily: cytoskeletal keratin

C;Keywords: coiled coil; heterotetramer; intermediate filament

F;4-179/Domain: head <HBD>

F;4-143/Region: E1 and V1 subdomains

F;14-179/Region: H1 subdomain

F;180-492/Domain: rod <ROD>

keratin K7, type I
keratin, 55K type
keratin K3 - rabbi
keratin, 67K type
hypothetical prote
keratin type II, h
RNA-directed RNA p
keratin 5, type II
hypothetical prote
RNA-directed RNA p
UDPglucose-glycopr
desmin - African c
desmin - chicken
hypothetical prote
OmpA-related prote
hypothetical prote

30 35 74.5 469 2 S05602
31 35 74.5 489 2 B24177
32 35 74.5 629 2 S42829
33 35 74.5 645 2 A44861
34 35 74.5 939 2 AF2503
35 34 72.3 479 2 A61368
36 34 72.3 525 1 RRXS15
37 34 72.3 590 2 A29904
38 34 72.3 857 2 T05352
39 34 72.3 878 1 RRXS1B
40 34 72.3 1447 2 S63669
41 33 70.2 458 2 A43554
42 33 70.2 463 1 DMCH
43 33 70.2 646 2 T34532
44 33 70.2 1055 2 A87364
45 32 68.1 249 2 B86231

F:180-214/Region: coil 1A
 F:215-226/Region: linker 1
 F:227-327/Region: coil 1B
 F:328-344/Region: linker 12
 F:345-363/Region: linker 2A
 F:364-371/Region: coil 2A
 F:372-492/Region: linker 2B
 F:430/Region: stutler
 F:493-643/Domain: tail <END>
 F:493-512/Region: H2 subdomain
 F:513-643/Region: V2 and E2 subdomains

Query Match 100.0%; Score 47; DB 1; Length 643;

Best Local Similarity 100.0%; Pred. No. 0.09; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLYQSK 10
 |||||
 Db 366 AEAESLYQSK 375

RESULT 2

IS9009

epidermal keratin subunit II - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: IS9009; A61205

R:Steinert, P.M.; Parry, D.A.D.; Racoosin, E.L.; Idler, W.W.; Steven, A.C.; Trus, B.L.; Proc. Natl. Acad. Sci. U.S.A. 81, 5709-5713, 1984

A:Title: The complete cDNA and deduced amino acid sequence of a type II mouse epidermal

A:Reference number: IS9009; MUID:85014838; PMID:6207530

A:Accession: IS9009

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-553 <RES>

A:Cross-references: UNIPROT:P50446; UNIPARC:UPI000016CE87; GB:K02108; NID:G1986334; PIDN:

R:Finch, J.; Andrews, K.; Krieg, P.; Fuerstenberger, G.; Slaga, T.; Ootsuyama, A.; Tanoc

Carcinogenesis 12, 1519-1522, 1991

A:Title: Identification of a cloned sequence activated during multi-stage carcinogenesis

A:Reference number: A61205; MUID:91316763; PMID:1713533

A:Accession: A61205

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 528-553 <FTN>

A:Cross-references: UNIPARC:UPI00001774C8

C:Genetics:

A:Gene: KER2

C:Superfamily: cytoskeletal keratin

Query Match 93.6%; Score 44; DB 2; Length 553;

Best Local Similarity 90.0%; Pred. No. 0.33;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLYQSK 10
 |||||
 Db 339 AEAESLYQTK 348

RESULT 3

A60093

cytokeratin, type II, early ectodermal - chicken (fragment)

C:Species: Gallus gallus (chicken)

C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993

C:Accession: A60093

R:Charlebois, T.S.; Spencer, D.H.; Tarkington, S.K.; Henry, J.J.; Grainger, R.M.

Development 108, 33-45, 1990

A:Title: Isolation of a chick cytokeratin cDNA clone indicative of regional specialization

A:Reference number: A60093; MUID:90276238; PMID:1693557

A:Accession: A60093

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-390 <CHA>

A:Cross-references: UNIPARC:UPI00001774C6

C:Superfamily: cytoskeletal keratin
 C:Keywords: intermediate filament

Query Match 87.2%; Score 41; DB 2; Length 390;
 Best Local Similarity 90.0%; Pred. No. 0.98;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AEAESLYQSK 10
 |||||
 Db 198 AEAESLYQSK 207

RESULT 4

I37942

keratin 4, type II, cytoskeletal - human

N:Alternate names: basic cytokeratin; cytokeratin 4

C:Species: Homo sapiens (man)

C:Date: 12-Aug-1996 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004

C:Accession: I37942; S01068; S21884; A30186; S31662

R:Wanner, R.; Forster, H.H.; Tilmans, I.; Mischke, D.

J. Invest. Dermatol. 100, 735-741, 1993

A:Title: Allelic variations of human keratins K4 and K5 provide polymorphic markers with

A:Reference number: I37942; MUID:93267125; PMID:7684424

A:Accession: I37942

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-127, I', 129-144 <WAN1>

A:Cross-references: UNIPROT:P19013; UNIPARC:UPI000016AB8C; EMBL:X67683; NID:G34020; PIDN:

R:Leube, R.E.; Bader, B.L.; Bosch, F.X.; Zimbelmann, R.; Achtsaetter, T.; Franke, W.W.

J. Cell Biol. 106, 1249-1261, 1988

A:Title: Molecular characterization and expression of the stratification-related cytokerat

A:Reference number: S01068; MUID:88198369; PMID:2452170

A:Accession: S01068

A:Molecule type: mRNA

A:Residues: 'S', 128-534 <LEU>

A:Cross-references: UNIPARC:UPI000016ABA3; EMBL:X07695; NID:G34072; PIDN:CAA30534.1; PID:

R:Wanner, R.; Tilmans, I.; Mischke, D.

submitted to the EMBL Data Library, July 1991

A:Reference number: S21884

A:Accession: S21884

A:Molecule type: DNA

A:Residues: 411-534 <WAN2>

A:Cross-references: UNIPARC:UPI000016ABA5; EMBL:X61028; NID:G34076; PIDN:CAA43362.1; PID:

A:Experimental source: allele K4a

C:Genetics:

A:Gene: GDB:KRT4; CYK4

A:Cross-references: GDB:120697; OMIM:123940

A:Map position: 12p11.2-12q11

A:Introns: 463/2; 475/1

C:Superfamily: cytoskeletal keratin

C:Keywords: coiled coil; intermediate filament

F:1-152/Domain: head #status predicted <HEA>

F:153-464/Domain: helical rod #status predicted <ROD>

F:465-534/Domain: tail #status predicted <TAI>

Query Match 87.2%; Score 41; DB 2; Length 534;
 Best Local Similarity 80.0%; Pred. No. 1.4;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLYQSK 10
 |||||
 Db 338 AEAALYQTK 347

RESULT 5

A29666

keratin, 65K type II cytoskeletal - human

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 20-Apr-2001

C:Accession: A29666

R:Klinge, E.M.; Sylvestre, Y.R.; Freedberg, I.M.; Blumenberg, M.

J. Mol. Evol. 24, 319-329, 1987

A:Title: Evolution of keratin genes: different protein domains evolve by different pathwa

A;Reference number: A29666; MUID:87254239; PMID:2439698

A;Accession: A29666

A;Molecule type: DNA

A;Residues: 1-629 <KUL>

A;Cross-references: UNIPARC:UPI0000161C35; GB:X05418; NID:G34040; PIDN:CAA28991.1; PID:G34047

A;Cross-references: UNIPARC:UPI0000161C35; GB:X05418; NID:G34040; PIDN:CAA28991.1; PID:G34047

A;Note: the authors translated the codon AAC for residue 63 as Asp and ACA for residue 2

A;Note: the complete translation is not annotated in GenBank entries HSKER65A, HSKER65B,

s mistranslated as a Met initiator codon

C;Genetics:

A;Introns: 215/3; 289/2; 309/3; 341/3; 396/3; 438/3; 512/2; 525/1

C;Superfamily: cytoskeletal keratin

C;Keywords: coiled coil

Query Match 87.2%; Score 41; DB 2; Length 629;

Best Local Similarity 80.0%; Pred. No. 1.6;

Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEAEELYQSK 10

Db 387 AEAEELYQTK 396

|||||:|||||

|||||:|||||

RESULT 6

KRMS2

keratin, type II cytoskeletal - mouse (fragment)

N;Alternate names: 67-kDa type II keratin

C;Species: Mus musculus (house mouse)

C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004

C;Accession: A02951

R;Steinert, P.M.; Parry, D.A.D.; Idler, W.W.; Johnson, L.D.; Steven, A.C.; Roop, D.R.

J. Biol. Chem. 260, 7142-7149, 1985

A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67,000

late filament subunits.

A;Reference number: A92535; MUID:85207740; PMID:2581964

A;Accession: A02951

A;Molecule type: mRNA

A;Residues: 1-581 <STE>

A;Cross-references: UNIPROT:P04104; UNIPARC:UPI0000173D5B; GB:M10937; NID:G198622; PID:G

C;Superfamily: cytoskeletal keratin

C;Keywords: coiled coil; intermediate filament

F;1-106/Domain: head (fragment) <HED>

F;1-70/Region: V1 subdomain (fragment)

F;71-106/Region: H1 subdomain

F;107-419/Domain: rod <ROD>

F;142-153/Region: linker 1

F;154-254/Region: coil 1B

F;255-271/Region: linker 12

F;272-290/Region: coil 2A

F;291-298/Region: linker 2

F;299-419/Region: coil 2B

F;357/Region: stutter

F;420-581/Domain: tail <END>

F;420-439/Region: H2 subdomain

F;440-581/Region: V2 and E2 subdomains

Query Match 85.1%; Score 40; DB 1; Length 581;

Best Local Similarity 80.0%; Pred. No. 2.4;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AEAEELYQSK 10

Db 293 AEAEELYQSK 302

|||||:|||||

|||||:|||||

RESULT 7

KRMS2

keratin 8, type II cytoskeletal - human

C;Species: Homo sapiens (man)

C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004

C;Accession: A34720; S06888; S12479; I37982; I37983; JS0487; A31942

R;Yamamoto, R.; Kao, L.C.; McKnight, C.E.; Strauss III, J.F.

Mol. Endocrinol. 4, 370-374, 1990

A;Title: Cloning and sequence of cDNA for human placental cytokeratin 8. Regulation of t

A;Reference number: A34720; MUID:90258929; PMID:1692965

A;Accession: A34720

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-483 <YAM>

A;Cross-references: UNIPROT:P05787; UNIPARC:UPI00001774C3; GB:M34225

R;Leube, R.E.; Bosch, F.X.; Romano, V.; Zimbelmann, R.; Hoefler, H.; Franke, W.W.

Differentiation 33, 69-85, 1986

A;Title: Cytokeratin expression in simple epithelia.

A;Reference number: S06888; MUID:87134779; PMID:2434381

A;Accession: S06888

A;Molecule type: mRNA

A;Residues: 205-483 <LEU>

A;Cross-references: UNIPARC:UPI000016ABAI; EMBL:X12882

R;Franke, W.W.

submitted to the EMBL Data Library, September 1988

A;Reference number: S12479

A;Accession: S12479

A;Molecule type: mRNA

A;Residues: 205-309, 'I', 311-483 <FRA>

A;Cross-references: UNIPARC:UPI000016A769; EMBL:X12882; NID:G30312; PIDN:CAA31376.1; PID

R;Waseem, A.; Alexander, C.M.; Steel, J.B.; Lane, E.B.

New Biol. 2, 464-478, 1990

A;Title: Embryonic simple epithelial keratins 8 and 18: chromosomal location emphasizes

A;Reference number: I37982; MUID:91145351; PMID:1705144

A;Accession: I37982

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-76, 'V', 78-416, 'S', 418-428, 'G', 430-431, 'S', 433-483 <RES>

A;Cross-references: UNIPARC:UPI0000161B3E; EMBL:X74929; NID:G400415; PIDN:CAAS2882.1; PI

A;Accession: I37983

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 151-201, 'VD', 202-271 <RE2>

A;Cross-references: UNIPARC:UPI000016ABCF; EMBL:X74981; NID:G400417; PIDN:CAAS2916.1; PI

R;Krauss, S.; Franke, W.W.

Gene 86, 241-249, 1990

A;Title: Organization and sequence of the human gene encoding cytokeratin 8.

A;Reference number: JS0487; MUID:90215304; PMID:1691124

A;Accession: JS0487

A;Molecule type: DNA

A;Residues: 1-76, 'V', 78-428, 'G', 434-483 <KRA>

A;Cross-references: UNIPARC:UPI000016A82B; GB:M34482; NID:G181572; PIDN:AAA35763.1; PID:

R;Kulesh, D.A.; Cecena, G.; Darmon, Y.M.; Vasseur, M.; Oshima, R.G.

Mol. Cell. Biol. 9, 1553-1565, 1989

A;Title: Posttranslational regulation of keratins: degradation of mouse and human kerati

A;Reference number: A31942; MUID:89261783; PMID:2471085

A;Accession: A31942

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-76, 'V', 78-231 <KUL>

A;Cross-references: UNIPARC:UPI000016A354; GB:M26512; NID:G177796; PIDN:AAA51542.1; PID:

C;Comment: This protein is one of the type II cytokeratins.

C;Genetics:

A;Gene: GDB:XRT8

A;Cross-references: GDB:I18830; OMIM:148060

A;Map position: 12p13.2-12q24.1

A;Introns: 108/3; 178/2; 198/3; 230/3; 327/3; 401/2; 421/1

C;Superfamily: cytoskeletal keratin

C;Keywords: coiled coil; intermediate filament

Qy 1 AEAEELYQSK 10

Db 276 AEAEELYQSK 285

|||||:|||||

|||||:|||||

RESULT 8

KRMS2

keratin 8, type II cytoskeletal - human

C;Species: Homo sapiens (man)

C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004

C;Accession: A34720; S06888; S12479; I37982; I37983; JS0487; A31942

R;Yamamoto, R.; Kao, L.C.; McKnight, C.E.; Strauss III, J.F.

Query Match 83.0%; Score 39; DB 2; Length 483;

Best Local Similarity 80.0%; Pred. No. 3.3;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AEAEELYQSK 10

Db 276 AEAEELYQSK 285

|||||:|||||

|||||:|||||

RESULT 9

```
I61769
keratin 6d, type II - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: I61769
R:Takahashi, K.; Paladini, R.D.; Coulombe, P.A.
J. Biol. Chem. 270, 18581-18592, 1995
A:Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
A:Reference number: A57398; MUID:95355491; PMID:7543104
A:Accession: I61769
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-384 <RES>
A:Cross-references: UNIPROT:P48667; UNIPARC:UPI000012DB17; GB:L42602; NID:G914823; GB:L4
28; GB:L42608; NID:G914829; GB:L42609; NID:G914830; GB:L42610; NID:G1488252; PIDN:AAB606
C:Genetics:
A:Gene: KRT6D
A:Introns: 72/2; 92/3; 124/3; 179/3; 221/3; 295/2; 307/1
A:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil

Query Match      80.9%; Score 38; DB 2; Length 384;
Best Local Similarity 80.0%; Pred. No. 4.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 AEAESLYQSK 10
      ||||| ||:|
Db      170 AEAESWYQTK 179

RESULT 9
KRHUEA
keratin 6a, type II - human
N:Alternate names: 56-kDa type II keratin; keratin cytoskeletal
C:Species: Homo sapiens (man)
C>Date: 15-Nov-1984 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: A57398; A02944
R:Takahashi, K.; Paladini, R.D.; Coulombe, P.A.
J. Biol. Chem. 270, 18581-18592, 1995
A:Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
A:Reference number: A57398; MUID:95355491; PMID:7543104
A:Accession: A57398
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-564 <TAK>
A:Cross-references: UNIPROT:P02538; UNIPARC:UPI000013CD4C; GB:L42575; NID:G908769; GB:L4
74; GB:L42581; NID:G908775; GB:L42582; NID:G908776; GB:L42583; NID:G908777; PIDN:AAC4176
R:Hanukoglu, I.; Fuchs, E.
Cell 33, 915-924, 1983
A:Title: The cDNA sequence of a type II cytoskeletal keratin reveals constant and variab
A:Reference number: A02944; MUID:83259278; PMID:6191871
A:Accession: A02944
A:Molecule type: mRNA
A:Residues: 208-394,'S',396-564 <HAN>
A:Cross-references: UNIPARC:UPI000016AB87; GB:J00269; NID:G34068; PIDN:CRAA24760.1; PID:G
A:Comment: The cytoskeletal and microfibrillar keratins are classified into two types, b
atin IF protein subunit appears to be a heterotetramer of two type I and two type II prd
C:Genetics:
A:Gene: GDB:KRT6A
A:Cross-references: GDB:128111; OMIM:148041
A:Map position: 12q12-12q21
A:Introns: 180/3; 252/2; 272/3; 304/3; 359/3; 401/3; 475/2; 487/1
A:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament
F:2-163/Domain: head <HED>
F:127-163/Region: E1 and V1 subdomains
F:162-476/Domain: rod <ROD>
F:199-210/Region: linker 1
F:211-311/Region: coil 1B
F:312-328/Region: linker 12
F:329-347/Region: coil 2A
F:348-355/Region: linker 2
A:Gene: GDB:KRT6B
A:Cross-references: GDB:128113; OMIM:148042
A:Map position: 12pter-12qter
A:Introns: 180/3; 252/2; 272/3; 304/3; 359/3; 401/3; 475/2; 487/1
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament
F:2-163/Domain: head <HED>
F:127-163/Region: E1 and V1 subdomains
F:162-476/Domain: rod <ROD>
F:164-198/Region: coil 1A
F:199-210/Region: linker 1
F:211-311/Region: coil 1B
F:312-328/Region: linker 12
F:329-347/Region: coil 2A
F:348-355/Region: linker 2
F:414/Region: stutler
F:477-564/Domain: tail <END>
F:477-496/Region: H2 subdomain
F:497-564/Region: V2 and E2 subdomains

Query Match      80.9%; Score 38; DB 1; Length 564;
Best Local Similarity 80.0%; Pred. No. 6.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 AEAESLYQSK 10
      ||||| ||:|
Db      350 AEAESWYQTK 359

RESULT 10
KRHUEB
keratin 6b, type II - human
N:Alternate names: 56K type II keratin; keratin, cytoskeletal
C:Species: Homo sapiens (man)
C>Date: 04-Dec-1986 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: I61767; A02945
R:Takahashi, K.; Paladini, R.D.; Coulombe, P.A.
J. Biol. Chem. 270, 18581-18592, 1995
A:Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
A:Reference number: A57398; MUID:95355491; PMID:7543104
A:Accession: I61767
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-564 <RES>
A:Cross-references: UNIPROT:P04259; UNIPARC:UPI0000167B38; GB:L42584; NID:G908780; GB:L42
85; GB:L42590; NID:G908786; GB:L42591; NID:G908787; GB:L42592; NID:G908788; PIDN:AAC41768
R:Tyner, A.L.; Eichman, M.J.; Fuchs, E.
Proc. Natl. Acad. Sci. U.S.A. 82, 4683-4687, 1985
A:Title: The sequence of a type II keratin gene expressed in human skin: conservation of
A:Reference number: A02945; MUID:85270392; PMID:2410904
A:Accession: A02945
A:Molecule type: DNA
A:Residues: 2-88,'AG','91-115','PA',118,'LC',122-158,'IG',161-254,'V',256-564 <TYN>
A:Cross-references: UNIPARC:UPI0000173D58; GB:W11229; GB:L00205; NID:G186714; PIDN:AAAS94
A:Note: Initiator Met not shown
C:Comment: There are two types of cytoskeletal and microfibrillar keratin, I (acidic) and
bligate heteropolymers, composed of complexes formed by the aggregation of at least one I
C:Genetics:
A:Gene: GDB:KRT6B
A:Cross-references: GDB:128113; OMIM:148042
A:Map position: 12pter-12qter
A:Introns: 180/3; 252/2; 272/3; 304/3; 359/3; 401/3; 475/2; 487/1
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament
F:2-163/Domain: head <HED>
F:127-163/Region: E1 and V1 subdomains
F:162-476/Domain: rod <ROD>
F:164-198/Region: coil 1A
F:199-210/Region: linker 1
F:211-311/Region: coil 1B
F:312-328/Region: linker 12
F:329-347/Region: coil 2A
F:348-355/Region: linker 2
F:414/Region: stutler
F:477-564/Domain: tail <END>
F:477-496/Region: H2 subdomain
F:497-564/Region: V2 and E2 subdomains

Query Match      80.9%; Score 38; DB 1; Length 564;
Best Local Similarity 80.0%; Pred. No. 6.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 AEAESLYQSK 10
      ||||| ||:|
Db      350 AEAESWYQTK 359
```

RESULT 11

I61770
keratin 6e, type II - human
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: I61770
R/Takahashi, K.; Paladini, R.D.; Coulombe, P.A.
J. Biol. Chem. 270, 18581-18592, 1995
A>Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
A:Reference number: A57398; MUID:95355491; PMID:7543104
A:Accession: I61770
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-564 <RES>
A:Cross-references: UNIPROT:P48668; UNIPARC:UPI0000167E31; GB:L42611; NID:g908802; PIDN:
C:Genetics:
A:Gene: KRT6E
A>Note: this may not be a distinct gene
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil

Query Match 80.9%; Score 38; DB 2; Length 564;
Best Local Similarity 80.0%; Pred. No. 6.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AEASLYQSK 10
||||| |||
Db 350 AEASWYQTK 359

RESULT 12

I61768
keratin 6c, type II - human
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: I61768
R/Takahashi, K.; Paladini, R.D.; Coulombe, P.A.
J. Biol. Chem. 270, 18581-18592, 1995
A>Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
A:Reference number: A57398; MUID:95355491; PMID:7543104
A:Accession: I61768
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-564 <RES>
A:Cross-references: UNIPROT:P48666; UNIPARC:UPI0000167E00; GB:L42593; NID:g908791; GB:L4
96; GB:L42599; NID:g908797; GB:L42600; NID:g908798; GB:L42601; NID:g908799; PIDN:AAC4176
C:Genetics:
A:Gene: KRT6C
A:Introns: 180/3; 252/2; 272/3; 304/3; 359/3; 401/3; 475/2; 487/1
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil

Query Match 80.9%; Score 38; DB 2; Length 564;
Best Local Similarity 80.0%; Pred. No. 6.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AEASLYQSK 10
||||| |||
Db 350 AEASWYQTK 359

RESULT 13

I61771
keratin 6f, type II - human
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: I61771
R/Takahashi, K.; Paladini, R.D.; Coulombe, P.A.
J. Biol. Chem. 270, 18581-18592, 1995
A>Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
A:Reference number: A57398; MUID:95355491; PMID:7543104

A:Accession: I61771
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-564 <RES>
A:Cross-references: UNIPROT:P48669; UNIPARC:UPI000013CD50; GB:L42612; NID:g908804; PIDN:
C:Genetics:
A:Gene: KRT6F
A>Note: this may not be a distinct gene
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil

Query Match 80.9%; Score 38; DB 2; Length 564;
Best Local Similarity 80.0%; Pred. No. 6.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AEASLYQSK 10
||||| |||
Db 350 AEASWYQTK 359

RESULT 14

I53169
cytokeratin 2 - human
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I53169
R/Collin, C.; Ohayoun, J.
Differentiation 51, 137-148, 1992
A>Title: Suprabasal marker proteins distinguishing keratinizing squamous epithelia: Cyto
A:Reference number: I53169; MUID:93114504; PMID:1282112
A:Accession: I53169
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-638 <RES>
A:Cross-references: UNIPROT:Q01546; UNIPARC:UPI000012DB04; GB:M99063; NID:g181389; PIDN:
C:Superfamily: cytoskeletal keratin

Query Match 80.9%; Score 38; DB 2; Length 638;
Best Local Similarity 70.0%; Pred. No. 7.1;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEASLYQSK 10
:|||||:
Db 370 SEAEALYQTK 379

RESULT 15

I38025
keratin-like protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C:Accession: I38025; S60680
R/Tomasetto, C.; Regnier, C.H.; Moog-Lutz, C.; Mattei, M.G.; Chenard, M.P.; Lidereau, R.
Genomics 28, 367-376, 1995
A>Title: Identification of four novel human genes amplified and overexpressed in breast
A:Reference number: I37080; MUID:96039245; PMID:7490069
A:Accession: I38025
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-257 <RES>
A:Cross-references: UNIPROT:Q14533; UNIPARC:UPI000016AD67; EMBL:X80197; NID:g951271; PID

Query Match 78.7%; Score 37; DB 2; Length 257;
Best Local Similarity 80.0%; Pred. No. 4.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AEASLYQSK 10
||||| |||
Db 43 AEASWYRSK 52

Search completed: July 5, 2006, 19:20:30
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RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP PRELIMINARY NUCLEOTIDE SEQUENCE [MRNA] OF 151-643.
 RX MEDLINE=85207740; PubMed=2581964;
 RA Steinert P.M., Parry D.A.D., Idler W.W., Johnson L.D., Steven A.C.,
 RA Roop D.R.;
 RT "Amino acid sequences of mouse and human epidermal type II keratins of
 RT Mr 67,000 provide a systematic basis for the structural and functional
 RT diversity of the end domains of keratin intermediate filament
 RT subunits.";
 RL J. Biol. Chem. 260:7142-7149(1985).
 RN [6]
 RP PROTEIN SEQUENCE OF 1-7.
 RC TISSUE=Placenta;
 RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;
 RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
 RA Thomas G.R., Vandekerckhove J.;
 RT "Exploring proteomes and analyzing protein processing by mass
 RT spectrometric identification of sorted N-terminal peptides.";
 RL Nat. Biotechnol. 21:566-569(2003).
 RN [7]
 RP CITRULLINATION.
 RX MEDLINE=96374388; PubMed=8780679; DOI=10.1006/bbrc.1996.1240;
 RA Senshu T., Kan S., Ogawa H., Marabe M., Asaga H.;
 RT "Preferential deimination of keratin K1 and filaggrin during the
 RT terminal differentiation of human epidermis.";
 RL Biochem. Biophys. Res. Commun. 225:712-719(1996).
 RN [8]
 RP VARIANT EHK PRO-160.
 RX MEDLINE=92386601; PubMed=1381288; DOI=10.1016/0092-8674(92)90315-4;
 RA Chipev C.C., Korge B.P., Markova N., Bale S.J., Digiovanna J.J.,
 RA Compton J.G., Steinert P.M.;
 RT "A leucine-->proline mutation in the H1 subdomain of keratin 1 causes
 RT epidermolytic hyperkeratosis.";
 RL Cell 70:821-828(1992).
 RN [9]
 RP VARIANT ALLELE 1B 559-GLY--TYR-565 DEL.
 RX MEDLINE=93107743; PubMed=1281859; DOI=10.1111/1523-1747.ep12614149;
 RA Korge B.P., Compton J.G., Steinert P.M., Mischke D.;
 RT "The two size alleles of human keratin 1 are due to a deletion in the
 RT glycine-rich carboxyl-terminal V2 subdomain.";
 RL J. Invest. Dermatol. 99:697-702(1992).
 RN [10]
 RP VARIANT EHK GLN-489.
 RX MEDLINE=92376531; PubMed=1380725;
 RA Rothnagel J.A., Dominy A.M., Dempsey L.D., Longley M.A.,
 RA Greenhalgh D.A., Gagne T.A., Huber M., Frenk E., Hohl D., Roop D.R.;
 RT "Mutations in the rod domains of keratins 1 and 10 in epidermolytic
 RT hyperkeratosis.";
 RL Science 257:1128-1130(1992).
 RN [11]
 RP VARIANT EHK CYS-481.
 RX MEDLINE=94216497; PubMed=7512983;
 RA Syder A.J., Yu Q.-C., Paller A.S., Giudice G., Pearson R., Fuchs E.;
 RT "Genetic mutations in the K1 and K10 genes of patients with
 RT epidermolytic hyperkeratosis. Correlation between location and disease
 RT severity.";
 RL J. Clin. Invest. 93:1533-1542(1994).
 RN [12]
 RP VARIANTS EHK GLY-154; SER-187 AND PRO-192.
 RX MEDLINE=94117869; PubMed=7507151; DOI=10.1111/1523-1747.ep12371725;
 RA Yang J.-W., Chipev C.C., Digiovanna J.J., Bale S.J., Marekov L.N.,
 RA Steinert P.M., Compton J.G.;
 RT "Mutations in the H1 and 1A domains in the keratin 1 gene in
 RT epidermolytic hyperkeratosis.";
 RL J. Invest. Dermatol. 102:17-23(1994).
 RN [13]
 RP VARIANTS EHK PRO-185 AND SER-187.
 RX MEDLINE=94117870; PubMed=7507152; DOI=10.1111/1523-1747.ep12371726;
 RA McLean W.H.I., Eady R.A.J., Dopping-Hepenstal P.J.C., McMillan J.R.,
 RA Leigh I.M., Navsaria H.A., Higgins C., Harper J.I., Paige D.G.,

RA Morley S.M.;
 RT "Mutations in the rod 1A domain of keratins 1 and 10 in bullous
 RT congenital ichthyosiform erythroderma (BCIE).";
 RL J. Invest. Dermatol. 102:24-30(1994).
 RN [14]
 RP VARIANT NEPK ILE-73.
 RX MEDLINE=95096501; PubMed=7528239; DOI=10.1111/1523-1747.ep12412771;
 RA Kimonis V., Digiovanna J.J., Yang J.-M., Doyle S.Z., Bale S.J.,
 RA Compton J.G.;
 RT "A mutation in the VI end domain of keratin 1 in non-epidermolytic
 RT palmar-plantar keratoderma.";
 RL J. Invest. Dermatol. 103:764-769(1994).
 RN [15]
 RP VARIANT EHK VAL-339.
 RX MEDLINE=99072666; PubMed=9856846;
 RX DOI=10.1046/j.1523-1747.1998.00389.x;
 RA Kremer H., Lavrijsen A.P., McLean W.H.I., Lane E.B., Melchers D.,
 RA Ruiters D.J., Mariman E.C., Steijlen P.M.;
 RT "An atypical form of bullous congenital ichthyosiform erythroderma is
 RT caused by a mutation in the L12 linker region of keratin 1.";
 RL J. Invest. Dermatol. 111:1224-1226(1998).
 RN [16]
 RP VARIANTS AEI PHE-478 AND THR-478.
 RX MEDLINE=99162195; PubMed=10053007;
 RA Sybert V.P., Francis J.S., Corden L.D., Smith L.T., Weaver M.,
 RA Stephens K., McLean W.H.I.;
 RT "Cyclic ichthyosis with epidermolytic hyperkeratosis: a phenotype
 RT conferred by mutations in the 2B domain of keratin K1.";
 RL Am. J. Hum. Genet. 64:732-738(1999).
 RN [17]
 RP VARIANT EHK THR-187.
 RX MEDLINE=99247363; PubMed=10232403;
 RA Arin M.J., Longley M.A., Kuster W., Huber M., Hohl D., Rothnagel J.A.,
 RA Roop D.R.;
 RT "An asparagine to threonine substitution in the 1A domain of keratin
 RT 1: a novel mutation that causes epidermolytic hyperkeratosis.";
 RL Exp. Dermatol. 8:124-127(1999).
 RN [18]
 RP VARIANT AEI PHE-478.
 RX MEDLINE=20062276; PubMed=10597140;
 RA Michael E.J., Schneiderman P., Grossman M.E., Cristiano A.M.;
 RT "Epidermolytic hyperkeratosis with polycyclic psoriasiform plaques
 RT resulting from a mutation in the keratin 1 gene.";
 RL Exp. Dermatol. 8:501-503(1999).
 RN [19]
 RP VARIANT EHK PRO-213.
 RX MEDLINE=20305470; PubMed=10844506;
 RX DOI=10.1046/j.1365-2230.2000.00625.x;
 RA Cserhalni-Friedman P.B., Squeo R., Gordon D., Garzon M.,
 RA Schneiderman P., Grossman M.E., Cristiano A.M.;
 RT "Epidermolytic hyperkeratosis in a Hispanic family resulting from a
 RT mutation in the keratin 1 gene.";
 RL Clin. Exp. Dermatol. 25:241-243(2000).
 RN [20]
 RP VARIANT EHK THR-478.
 RX MEDLINE=20151078; PubMed=10688370;
 RX DOI=10.1034/j.1600-0625.2000.009001016.x;
 RA Arin M.J., Longley M.A., Epstein E.H. Jr., Rothnagel J.A., Roop D.R.;
 RT "Identification of a novel mutation in keratin 1 in a family with
 RT epidermolytic hyperkeratosis.";
 RL Exp. Dermatol. 9:16-19(2000).
 RN [21]
 RP VARIANT EHK ASP-154.
 RX MEDLINE=21423058; PubMed=11531804;
 RX DOI=10.1046/j.1365-2133.2001.04327.x;
 RA Whittock N.V., Ashton G.H.S., Griffiths W.A.D., Eady R.A.J.,
 RA McGrath J.A.;
 RT "New mutations in keratin 1 that cause bullous congenital
 RT ichthyosiform erythroderma and keratin 2e that cause ichthyosis
 RT bullosa of Siemens.";
 RL Br. J. Dermatol. 145:330-335(2001).
 RN [22]
 RP INVOLVEMENT IN IHCW.

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RX MEDLINE=21184521; PubMed=11286616;
RX DOI=10.1046/j.1523-1747.2001.01292.x;

Query Match      100.0%; Score 47; DB 1; Length 643;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAEESLYQSK 10
Db 366 AEAEESLYQSK 375

RESULT 2
Q4R3D5_MACFA
ID Q4R3D5_MACFA PRELIMINARY; PRT; 147 AA.
AC Q4R3D5;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Testis cDNA clone: Q4R3D5-17726, similar to human keratin protein K6irs
DE (K6IRS2).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15944441; DOI=10.1093/molbev/msi187;
RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen C.-K.J., Wu C.I., Hashimoto K.;
RT "Substitution Rate and Structural Divergence of 5'UTR Evolution:
RT Comparative Analysis Between Human and Cynomolgus Monkey cDNAs.";
RL Mol. Biol. Evol. 22:1976-1982(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG International consortium for macaque cDNA sequencing and analysis;
RT "DNA sequences of macaque genes expressed in brain or testis and its
RT evolutionary implications.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AB179331; BAE02382.1; -; mRNA.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893.SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
KW Keratin.
SQ SEQUENCE 147 AA; 16859 MW; 9680F74B1FE850F2 CRC64;

Query Match      87.2%; Score 41; DB 2; Length 147;
Best Local Similarity 80.0%; Pred. No. 3.2;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAEESLYQSK 10
Db 109 AEAEESLYQSK 118

RESULT 3
Q80VP7_MOUSE
ID Q80VP7_MOUSE PRELIMINARY; PRT; 324 AA.
AC Q80VP7;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Hypothetical protein MGC54654.
GN Name=MGC54654;
OS Mus musculus (Mouse).

RX MEDLINE=21184521; PubMed=11286616;
RX DOI=10.1046/j.1523-1747.2001.01292.x;

Query Match      100.0%; Score 47; DB 1; Length 643;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAEESLYQSK 10
Db 366 AEAEESLYQSK 375

RESULT 2
Q4R3D5_MACFA
ID Q4R3D5_MACFA PRELIMINARY; PRT; 147 AA.
AC Q4R3D5;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Testis cDNA clone: Q4R3D5-17726, similar to human keratin protein K6irs
DE (K6IRS2).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15944441; DOI=10.1093/molbev/msi187;
RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen C.-K.J., Wu C.I., Hashimoto K.;
RT "Substitution Rate and Structural Divergence of 5'UTR Evolution:
RT Comparative Analysis Between Human and Cynomolgus Monkey cDNAs.";
RL Mol. Biol. Evol. 22:1976-1982(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG International consortium for macaque cDNA sequencing and analysis;
RT "DNA sequences of macaque genes expressed in brain or testis and its
RT evolutionary implications.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AB179331; BAE02382.1; -; mRNA.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893.SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
KW Keratin.
SQ SEQUENCE 147 AA; 16859 MW; 9680F74B1FE850F2 CRC64;

Query Match      87.2%; Score 41; DB 2; Length 147;
Best Local Similarity 80.0%; Pred. No. 3.2;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAEESLYQSK 10
Db 109 AEAEESLYQSK 118

RESULT 3
Q80VP7_MOUSE
ID Q80VP7_MOUSE PRELIMINARY; PRT; 324 AA.
AC Q80VP7;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Hypothetical protein MGC54654.
GN Name=MGC54654;
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RG NIH MGC Project;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC046626; AAH46626.1; -; mRNA.
DR HSSP; P08670; IGK.
DR Ensembl; ENSMUSG00000046162; Mus musculus.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893.SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
KW Hypothetical protein.
SQ SEQUENCE 324 AA; 35165 MW; 0E4D7E25144435DD CRC64;

Query Match      87.2%; Score 41; DB 2; Length 324;
Best Local Similarity 80.0%; Pred. No. 7.7;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAEESLYQSK 10
Db 300 AEAEESLYQSK 309

RESULT 4
Q32MB2_HUMAN
ID Q32MB2_HUMAN PRELIMINARY; PRT; 381 AA.
AC Q32MB2;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE K6IR3 protein.
GN Name=K6IR3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
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RP TISSUE=PCR rescued clones;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Toshiyuki S., Carinci P., Prange C.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Rutterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RG NIH MGC Project;
 RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
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 CC
 CC
 DR EMBL; BC109213; AA109214.1; -; mRNA.
 DR EMBL; BC109212; AA109213.1; -; mRNA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 SQ SEQUENCE 381 AA; 42010 MW; 9049439791F7B1A8 CRC64;
 Query Match 87.2%; Score 41; DB 2; Length 381;
 Best Local Similarity 80.0%; Pred. No. 9.2;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEAEALYQSK 10
 DB 319 AEAEALYQTK 328
 RESULT 5
 Q8NA87 HUMAN
 ID Q8NA87_HUMAN PRELIMINARY; PRT; 398 AA.
 AC Q8NA87
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2002, sequence version 1.
 DT CDNA FLJ35741 fis, clone TEST12004163, moderately similar to Mus
 DE musculus type II cytochrome.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Testis;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohyashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,

RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Moniyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45 (2004).
 CC -!- SIMILARITY: Belongs to the intermediate filament family.
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 CC
 CC
 DR EMBL; AK093060; BAC04039.1; -; mRNA.
 DR HSSP; P08670; 1GK7.
 DR GO; GO:0005001; C:intermediate filament; IEA.
 DR GO; GO:0005198; P:structural molecule activity; IEA.
 DR InterPro; IPR001664; IF.
 DR InterPro; IPR003054; Keratin-II.
 DR PANTHER; PTHR18993:SF5; Keratin-II; 1.
 DR Pfam; PF00038; Filament; 1.
 DR PRINTS; PR01276; TYPE2KERATIN.
 DR PROSITE; PS00226; IF; 1.
 KW Intermediate filament.
 SQ SEQUENCE 398 AA; 44698 MW; D5DD16028B8EBA3D CRC64;
 Query Match 87.2%; Score 41; DB 2; Length 398;
 Best Local Similarity 80.0%; Pred. No. 9.6;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEAEALYQSK 10
 DB 199 AEAEALYQTK 208
 RESULT 6
 Q5HYM7 HUMAN
 ID Q5HYM7_HUMAN PRELIMINARY; PRT; 410 AA.
 AC Q5HYM7
 DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
 DT 15-FEB-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Hypothetical protein DKFZp686B15196.
 GN Name=DKFZp686B15196;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Esophagus tumor;
 RG The German cDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the intermediate filament family.
 CC


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DR EMBL; BX647095; CAI46001.1; -; mRNA.
DR Ensembl; ENSG00000170423; Homo sapiens.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893.SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Hypothetical protein; Intermediate filament.
SQ SEQUENCE 410 AA; 44990 MW; 116584182471A250 CRC64;

Query Match 87.2%; Score 41; DB 2; Length 410;
Best Local Similarity 80.0%; Pred. No. 9.9; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 2;

Qy 1 AEASLYQSK 10
Db 188 AEALYQTK 197
|||||:|:|

RESULT 7
K2CO CHICK
ID K2CO CHICK STANDARD; PRT; 492 AA.
AC 093532;
DT 19-SEP-2003, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1998, sequence version 1.
DT 07-FEB-2006, entry version 30.
DE Keratin, type II cytoskeletal cochlear (Cytokeratin otokeratin).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], TISSUE SPECIFICITY, AND DEVELOPMENTAL
STAGE.
RC STRAIN=White leghorn; TISSUE=Basilar papilla;
RX MEDLINE=98409669; PubMed=9736748; DOI=10.1073/pnas.95.19.11400;
RA Heller S., Sheane C.A., Javed Z., Hudspeth A.J.;
RT "Molecular markers for cell types of the inner ear and candidate genes
for hearing disorders.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:11400-11405 (1998).
CC -!- SUBUNIT: Heterotrimer of two type I and two type II keratins (By
similarity).
CC -!- TISSUE SPECIFICITY: Abundant in the cochlea of the inner ear,
where it is found in the cells of the tegmentum vasculosum. Lower
levels also found in the heart and forebrain.
CC -!- DEVELOPMENTAL STAGE: Specifically expressed at the late
developmental stages in the cochlea.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
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-----
DR EMBL; AF072698; AAC64042.1; -; mRNA.
DR HSPSP; P08670; 1GK7.
DR Ensembl; ENSGALG0000010250; Gallus gallus.
DR InterPro; IPR001664; IF.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893.SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Coiled coil; Intermediate filament; Keratin.
FT CHAIN 1 492 Keratin, type II cytoskeletal cochlear.
/FTid=PRO_0000063746.
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FT REGION 1 113 Head.
FT REGION 114 421 Rod.
FT REGION 114 149 Coiled 1A.
FT REGION 150 166 Linker 1.
FT REGION 167 259 Coiled 1B.
FT REGION 260 282 Linker 12.
FT REGION 283 421 Coiled 2.
FT REGION 422 492 Tail.
SQ SEQUENCE 492 AA; 53803 MW; A01A66426B9F3941 CRC64;

Query Match 87.2%; Score 41; DB 1; Length 492;
Best Local Similarity 90.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AEASLYQSK 10
Db 299 AEASLYQSK 308
|||||:|:|

RESULT 8
Q8WVZO HUMAN
ID Q8WVZO HUMAN PRELIMINARY; PRT; 510 AA.
AC Q8WVZO;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Keratin protein K6lrs.
GN Name=KRT6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Porter R.M., McLean W.H.I.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
-----
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DR EMBL; AY033495; AAK55108.1; -; mRNA.
DR HSPSP; P08670; 1GK7.
DR Ensembl; ENSG00000170486; Homo sapiens.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893.SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
SQ SEQUENCE 510 AA; 55749 MW; 93AAAF9D75378EE7 CRC64;

Query Match 87.2%; Score 41; DB 2; Length 510;
Best Local Similarity 80.0%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEASLYQSK 10
Db 312 AEATLYQTK 321
|||||:|:|

RESULT 9
Q8WVY9 HUMAN
ID Q8WVY9 HUMAN PRELIMINARY; PRT; 511 AA.
AC Q8WVY9;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Keratin protein K6lrs.
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GN Name=KRT6;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Porter R.M., McLean W.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA McLean W.H.1.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
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CC
DR EMBL; AY033496; AAK55109.1; -; Genomic_DNA.
DR HSSP; P08670; 1GK7.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
SQ SEQUENCE 511 AA; 55877 MW; 61E930C382063731 CRC64;

Query Match 87.2%; Score 41; DB 2; Length 511;
Best Local Similarity 80.0%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 AEAESLYQSK 10
Db |||||:||||: 321

RESULT 10
ID Q8N1N4 HUMAN PRELIMINARY; PRT; 520 AA.
AC Q8N1N4;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-MAR-2006, entry version 20.
DE CDNA FLJ39100 fis, clone NTONG2001587, moderately similar to KERATIN,
DE TYPE II CYTOSKELETAL 4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=tongue;
RX PubMed=14702039; DOI=10.1038/ngi1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosiiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuma N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoa K., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hoshino T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
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RA Musahino K., Yuuki H., Oshima A., Sasaki N., Aoteuka S.,
RA Yoshikawa Y., Matsuura H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsuura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs."
RL Nat. Genet. 36:40-45(2004).
CC -!- SIMILARITY: Belongs to the intermediate filament family.
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CC
DR EMBL; AK096419; BAC04782.1; -; mRNA.
DR HSSP; P08670; 1GK7.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR011598; HLH_DNA_bd.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin I.
DR InterPro; IPR003054; Keratin II.
DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament.
SQ SEQUENCE 520 AA; 56820 MW; 1B3C01F3F9DC9158 CRC64;

Query Match 87.2%; Score 41; DB 2; Length 520;
Best Local Similarity 80.0%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 AEAESLYQSK 10
Db |||||:||||: 307

RESULT 11
ID Q7RTT2 HUMAN PRELIMINARY; PRT; 521 AA.
AC Q7RTT2;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-MAR-2006, entry version 13.
DE Keratin 5b.
GN Name=K5B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21539571; PubMed=11683385;
RA Hesse M., Magin T.M., Weber K.;
RT "Genes for intermediate filament proteins and the draft sequence of
RT the human genome: novel keratin genes and a surprisingly high number
RT of pseudogenes related to keratin genes 8 and 18."
RL J. Cell Sci. 114:2569-2575(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
```

```

RA Hesse M., Magin T.M., Weber K.;
RL Submitted (Oct-2002) to the EMBL/GenBank/DBJ databases.
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
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CC -----
DR EMBL; BK000646; DAA00377.1; -; Genomic_DNA.
DR HSP; P08670; 1GK7.
DR Ensemble; ENSG00000170423; Homo sapiens.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
SQ SEQUENCE 521 AA; 56965 MW; 94A0C125C9077F08 CRC64;

Query Match 87.2%; Score 41; DB 2; Length 521;
Best Local Similarity 80.0%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEAEALYQSK 10
Db 298 AEAEALYQTK 307
|||||:|:|:|

RESULT 12
ID Q3SY84 HUMAN PRELIMINARY; PRT; 523 AA.
AC Q3SY84;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Keratin 6 IRS.
GN Name=KRT6IRS;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----

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RG NIH MGC Project;
RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
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CC -----
DR EMBL; BC103918; AA103919.1; -; mRNA.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR003054; Keratin_II.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
SQ SEQUENCE 523 AA; 57221 MW; 7861868BFF46D16 CRC64;

Query Match 87.2%; Score 41; DB 2; Length 523;
Best Local Similarity 80.0%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEAEALYQSK 10
Db 317 AEAEALYQTK 326
|||||:|:|:|

RESULT 13
ID Q3SY85 HUMAN PRELIMINARY; PRT; 523 AA.
AC Q3SY85;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Keratin 6 IRS.
GN Name=KRT6IRS;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----

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CC -----
DR EMBL; BG103917; AAI03918.1; -; mRNA.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR003054; Keratin_II.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
SQ SEQUENCE 523 AA; 57249 MW; 797F5644FF3A73C6 CRC64;

Query Match 87.2%; Score 41; DB 2; Length 523;
Best Local Similarity 80.0%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAEALYQSK 10
Db 317 AEAEALYQTK 326

RESULT 14
Q96DU2 HUMAN PRELIMINARY; PRT; 523 AA.
AC Q96DU2
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Keratin 6 IRS.
GN Names=KRT6IRS;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Scalp;
RA Rogers M.A., Langbein L., Winter H., Praetzel S., Ehmann C.,
RA Schweizer J.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----
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CC -----
DR EMBL; AJ308599; CAC43429.1; -; mRNA.
DR HSSP; P08670; 1GK7.
DR Ensembl; ENSG00000139648; Homo sapiens.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR18893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
SQ SEQUENCE 523 AA; 57292 MW; 797F5655EE3A62D7 CRC64;

Query Match 87.2%; Score 41; DB 2; Length 523;
Best Local Similarity 80.0%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAEALYQSK 10
Db 317 AEAEALYQTK 326

RESULT 15
Q5RCY8_PONPY
Q5RCY8_PONPY PRELIMINARY; PRT; 523 AA.
```

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AC Q5RCY8;
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 21-DEC-2004, sequence version 1.
DE 07-FEB-2006, entry version 7.
DE Hypothetical protein DKFZp468M2112.
GN Name=DKFZp468M2112;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RG The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----
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CC -----
DR EMBL; CR858130; CAH90369.1; -; mRNA.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR18893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Hypothetical protein; Intermediate filament.
SQ SEQUENCE 523 AA; 57249 MW; 797F5644FF3A73C6 CRC64;

Query Match 87.2%; Score 41; DB 2; Length 523;
Best Local Similarity 80.0%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAEALYQSK 10
Db 317 AEAEALYQTK 326

Search completed: July 5, 2006, 19:01:32
Job time : 102.43 secs
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OM protein - protein search, using sw model

Run on: July 5, 2006, 18:28:26 ; Search time 86.8932 Seconds
(without alignments)
52.618 Million cell updates/sec

Title: US-10-774-928A-7

Perfect score: 47

Sequence: 1 AEAESLYQSK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	10	6	AAO26387 Psoriasis
2	47	100.0	10	9	ADV04412 Leishmani
3	47	100.0	12	8	AD119066 Rat pepti
4	47	100.0	644	8	ADQ17549 Human sof
5	47	100.0	644	9	AEA15501 Human pol
6	41	87.2	55	4	ABB42646 Peptide #
7	41	87.2	55	4	AAM36459 Peptide #
8	41	87.2	55	4	ABB25991 Protein #
9	41	87.2	55	4	AAM76351 Human bon
10	41	87.2	55	4	AAM63536 Human bra
11	41	87.2	55	4	ABG58058 Human liv
12	41	87.2	55	5	ABG45643 Human pep
13	41	87.2	314	7	AD136103 Human NOV
14	41	87.2	327	7	ADJ69669 Human hea
15	41	87.2	336	7	ADJ70556 Human hea
16	41	87.2	398	7	ADB65234 Human pro
17	41	87.2	420	8	ADP29879 Human sec
18	41	87.2	508	8	ADS10914 Human the
19	41	87.2	511	5	ABG94648 Human NOV
20	41	87.2	511	7	ADL36000 Human NOV
21	41	87.2	511	9	AEA15498 Human pol
22	41	87.2	520	7	ADB75609 Prostate
23	41	87.2	520	7	ADC31845 Human nov

ALIGNMENTS

RESULT 1
AAO26387
ID AAO26387 standard; peptide; 10 AA.
XX
AC AAO26387;
XX
DT 30-JAN-2003 (first entry)
XX
DE Psoriasis treating immunotherapeutic peptide, SEQ ID No 7.
XX
KW Antipsoriatic; immunostimulant; gene therapy; pharmaceutical composition;
KW vaccine; immunogenic variant; immunotherapeutic agent; psoriasis;
KW gene therapy.
XX
OS Leishmania sp.
XX
PN W0200274239-A2.
XX
PD 26-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006496.
XX
PR 16-MAR-2001; 2001US-00809003.
XX
PA (AKIV-) AKIVA LLC.
XX
PI O'daly JA;
XX
DR WPI; 2003-018763/01.
XX
PT New polypeptide and immunogenic variants comprising amino acid sequences
PT of particulate antigens, useful for the treatment and clinical remission
PT of psoriasis.
XX
PS Claim 1; Page 43; 56pp; English.
XX
CC The invention relates to a polypeptide comprising an isolated amino acid
CC sequence or immunogenic variants selected from any of 14 fully defined
CC sequences of 7-16 amino acids, given in the specification. The
CC immunotherapeutic agents and a pharmaceutical compositions comprising
CC polynucleotides and vectors of the invention are useful for the treatment
CC and clinical remission of psoriasis. The isolated nucleic acids are
CC useful as probes. The sequences of the invention can be used in the
CC treatment of disorders by gene therapy. This sequence represents one of
CC the 14 immunotherapeutic peptides of the invention
XX

Adm05027 Human pro
Aec87957 Human GDN
Abg94649 Human NOV
Abb78802 Human NOV
Adl36002 Human NOV
Aae32116 Human cyt
Aea15496 Human cyt
Aae15496 Human DIT
Abg60120 Human pol
Abj04655 Protein o
Abb83482 Human cyt
Aea15497 Human pol
Aad43881 57kd kera
Adf09537 Human ker
Aea15503 Human pol
Abj04646 Protein o
Aea15499 Human pol
Abb78799 Human NOV
Aea20229 Novel hum
Abg94647 Human NOV
Adl35998 Human NOV
Ada54878 Human pro
Aea15502 Human pol

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SQ Sequence 10 AA;
Query Match 100.0%; Score 47; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEASLYQSK 10
   |||||
Db 1 AEASLYQSK 10

RESULT 2
ADV04412
ID ADV04412 standard; peptide; 10 AA.
XX
AC ADV04412;
XX
DT 24-FEB-2005 (first entry)
XX
DE Leishmania immunotherapeutic peptide SEQ ID NO: 7.
XX
KW T-lymphocyte; immunogenicity; antigen; antipsoriatic; immunostimulant;
KW psoriasis.
XX
OS Leishmania sp.
XX
PN US2004241168-A1.
XX
PD 02-DEC-2004.
XX
PF 09-FEB-2004; 2004US-00774928.
XX
PR 16-MAR-2001; 2001US-00809003.
PR 17-OCT-2003; 2003US-00687892.
XX
PA (ODAL/) ODALY J A.
PI Odaly JA;
XX
DR WPI; 2005-011563/01.
XX
PT Inhibiting selectively T-cell rolling in human, by administering compound
PT interfering with cutaneous lymphocyte antigen-E selectin interaction and
PT leukocyte function associated antigen-1 interaction.
XX
PS Claim 18; SEQ ID NO 7; 21pp; English.
XX
CC The invention relates to a novel method for selectively inhibiting T-cell
CC rolling in a human host, comprising administering a compound that
CC selectively interferes with the cutaneous lymphocyte antigen (CLA)-E
CC selectin interaction and leukocyte function associated antigen (LFA)-
CC 1/intercellular adhesion molecule (ICAM) and very late antigen
CC (VLA)/vascular cell adhesion molecule (VCAM) interactions. The compound
CC includes an immunotherapeutic agent, which comprises a purified protein
CC extract that is isolated by diethylaminoethyl Sephadex chromatography of
CC a Nonidet P-40 insoluble particulate antigen fraction derived from
CC isolated killed cells of amastigotes from one or more species of the
CC Leishmania genus, where the particulate antigen fraction is solubilized
CC with 8M urea and 0.025 M Tris(hydroxymethyl)aminomethane pH 8.3 applied
CC to diethylaminoethyl Sephadex and is eluted with a solution comprising
CC 0.1 M sodium chloride, 8 M urea and 0.025 M
CC Tris(hydroxymethyl)aminomethane pH 8.3, and the purified protein extract
CC includes polypeptides having apparent molecular weights of 73, 80 and 82
CC kDa, after total reduction and alkylation. The species is L. amazonensis,
CC L. venezuelensis, L. brasiliensis and/or L. chagasi. A compound of the
CC invention has antipsoriatic and immunostimulant activity, and inhibits T-
CC cell rolling by interfering with CLA-E selectin interaction and LFA-
CC 1/ICAM and VLA/VCAM interactions. The method is useful for selectively
CC inhibiting T-cell rolling in a human host, and for treating psoriasis.
CC The present sequence represents a Leishmania peptide used in the
CC invention.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 47; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEASLYQSK 10
   |||||
Db 1 AEASLYQSK 10

RESULT 3
ADI19066
ID ADI19066 standard; peptide; 12 AA.
XX
AC ADI19066;
XX
DT 15-APR-2004 (first entry)
XX
DE Rat peptide #1 used in the exemplification of the invention.
XX
KW Detrusor estrogen-regulated protein; DERP; DERP-related disorder;
KW impaired detrusor contractility; urinary retention; Alzheimer's disease;
KW cardiovascular disease; osteoporosis; smooth muscle function; neurotropic;
KW neuroprotective; osteopathic; immunostimulant; therapy; rat.
XX
OS Rattus norvegicus.
XX
PN US2003232374-A1.
XX
PD 18-DEC-2003.
XX
PF 22-MAY-2003; 2003US-00444575.
PR 23-MAY-2002; 2002US-0382830P.
XX
PA (KUCH/) KUCHEL G A.
PI Kuchel GA, Zhu Q;
XX
DR WPI; 2004-052160/05.
XX
PT Novel purified immunogenic detrusor estrogen-regulated polypeptide
PT fragment useful for generating antibodies and as screening reagents.
XX
PS Example 11; SEQ ID NO 16; 48pp; English.
XX
CC The present invention relates to a immunogenic polypeptide fragment
CC comprising ten to fifty consecutive amino acids of a fully defined
CC detrusor estrogen-regulated protein (DERP). The invention is useful for
CC diagnosing DERP-related disorder such as impaired detrusor contractility,
CC urinary retention, Alzheimer's disease, cardiovascular disease,
CC osteoporosis, or their combinations. The invention is also useful for
CC generating antibodies, as reagents in diagnostic assays, as identifiers
CC of other gene products involved in the regulation of bladder and smooth
CC muscle function, as screening reagents useful for detecting compounds
CC that are used in the regulation of bladder and smooth muscle function,
CC and as pharmaceutical agents useful for treating symptoms relating to
CC bladder and smooth muscle function. The present sequence is rat peptide
CC used in the exemplification of the invention.
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 47; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEASLYQSK 10
   |||||
Db 3 AEASLYQSK 12

RESULT 4
Sequence 10 AA;
```

```
ADQ17549
ID ADQ17549 standard; protein; 644 AA.
XX
AC ADQ17549;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 366.
XX
KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX
OS Homo sapiens.
XX
PN WO2004048938-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US038193.
XX
PR 26-NOV-2002; 2002US-0429739P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Aziz N, Ginsburg WM, Zlotnik A;
XX
DR WPI; 2004-441208/41.
XX
PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
PS Example 2; SEQ ID NO 366; 210pp; English.
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 644 AA;

Query Match 100.0%; Score 47; DB 8; Length 644;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAEESLYQSK 10
DB 367 AEAEESLYQSK 376

RESULT 5
AEAL5501
ID AEAL5501 standard; protein; 644 AA.
XX
AC AEAL5501;
XX
DT 28-JUL-2005 (first entry)
XX
DE Human polypeptide #120.
XX
KW Diagnosis; prognosis; cancer; breast tumor; ovary tumor; stomach tumor;
KW colon tumor; esophagus tumor; bladder tumor; non-small-cell lung cancer;
KW cytostatic; neoplasm.
XX

OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX

Query Match 100.0%; Score 47; DB 9; Length 644;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAEESLYQSK 10
DB 367 AEAEESLYQSK 376

RESULT 6
ABB42646
ID ABB42646 standard; peptide; 55 AA.
XX
AC ABB42646;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #10152 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX

Claim 7; SEQ ID NO 463; 464pp; English.

The invention relates to a method of predicting response to cancer
treatment comprising detection of at least 2 markers, where the markers
are genes and fragments or genomic nucleic acid sequences that are
located on one chromosomal region, which is altered in malignant
neoplasia. The invention also relates to a method for the prediction,
diagnosis or prognosis of malignant neoplasia, methods for detecting,
deregulations in malignant neoplasia and breast cancer, a method of
determining the phenotype of a cell or tissue, a method for identifying
genomic regions which are altered on the chromosomal level and encode
genes that are linked by function and are differentially expressed in
malignant neoplasia and breast cancer, methods of screening for agents
which regulate the activity of a polypeptide or a polynucleotide and
antibodies that specifically bind to a full length or partial
polypeptide. The method is useful for predicting response to cancer
treatment. The methods and compositions are useful for predicting,
diagnosing, prognosing, preventing or treating malignant neoplasia
including breast cancer, ovarian cancer, gastric cancer, colon cancer,
esophageal cancer, mesenchymal cancer, bladder cancer or non-small-cell
lung cancer. This sequence represents a human polypeptide used in the
scope of the invention.

Sequence 644 AA;

Query Match 100.0%; Score 47; DB 9; Length 644;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAEESLYQSK 10
DB 367 AEAEESLYQSK 376

RESULT 6
ABB42646
ID ABB42646 standard; peptide; 55 AA.
XX
AC ABB42646;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #10152 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
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XX 30-JAN-2001; 2001WO-US0000669.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human fetal liver.
XX
XX Claim 27; SEQ ID NO 35281; 639pp + Sequence Listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for measuring
XX human gene expression in a sample derived from human foetal liver. The
XX single exon nucleic acid probes may be used for predicting, measuring and
XX displaying gene expression in samples derived from human fetal liver. The
XX present sequence is a peptide encoded by a single exon nucleic acid probe
XX of the invention. Note: The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 55 AA;
XX
XX Query Match 87.2%; Score 41; DB 4; Length 55;
XX Best Local Similarity 80.0%; Pred. No. 2.5;
XX Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AEAESLYQSK 10
XX Db 46 AEAELYQTK 55
XX
XX RESULT 7
XX ID AAM36459 standard; protein; 55 AA.
XX
XX AC AAM36459;
XX
XX DT 17-OCT-2001 (first entry)
XX
XX DE Peptide #10496 encoded by probe for measuring placental gene expression.
XX
XX KW Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder.
XX
XX OS Homo sapiens.
XX
XX PN WO200157272-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 30-JAN-2001; 2001WO-US0000663.
XX
XX PR 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX PA
XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts.
XX
XX Claim 15; SEQ ID NO 27761; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart (see
XX ABA21535-ABA41305). The present sequence is a protein encoded by one such
XX probe. The probes may be used for predicting, measuring and displaying
XX gene expression in samples derived from the human heart via microarrays.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human placenta.
XX
XX Claim 27; SEQ ID NO 36728; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP:
XX see AA131315-AA157546). The present sequence is a peptide encoded by one
XX such probe. The probes are useful for producing a microarray for
XX predicting, measuring and displaying gene expression in samples derived
XX from human placenta. The probes are useful for antenatal diagnosis of
XX human genetic disorders
XX
XX Sequence 55 AA;
XX
XX Query Match 87.2%; Score 41; DB 4; Length 55;
XX Best Local Similarity 80.0%; Pred. No. 2.5;
XX Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AEAESLYQSK 10
XX Db 46 AEAELYQTK 55
XX
XX RESULT 8
XX ID ABB25991 standard; protein; 55 AA.
XX
XX AC ABB25991;
XX
XX DT 23-JAN-2002 (first entry)
XX
XX DE Protein #7990 encoded by probe for measuring heart cell gene expression.
XX
XX KW Human; gene expression; heart; microarray; vascular system;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease.
XX
XX OS Homo sapiens.
XX
XX PN WO200157274-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 30-JAN-2001; 2001WO-US0000666.
XX
XX PR 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX PA
XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts.
XX
XX Claim 15; SEQ ID NO 27761; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart (see
XX ABA21535-ABA41305). The present sequence is a protein encoded by one such
XX probe. The probes may be used for predicting, measuring and displaying
XX gene expression in samples derived from the human heart via microarrays.
XX

```


CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 55 AA;

Query Match 87.2%; Score 41; DB 4; Length 55;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLYQSK 10
DB 46 AEAELYQTK 55
||||:||||:

RESULT 9
AMW76351
ID AAMW76351 standard; protein; 55 AA.

XX AC AAMW76351;

XX DT 06-NOV-2001 (first entry)

XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 36657.

XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma.

XX OS Homo sapiens.

XX PN WO200157276-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000668.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human bone marrow.

XX PS Example 4; SEQ ID NO 36657; 658pp + Sequence Listing; English.

XX CC The present invention provides a number of single exon nucleic acid

XX CC probes which are derived from genomic sequences expressed in the human

XX CC bone marrow. They can be used to measure gene expression in bone marrow

XX CC samples, which may enable the improved diagnosis and treatment of cancers

XX CC such as lymphoma, leukaemia and myeloma. The present sequence is a

XX CC protein encoded by one of the probes of the invention

XX SQ Sequence 55 AA;

Query Match 87.2%; Score 41; DB 4; Length 55;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLYQSK 10

DB 46 AEAELYQTK 55
||||:||||:

RESULT 10

AAM63536
ID AAM63536 standard; protein; 55 AA.

XX AC AAM63536;

XX DT 05-NOV-2001 (first entry)

XX DE Human brain expressed single exon probe encoded protein SEQ ID NO: 35641.

XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;

XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

XX OS Homo sapiens.

XX PN WO200157275-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000667.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483446/52.

XX PT Single exon nucleic acid probes for analyzing gene expression in human

XX PT brains.

XX PS Example 4; SEQ ID NO 35641; 650pp + Sequence Listing; English.

XX CC The present invention provides a number of single exon nucleic acid

XX CC probes which are derived from genomic sequences expressed in the human

XX CC brain. They can be used to measure gene expression in brain cell samples,

XX CC which may enable the diagnosis and improved treatment of nervous system

XX CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

XX CC epilepsy and cancers. The present sequence is a protein encoded by one of

XX CC the probes of the invention

XX SQ Sequence 55 AA;

Query Match 87.2%; Score 41; DB 4; Length 55;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLYQSK 10
DB 46 AEAELYQTK 55
||||:||||:

RESULT 11

ABG58058
ID ABG58058 standard; peptide; 55 AA.

XX AC ABG58058;

XX DT 25-FEB-2003 (first entry)

XX DE Human liver peptide, SEQ ID No 36706.

KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
 KW hypercholesterolaemia; coronary heart disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200157273-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000664.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488898/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human adult liver.
 XX
 PS Claim 27; SEQ ID NO 36706; 658pp; English.
 XX
 CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/ fragments). The probe hybridises at high
 CC stringency to a nucleic acid molecule expressed in the human adult liver.
 CC (I) may be used for predicting, measuring and displaying gene expression
 CC in samples derived from human adult liver. The genes identified may be
 CC involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
 CC associated with coronary heart disease. ABG47348-ABG59930 represent human
 CC liver single exon encoded peptides of the invention. Note: The sequence
 CC information for this patent does not appear in the printed specification
 CC but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 55 AA;
 Query Match 87.2%; Score 41; DB 4; Length 55;
 Best Local Similarity 80.0%; Pred. No. 2.5;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEAEELYQSK 10
 Db |||||:|:|:
 46 AEAEELYQTK 55
 RESULT 12
 ABG45643
 ID ABG45643 standard; peptide; 55 AA.
 XX
 AC ABG45643;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 35308.
 XX
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;

KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200186003-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000665.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2002-114183/15.
 XX
 PT Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 XX
 PS Claim 27; SEQ ID NO 35308; 634pp; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC ; the novel set of probes which hybridise at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a peptide/protein encoded by a single exon probe of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 55 AA;
 Query Match 87.2%; Score 41; DB 5; Length 55;
 Best Local Similarity 80.0%; Pred. No. 2.5;

Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAEELYQSK 10
 Db 46 AEAEELYQTK 55
 RESULT 13
 ADJ36103
 ID ADL36103 standard; protein; 314 AA.
 XX
 AC ADL36103;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human NOVX-related polypeptide #29.
 XX
 KW Human; NOVX; Alzheimer's disease; Parkinson's disease; stroke; epilepsy;
 KW multiple sclerosis; addiction; anxiety; pain; acne; alopecia;
 KW inflammation; rheumatoid arthritis; AIDS; cancer; psoriasis;
 KW hypertension; renal disorder; bone disease; haematopoietic disorder;
 KW wound; bacterial infection; viral infection; fungal infection;
 KW protozoal infection; urinary retention; osteoporosis;
 KW myocardial infarction; diabetes; ulcer; cirrhosis; depression.
 XX
 KW Homo sapiens.
 OS
 XX
 XX US2003207800-A1.
 XX
 XX 06-NOV-2003.
 XX
 XX 13-NOV-2001; 2001US-00015115.
 XX
 XX 08-NOV-1999; 99US-0164240P.
 PR 13-NOV-2000; 2000US-0248153P.
 PR 17-NOV-2000; 2000US-0249598P.
 PR 02-FEB-2001; 2001US-0266127P.
 PR 16-FEB-2001; 2001US-0269562P.
 PR 10-JUL-2001; 2001US-0304348P.
 PR 31-JUL-2001; 2001US-0309261P.
 PR 17-AUG-2001; 2001US-0313283P.
 XX
 PA (MALV/) MALYANKAR U M.
 PA (SHEN/) SHENOY S G.
 PA (SPYI/) SPYTEK K A.
 PA (ZERR/) ZERHUSEN B D.
 PA (PATT/) PATTURAJAN M.
 PA (GUOX/) GUO X.
 PA (KEKU/) KEKUDA R.
 PA (GANG/) GANGOLLI E A.
 PA (SHIM/) SHIMKETS R A.
 PA (TAUP/) TAUPIER R J.
 PA (LILL/) LI L.
 PA (PADI/) PADIGARU M.
 XX
 PI Malyankar UM, Shenoy SG, Spytek KA, Zerhusen BD, Patturajan M;
 PI Guo X, Kekuda R, Gangolli EA, Shimkets RA, Taupier RJ, Li L;
 PI Padigar M;
 XX
 WPI; 2003-875894/81.
 XX
 XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
 PT preventing or treating NOVX-associated disorders (e.g. stroke, epilepsy,
 PT AIDS, pain, diabetes or cancer) and in chromosome mapping, tissue typing
 PT or pharmacogenomics.
 XX
 PS Disclosure; SEQ ID NO 206; 233pp; English.
 XX
 CC The invention relates to human NOVX polypeptides and the polynucleotides
 CC encoding them. The invention also relates to antibodies that bind
 CC immunospecifically to the polypeptides. The NOVX polypeptides,
 CC polynucleotides and antibodies are useful in diagnosing, treating or
 CC preventing NOVX-associated disorders such as Alzheimer's disease,

CC Parkinson's disease, stroke, epilepsy, multiple sclerosis, addiction,
 CC anxiety, pain, acne, alopecia, inflammation, rheumatoid arthritis, AIDS,
 CC cancer, psoriasis, hypertension, renal disorders, bone diseases,
 CC haematopoietic disorders, wounds, infection (e.g. bacterial, viral,
 CC fungal or protozoal), urinary retention, osteoporosis, myocardial
 CC infarction, diabetes, ulcer, cirrhosis or depression. The polypeptides
 CC are also useful as vaccines. This sequence represents a human NOVX-
 CC related polypeptide of the invention.
 XX
 SQ Sequence 314 AA;
 Query Match 87.2%; Score 41; DB 7; Length 314;
 Best Local Similarity 80.0%; Pred. No. 16;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEAEELYQSK 10
 Db 189 AEAEELYQTK 198
 RESULT 14
 ADJ69669
 ID ADJ69669 standard; protein; 327 AA.
 XX
 AC ADJ69669;
 XX
 XX 06-MAY-2004 (first entry)
 DT
 DE Human heat mitochondrial protein as a therapeutic target SeqID1475.
 XX
 KW mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytostatic.
 XX
 OS Homo sapiens.
 XX
 XX WO2003087768-A2.
 PN
 XX 23-OCT-2003.
 PD
 XX 04-APR-2003; 2003WO-US010870.
 PF
 XX 12-APR-2002; 2002US-0372843P.
 PR 17-JUN-2002; 2002US-0389987P.
 PR 20-SEP-2002; 2002US-0412418P.
 XX
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 XX
 XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;
 PI Warnock DE;
 XX
 WPI; 2003-845369/78.
 DR
 XX
 PT Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function,
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 XX
 PS Claim 1; SEQ ID NO 1475; 180pp; English.
 XX
 CC This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,

CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytotatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 327 AA;

Query Match 87.2%; Score 41; DB 7; Length 327;
Best Local Similarity 80.0%; Pred. No. 17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 AEAESLYQSK 10
| | | | | | | | | |
Db 131 AEAALYQTK 140

RESULT 15

ADJ70556
ID ADJ70556 standard; protein; 336 AA.

XX
AC ADJ70556;

XX
DT 06-MAY-2004 (first entry)

XX
DE Human heat mitochondrial protein as a therapeutic target SeqID2362.

XX
DE Mitochondrial; human; screening assay; diabetes mellitus;

KW Huntington's disease; osteoarthritis;

KW Leber's hereditary optic neuropathy; LHON;

KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;

KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;

KW osteopathic; ophthalmological; cytotatic.

XX
OS Homo sapiens.

XX
PN WO2003087768-A2.

XX
PD 23-OCT-2003.

XX
PF 04-APR-2003; 2003WO-US010870.

XX
PR 12-APR-2002; 2002US-0372843P.

PR 17-JUN-2002; 2002US-0389987P.

PR 20-SEP-2002; 2002US-0412418P.

XX
PA (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.

XX
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;

PI Warnock DE;

XX
WPI; 2003-845369/78.

XX
PT Identifying a mitochondrial target for drug screening assays and for

PT treating diseases associated with altered mitochondrial function,

PT comprises detecting a modified polypeptide in a sample and correlating

PT with the disease.

XX
PS Claim 1; SEQ ID NO 2362; 180pp; English.

XX
CC This invention relates to novel mitochondrial targets that can be used

CC for therapeutic intervention in treating a disease associated with

CC altered mitochondrial function. Specifically, it refers to a method for

CC identifying proteins of the human heart mitochondrial proteome that are

CC useful for drug screening assays, as well as therapeutic targets. The

CC present invention describes a method for identifying such proteins that

CC can be used in the treatment of various diseases associated with altered

CC mitochondrial function including diabetes mellitus, Huntington's disease,

CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial

CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytotatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 336 AA;

Query Match 87.2%; Score 41; DB 7; Length 336;
Best Local Similarity 80.0%; Pred. No. 17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 AEAESLYQSK 10

Db 235 AEAALYQTK 244

Search completed: July 5, 2006, 18:43:53

Job time : 87.8932 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 5, 2006, 20:38:52 ; Search time 73.2039 Seconds
(without alignments)
63.277 Million cell updates/sec

Title: US-10-774-928A-7

Perfect score: 47

Sequence: 1 AEAESLYQSK 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	10	5	US-10-774-928-7
2	47	100.0	12	4	US-10-444-575-16
3	47	100.0	644	5	US-10-723-860-366
4	41	87.2	55	3	US-09-864-761-41289
5	41	87.2	222	4	US-10-231-913-263
6	41	87.2	315	4	US-10-231-913-259
7	41	87.2	318	4	US-10-231-913-261
8	41	87.2	327	4	US-10-408-765A-1475
9	41	87.2	336	4	US-10-015-115-126
10	41	87.2	336	4	US-10-408-765A-2362
11	41	87.2	398	4	US-10-104-047-3388
12	41	87.2	398	6	US-11-072-512-3388
13	41	87.2	441	4	US-10-015-115-124
14	41	87.2	441	4	US-10-231-913-85
15	41	87.2	441	4	US-10-231-913-115
16	41	87.2	511	4	US-10-015-115-46
17	41	87.2	520	4	US-10-205-823-433
18	41	87.2	520	4	US-10-108-260A-3712
19	41	87.2	520	6	US-11-051-454-433
20	41	87.2	521	3	US-09-976-782-10
21	41	87.2	521	4	US-10-015-115-48
22	41	87.2	523	4	US-10-015-115-123
23	41	87.2	523	4	US-10-231-913-83
24	41	87.2	523	4	US-10-231-913-113
25	41	87.2	523	4	US-10-473-574-14
26	41	87.2	524	4	US-10-015-115-125
27	41	87.2	524	4	US-10-231-913-84

Sequence 114, Appl
Sequence 32, Appl
Sequence 11, Appl
Sequence 182, Appl
Sequence 86, Appl
Sequence 87, Appl
Sequence 86, Appl
Sequence 87, Appl
Sequence 14, Appl
Sequence 4, Appl
Sequence 44, Appl
Sequence 2446, Ap
Sequence 2878, Ap
Sequence 21, Appl
Sequence 5, Appl
Sequence 18, Appl
Sequence 49505, A

28 41 87.2 524 4 US-10-231-913-114
29 41 87.2 526 4 US-10-231-913-32
30 41 87.2 529 4 US-10-250-613-11
31 41 87.2 529 6 US-11-124-368A-182
32 41 87.2 534 3 US-09-976-782-86
33 41 87.2 534 3 US-09-976-782-87
34 41 87.2 534 4 US-10-231-913-86
35 41 87.2 534 4 US-10-231-913-87
36 41 87.2 534 5 US-10-367-057-38
37 41 87.2 536 4 US-10-231-913-14
38 41 87.2 542 3 US-09-976-782-4
39 41 87.2 549 4 US-10-015-115-44
40 41 87.2 608 4 US-10-094-749-2446
41 40 85.1 390 4 US-10-408-765A-2878
42 39 83.0 279 6 US-11-013-684-21
43 39 83.0 398 5 US-10-883-020-5
44 39 83.0 422 3 US-09-779-307-18
45 39 83.0 429 5 US-10-450-763-49905

ALIGNMENTS

RESULT 1

US-10-774-928-7

; Sequence 7, Application US/10774928

; Publication No. US20040241168A1

; GENERAL INFORMATION:

; APPLICANT: O'Daly, Jose

; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission

; TITLE OF INVENTION: Psoriasis

; FILE REFERENCE: 302178

; CURRENT APPLICATION NUMBER: US/10/774,928

; CURRENT FILING DATE: 2004-02-09

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 7

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Leishmania

US-10-774-928-7

Query Match

Best Local Similarity 100.0%; Score 47; DB 5; Length 10;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEAESLYQSK 10

Db 1 AEAESLYQSK 10

RESULT 2

US-10-444-575-16

; Sequence 16, Application US/10444575

; Publication No. US20030232374A1

; GENERAL INFORMATION:

; APPLICANT: University of Connecticut Health Center

; APPLICANT: Kuchel, George A

; APPLICANT: Zhu, Qing

; TITLE OF INVENTION: Compositions and Methods Relating to Detrusor Estrogen-Regulated

; FILE REFERENCE: UCT-0035

; CURRENT APPLICATION NUMBER: US/10/444,575

; CURRENT FILING DATE: 2003-05-22

; PRIOR APPLICATION NUMBER: US 60/382,830

; PRIOR FILING DATE: 2002-05-23

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 16

; LENGTH: 12

; TYPE: PRT

; ORGANISM: Rattus norvegicus

US-10-444-575-16

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Query Match      100.0%; Score 47; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.031; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY      1 AEAESLYQSK 10
        |||||
Db      3 AEAESLYQSK 12

RESULT 3
US-10-723-860-366
; Sequence 366, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 366
; LENGTH: 644
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-366

Query Match      100.0%; Score 47; DB 5; Length 644;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AEAESLYQSK 10
        |||||
Db      367 AEAESLYQSK 376

RESULT 4
US-09-864-761-41289
; Sequence 41289, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 41289
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC024196.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: EST_HUMAN HIT: BE747524.1, EVALUE 2.00e-18
; OTHER INFORMATION: SWISSPROT HIT: P19013, EVALUE 2.00e-19
US-09-864-761-41289
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Query Match      87.2%; Score 41; DB 3; Length 55;
Best Local Similarity 80.0%; Pred. No. 2.2;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY      1 AEAESLYQSK 10
        |||||
Db      46 AEAALYQTK 55
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RESULT 5
US-10-231-913-263
; Sequence 263, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigaru, Muralidhara
```

APPLICANT: Spaderna, Steven K.
APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-216
CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 60/251,660
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/255,029
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/260,326
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/263,800
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/269,942
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/286,183
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/313,627
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/318,712
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 263
LENGTH: 222
TYPE: PRT
ORGANISM: Homo sapiens
US-10-231-913-263

Query Match 87.2%; Score 41; DB 4; Length 222;
Best Local Similarity 80.0%; Pred. No. 9.6;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLYQSK 10
Db 138 AEAEALYQTK 147
|||||:|||||

RESULT 6
US-10-231-913-259
Sequence 259, Application US/10231913
Publication No. US20040005576A1
GENERAL INFORMATION:
APPLICANT: Guo, Xiaojia S.
APPLICANT: Li, Li
APPLICANT: Patturajan, Meera
APPLICANT: Shimkets, Richard A.
APPLICANT: Casman, Stacie J.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Tchernev, Velizar T.
APPLICANT: Vernet, Corine A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Alsobrook II, John P.
APPLICANT: Edinger, Schlomit
APPLICANT: Peyman, John A.
APPLICANT: Stone, David J.
APPLICANT: Ellerman, Karen
APPLICANT: Gangolli, Esha A.
APPLICANT: Boldog, Ference L.
APPLICANT: Colman, Steven D.
APPLICANT: Eisen, Andrew J.
APPLICANT: Liu, Xiaohong
APPLICANT: Padigar, Muralidhara
APPLICANT: Spaderna, Steven K.
APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-216
CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 60/251,660
PRIOR FILING DATE: 2000-12-06

PRIOR APPLICATION NUMBER: 60/255,029
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/260,326
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/263,800
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/269,942
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/286,183
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/313,627
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/318,712
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 259
LENGTH: 315
TYPE: PRT
ORGANISM: Homo sapiens
US-10-231-913-259

Query Match 87.2%; Score 41; DB 4; Length 315;
Best Local Similarity 80.0%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLYQSK 10
Db 190 AEAEALYQTK 199
|||||:|||||

RESULT 7
US-10-231-913-261
Sequence 261, Application US/10231913
Publication No. US20040005576A1
GENERAL INFORMATION:
APPLICANT: Guo, Xiaojia S.
APPLICANT: Li, Li
APPLICANT: Patturajan, Meera
APPLICANT: Shimkets, Richard A.
APPLICANT: Casman, Stacie J.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Tchernev, Velizar T.
APPLICANT: Vernet, Corine A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Alsobrook II, John P.
APPLICANT: Edinger, Schlomit
APPLICANT: Peyman, John A.
APPLICANT: Stone, David J.
APPLICANT: Ellerman, Karen
APPLICANT: Gangolli, Esha A.
APPLICANT: Boldog, Ference L.
APPLICANT: Colman, Steven D.
APPLICANT: Eisen, Andrew J.
APPLICANT: Liu, Xiaohong
APPLICANT: Padigar, Muralidhara
APPLICANT: Spaderna, Steven K.
APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-216
CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 60/251,660
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/255,029
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/260,326
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/263,800
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/269,942
PRIOR FILING DATE: 2001-02-20

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; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 261
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-913-261

Query Match      87.2%; Score 41; DB 4; Length 318;
Best Local Similarity 80.0%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 AEAESLYQSK 10
      |||||:||||:|
Db      195 AEAELYQTK 204

RESULT 8
US-10-408-765A-1475
; Sequence 1475, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1475
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1475

Query Match      87.2%; Score 41; DB 4; Length 327;
Best Local Similarity 80.0%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 AEAESLYQSK 10
      |||||:||||:|
Db      131 AEAELYQTK 140

RESULT 9
US-10-015-115-126
; Sequence 126, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangolli, Esha A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li

; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015,115
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/248,153
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/249,598
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/264,240
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/266,127
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/269,562
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/304,348
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/309,261
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,283
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 126
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-115-126

Query Match      87.2%; Score 41; DB 4; Length 336;
Best Local Similarity 80.0%; Pred. No. 15;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 AEAESLYQSK 10
      |||||:||||:|
Db      235 AEAELYQTK 244

RESULT 10
US-10-408-765A-2362
; Sequence 2362, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2362
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2362

Query Match      87.2%; Score 41; DB 4; Length 336;
Best Local Similarity 80.0%; Pred. No. 15;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 AEAESLYQSK 10
      |||||:||||:|
Db      235 AEAELYQTK 244
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RESULT 11
US-10-04-047-3388
; Sequence 3388, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: HI-A0105
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3388
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-04-047-3388

Query Match 87.2%; Score 41; DB 4; Length 398;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEESLYQSK 10
||||:||||:
Db 199 AEATLYQTK 208

RESULT 12
US-11-072-512-3388
; Sequence 3388, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KENJI
; APPLICANT: NAGAI, KENJI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3388
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3388

Query Match 87.2%; Score 41; DB 6; Length 398;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEESLYQSK 10

Db 199 AEATLYQTK 208
||||:||||:
RESULT 13
US-10-015-115-124
; Sequence 124, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangolli, Baha A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015,115
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/248,153
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/249,598
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/264,240
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/286,127
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/269,562
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/304,348
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/309,261
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,283
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-115-124

Query Match 87.2%; Score 41; DB 4; Length 441;
Best Local Similarity 80.0%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEESLYQSK 10
||||:||||:
Db 235 AEATLYQTK 244

RESULT 14
US-10-231-913-85
; Sequence 85, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Feynman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-913-85

Query Match 87.2%; Score 41; DB 4; Length 441;
Best Local Similarity 80.0%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAEALYQSK 10
DB 235 AEAEALYQTK 244
|||||:|

RESULT 15
US-10-231-913-115
; Sequence 115, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Feynman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Boldog, Ference L.

; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 115
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-913-115

Query Match 87.2%; Score 41; DB 4; Length 441;
Best Local Similarity 80.0%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAEALYQSK 10
DB 235 AEAEALYQTK 244
|||||:|

Search completed: July 5, 2006, 20:51:59
Job time: 73.2039 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 20:39:32 ; Search time 5.72816 Seconds
(without alignments)
46.842 Million cell updates/sec

Title: US-10-774-928A-7

Perfect score: 47

Sequence: 1 AEAEELYQSK 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 112942

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 3: /EMC_Celerra_SID33/prodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC_Celerra_SID33/prodata/1/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC_Celerra_SID33/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 6: /EMC_Celerra_SID33/prodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Celerra_SID33/prodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SID33/prodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	41	87.2	520	7	US-11-293-697-3712
2	39	83.0	483	7	US-11-105-233-180
3	35	74.5	469	6	US-10-505-328-457
4	34	72.3	639	6	US-10-449-902-41447
5	33	70.2	221	6	US-10-449-902-30681
6	33	70.2	984	6	US-10-449-902-56454
7	32	68.1	282	6	US-10-449-902-54246
8	32	68.1	576	6	US-10-953-349-32301
9	32	68.1	626	6	US-10-449-902-54896
10	32	68.1	645	7	US-11-354-079-3
11	32	68.1	662	6	US-10-449-902-54986
12	32	68.1	689	6	US-10-953-349-32300
13	32	68.1	689	6	US-10-449-902-35350
14	32	68.1	745	6	US-10-953-349-32239
15	31	66.0	220	6	US-10-449-902-30877
16	31	66.0	220	6	US-10-449-902-33167
17	31	66.0	378	7	US-11-174-307B-5390
18	31	66.0	423	6	US-10-449-902-37702
19	31	66.0	546	6	US-10-471-571A-3376
20	31	66.0	599	7	US-11-293-697-2702
21	31	66.0	637	7	US-11-293-697-2455
22	31	66.0	869	6	US-10-471-571A-4926
23	30	63.8	402	7	US-11-174-307B-282
24	30	63.8	450	7	US-11-293-697-4090
25	30	63.8	474	6	US-10-449-902-31122

Sequence 54681, A
Sequence 41136, A
Sequence 54848, A
Sequence 50919, A
Sequence 2, Appli
Sequence 37142, A
Sequence 35627, A
Sequence 289, App
Sequence 52901, A
Sequence 53911, A
Sequence 4, Appli
Sequence 10587, A
Sequence 10587, A
Sequence 41065, A
Sequence 54909, A
Sequence 43668, A
Sequence 35135, A
Sequence 12, Appl
Sequence 468, App
Sequence 3730, Ap

26 30 63.8 527 6 US-10-449-902-54681
27 30 63.8 754 6 US-10-449-902-41136
28 29 61.7 265 6 US-10-449-902-54848
29 29 61.7 347 6 US-10-449-902-50919
30 29 61.7 403 7 US-11-270-040-2
31 29 61.7 442 6 US-10-449-902-37142
32 29 61.7 458 6 US-10-449-902-35627
33 29 61.7 466 7 US-11-289-102-289
34 29 61.7 514 6 US-10-449-902-52901
35 29 61.7 514 6 US-10-449-902-53911
36 29 61.7 551 7 US-11-270-040-4
37 29 61.7 778 6 US-10-953-349-10587
38 29 61.7 792 6 US-10-953-349-10587
39 29 61.7 1061 6 US-10-449-902-41065
40 29 61.7 1191 6 US-10-449-902-54909
41 29 61.7 1511 6 US-10-449-902-43668
42 28 59.6 95 6 US-10-953-349-35135
43 28 59.6 95 7 US-11-225-400-12
44 28 59.6 100 7 US-11-197-712-468
45 28 59.6 155 7 US-11-293-697-3730

ALIGNMENTS

RESULT 1
US-11-293-697-3712
; Sequence 3712, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3712
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3712

Query Match 87.2%; Score 41; DB 7; Length 520;
Best Local Similarity 80.0%; Pred. No. 0.51;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEAEELYQSK 10
Db 298 AEAEELYQTK 307
|||||:|

RESULT 2

US-11-105-233-180
; Sequence 180, Application US/11105233
; Publication No. US20060134653A1
; GENERAL INFORMATION:
; APPLICANT: Thiagalingam et al
; TITLE OF INVENTION: Differential Expression of Genes in MSI
; TITLE OF INVENTION: Tumors
; FILE REFERENCE: 1657/2001
; CURRENT APPLICATION NUMBER: US/11/105,233
; CURRENT FILING DATE: 2005-04-13
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 180
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-233-180

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Query Match      83.0%; Score 39; DB 7; Length 483;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;

QY      1 AEAESLYQSK 10
      |||||:|:|
Db      276 AEAESMYQIK 285

RESULT 3
US-10-505-928-457
; Sequence 457, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 457
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-457

Query Match      74.5%; Score 35; DB 6; Length 469;
Best Local Similarity 70.0%; Pred. No. 8.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 AEAESLYQSK 10
      |||||:|:|
Db      277 AEAESWYQTK 286

RESULT 4
US-10-449-902-41447
; Sequence 41447, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41447
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-41447

Query Match      72.3%; Score 34; DB 6; Length 639;
Best Local Similarity 60.0%; Pred. No. 20;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 AEAESLYQSK 10
      |||||:|:|
Db      474 AEAEGVQTR 483

RESULT 5
US-10-449-902-41447
; Sequence 41447, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41447
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-41447

Query Match      70.2%; Score 33; DB 6; Length 984;
Best Local Similarity 60.0%; Pred. No. 52;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 AEAESLYQSK 10
      |||||:|:|
Db      182 AHADSLYESR 191

RESULT 6
US-10-449-902-56454
; Sequence 56454, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56454
; LENGTH: 984
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-56454

Query Match      70.2%; Score 33; DB 6; Length 984;
Best Local Similarity 60.0%; Pred. No. 52;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 AEAESLYQSK 10
      |||||:|:|
Db      182 AHADSLYESR 191

RESULT 7
US-10-449-902-54246
; Sequence 54246, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
```

; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54246
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-54246

Query Match 68.1%; Score 32; DB 6; Length 282;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEAEELYQ 8
Db 26 AEESLYE 33

RESULT 8

US-10-953-349-32301
; Sequence 32301, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32301
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-32301

Query Match 68.1%; Score 32; DB 6; Length 576;
Best Local Similarity 70.0%; Pred. No. 46;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AEAEELYQSK 10
Db 378 AEQALYQSK 387

RESULT 9

US-10-449-902-54896
; Sequence 54896, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54896
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-54896

Query Match 68.1%; Score 32; DB 6; Length 626;
Best Local Similarity 70.0%; Pred. No. 51;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AEAEELYQSK 10
Db 493 AEQALYQSK 502

RESULT 10

US-11-354-079-3
; Sequence 3, Application US/11354079
; Publication No. US20060141522A1
; GENERAL INFORMATION:

; APPLICANT: Young et al.
; TITLE OF INVENTION: Heregulin-Like Factor
; FILE REFERENCE: PF383D2
; CURRENT APPLICATION NUMBER: US/11/354,079
; CURRENT FILING DATE: 2006-02-15
; PRIOR APPLICATION NUMBER: 10/609,370
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: 09/097,681
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/049,942
; PRIOR FILING DATE: 1997-06-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-354-079-3

Query Match 68.1%; Score 32; DB 7; Length 645;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 EAESLYQSK 10
Db 239 EAELYQKR 247

RESULT 11

US-10-449-902-54986
; Sequence 54986, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54986
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Oryza sativa

US-10-449-902-54986

Query Match 68.1%; Score 32; DB 6; Length 662;
Best Local Similarity 70.0%; Pred. No. 54;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEAESLYQSK 10
|||:||||
Db 481 AEQEALYGSK 490

RESULT 12

US-10-953-349-32300
; Sequence 32300, Application US/10953349
; Publication No. US20060107345A1

GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32300
; LENGTH: 689
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-32300

Query Match 68.1%; Score 32; DB 6; Length 689;
Best Local Similarity 70.0%; Pred. No. 57;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEAESLYQSK 10
|||:||||
Db 491 AEQEALYGSK 500

RESULT 13

US-10-449-902-35350
; Sequence 35350, Application US/10449902
; Publication No. US20060123505A1

GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35350
; LENGTH: 689
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-35350

Query Match 68.1%; Score 32; DB 6; Length 689;
Best Local Similarity 70.0%; Pred. No. 57;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEAESLYQSK 10
|||:||||
Db 493 AEQEALYGSK 502

RESULT 14

US-10-953-349-32299
; Sequence 32299, Application US/10953349
; Publication No. US20060107345A1

GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32299
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-32299

Query Match 68.1%; Score 32; DB 6; Length 745;
Best Local Similarity 70.0%; Pred. No. 62;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEAESLYQSK 10
|||:||||
Db 547 AEQEALYGSK 556

RESULT 15

US-10-449-902-30877
; Sequence 30877, Application US/10449902
; Publication No. US20060123505A1

GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30877
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-30877

Query Match 66.0%; Score 31; DB 6; Length 220;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLY 7
|||:||||
Db 149 AEAESMY 155

Search completed: July 5, 2006, 20:53:03
Job time : 6.72816 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 19:18:42 ; Search time 22.5243 Seconds
(without alignments)
38.861 Million cell updates/sec

Title: US-10-774-928A-7

Perfect score: 47

Sequence: 1 AEAESLYQSK 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SID33/prodata/2/iaa/5 COMB pep.*
- 2: /EMC_Celerra_SID33/prodata/2/iaa/6 COMB pep.*
- 3: /EMC_Celerra_SID33/prodata/2/iaa/7 COMB pep.*
- 4: /EMC_Celerra_SID33/prodata/2/iaa/H COMB pep.*
- 5: /EMC_Celerra_SID33/prodata/2/iaa/PCITUS COMB pep.*
- 6: /EMC_Celerra_SID33/prodata/2/iaa/RE COMB pep.*
- 7: /EMC_Celerra_SID33/prodata/2/iaa/backfiles1 pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	10	2	US-09-809-003A-7
2	47	100.0	637	2	US-09-949-016-8152
3	47	100.0	643	2	US-09-538-092-844
4	41	87.2	398	2	US-10-104-047-3388
5	41	87.2	608	2	US-10-094-749-2446
6	39	83.0	443	2	US-09-949-016-10582
7	39	83.0	482	2	US-09-538-092-858
8	39	83.0	483	2	US-09-919-497-79
9	39	83.0	502	2	US-09-949-016-11033
10	38	80.9	551	1	US-09-067-351-2
11	38	80.9	551	2	US-09-360-490-2
12	38	80.9	564	2	US-09-949-016-6628
13	38	80.9	569	2	US-09-949-016-11035
14	38	80.9	569	2	US-09-949-016-11036
15	37	78.7	235	2	US-09-620-405B-487
16	37	78.7	235	2	US-09-604-287A-487
17	37	78.7	235	2	US-09-834-759-487
18	37	78.7	235	2	US-10-076-622-487
19	37	78.7	235	2	US-10-124-805-487
20	37	78.7	274	2	US-09-949-016-9095
21	37	78.7	493	2	US-09-949-016-6203
22	37	78.7	505	2	US-09-620-405B-478
23	37	78.7	505	2	US-09-620-405B-485
24	37	78.7	505	2	US-09-604-287A-478
25	37	78.7	505	2	US-09-604-287A-485
26	37	78.7	505	2	US-09-834-759-478

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27 37 78.7 505 2 US-09-834-759-485 Sequence 485, App
28 37 78.7 505 2 US-09-590-751A-478 Sequence 478, App
29 37 78.7 505 2 US-09-551-621A-478 Sequence 478, App
30 37 78.7 505 2 US-09-551-621A-478 Sequence 478, App
31 37 78.7 505 2 US-10-076-622-478 Sequence 478, App
32 37 78.7 505 2 US-10-076-622-485 Sequence 485, App
33 37 78.7 505 2 US-10-124-805-478 Sequence 478, App
34 37 78.7 505 2 US-10-124-805-485 Sequence 485, App
35 37 78.7 528 2 US-09-949-016-9678 Sequence 9678, App
36 37 78.7 687 2 US-09-302-626B-173 Sequence 173, App
37 37 78.7 707 2 US-08-772-270A-4 Sequence 4, Appli
38 37 78.7 707 2 US-09-062-126-4 Sequence 11034, A
39 35 74.5 384 2 US-09-949-016-11034 Sequence 3, Appli
40 35 74.5 459 2 US-09-077-606-3 Sequence 9096, Ap
41 35 74.5 476 1 US-09-949-016-9096 Sequence 1, Appli
42 35 74.5 546 1 US-09-067-351-1 Sequence 41, Appli
43 35 74.5 546 2 US-09-360-490-1 Sequence 41, Appli
44 35 74.5 645 2 US-09-919-172-41 Sequence 7138, Ap
45 34 72.3 136 2 US-09-543-681A-7138

```

ALIGNMENTS

RESULT 1

US-09-809-003A-7
; Sequence 7, Application US/09809003A
; Patent No. 6673351

; GENERAL INFORMATION:

; APPLICANT: O'Daly, Jose

; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission

; TITLE OF INVENTION: Psoriasis

; FILE REFERENCE: 302178

; CURRENT APPLICATION NUMBER: US/09/809,003A

; CURRENT FILING DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 7

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Leishmania

; US-09-809-003A-7

Query Match 100.0%; Score 47; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.004;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEAESLYQSK 10

DB 1 AEAESLYQSK 10

RESULT 2

US-09-949-016-8152

; Sequence 8152, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR FILING DATE: 2000-10-20

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8152

; LENGTH: 637

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; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8152

Query Match      100.0%; Score 47; DB 2; Length 637;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AEAESLYQSK 10
Db      367 AEAESLYQSK 376
|||||

RESULT 3
US-09-538-092-844
; Sequence 844, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 844
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P04264
US-09-538-092-844

Query Match      100.0%; Score 47; DB 2; Length 643;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AEAESLYQSK 10
Db      366 AEAESLYQSK 375
|||||

RESULT 4
US-10-104-047-3388
; Sequence 3388, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3388
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3388

Query Match      87.2%; Score 41; DB 2; Length 398;
Best Local Similarity 80.0%; Pred. No. 3.9;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 AEAESLYQSK 10
Db      366 AEAESLYQSK 375
|||||

RESULT 5
US-10-094-749-2446
; Sequence 2446, Application US/10094749
; Patent No. 6979557
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOMYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: NASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2446
; LENGTH: 608
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2446

Query Match      87.2%; Score 41; DB 2; Length 608;
Best Local Similarity 80.0%; Pred. No. 6.2;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 AEAESLYQSK 10
Db      412 AEAALYQTK 421
|||||

RESULT 6
US-09-949-016-10582
; Sequence 10582, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10582
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LENGTH: 443
TYPE: PRT
ORGANISM: Human
US-09-949-016-10582

Query Match 83.0%; Score 39; DB 2; Length 443;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 AEAESLYQSK 10
Db 236 AEAESMYQIK 245

RESULT 7

US-09-538-092-858
Sequence 858, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuratPatSeqFormatter Version 0.9
SEQ ID NO 858
LENGTH: 482
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P05787
US-09-538-092-858

Query Match 83.0%; Score 39; DB 2; Length 482;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 AEAESLYQSK 10
Db 275 AEAESMYQIK 284

RESULT 8

US-09-919-497-79
Sequence 79, Application US/09919497
Patent No. 6773883
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.0
SEQ ID NO 79
LENGTH: 483
TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-497-79

Query Match 83.0%; Score 39; DB 2; Length 483;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 AEAESLYQSK 10
Db 276 AEAESMYQIK 285

RESULT 9

US-09-949-016-11033
Sequence 11033, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11033
LENGTH: 502
TYPE: PRT
ORGANISM: Human
US-09-949-016-11033

Query Match 83.0%; Score 39; DB 2; Length 502;
Best Local Similarity 80.0%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 AEAESLYQSK 10
Db 295 AEAESMYQIK 304

RESULT 10

US-09-067-351-2
Sequence 2, Application US/09067351
Patent No. 5994081
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Baughn, Mariah
TITLE OF INVENTION: HUMAN KERATINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,351
FILING DATE: Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0511 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555

```
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 551 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: KERANOT02
;   CLONE: 2029060
; US-09-067-351-2

Query Match      80.9%; Score 38; DB 1; Length 551;
Best Local Similarity 80.0%; Pred. No. 22;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 AEAESLYQSK 10
Db      336 AEAESWYQTK 345

RESULT 12
US-09-949-016-6628
; Sequence 6628, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSeq for Windows Version 4.0
;   SEQ ID NO 6628
;   LENGTH: 564
;   TYPE: PRT
;   ORGANISM: Human
; US-09-949-016-6628

Query Match      80.9%; Score 38; DB 2; Length 564;
Best Local Similarity 80.0%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 AEAESLYQSK 10
Db      350 AEAESWYQTK 359

RESULT 13
US-09-949-016-11035
; Sequence 11035, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSeq for Windows Version 4.0
;   SEQ ID NO 11035
;   LENGTH: 569
;   TYPE: PRT
;   ORGANISM: Human
; US-09-949-016-11035

Query Match      80.9%; Score 38; DB 2; Length 569;
Best Local Similarity 80.0%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 AEAESLYQSK 10
Db      355 AEAESWYQTK 364
```

```
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 551 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: KERANOT02
;   CLONE: 2029060
; US-09-067-351-2

Query Match      80.9%; Score 38; DB 1; Length 551;
Best Local Similarity 80.0%; Pred. No. 22;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 AEAESLYQSK 10
Db      336 AEAESWYQTK 345

RESULT 11
US-09-360-490-2
; Sequence 2, Application US/09360490
; Patent No. 6221843
; GENERAL INFORMATION:
;   APPLICANT: Tang, Y. Tom
;   APPLICANT: Hillman, Jennifer L.
;   APPLICANT: Corley, Neil C.
;   APPLICANT: Baughn, Mariah
;   TITLE OF INVENTION: HUMAN KERATINS
;   NUMBER OF SEQUENCES: 6
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;   STREET: 3174 PORTER DRIVE
;   CITY: PALO ALTO
;   STATE: CALIFORNIA
;   COUNTRY: USA
;   ZIP: 94304
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/360,490
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/067,351
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: CERRONE, MICHAEL C.
;   REGISTRATION NUMBER: 39,132
;   REFERENCE/DOCKET NUMBER: PF-0511 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (650) 855-0555
;   TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 551 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: KERANOT02
;   CLONE: 2029060
; US-09-360-490-2

Query Match      80.9%; Score 38; DB 2; Length 551;
Best Local Similarity 80.0%; Pred. No. 22;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;
```

RESULT 14

US-09-949-016-11036
; Sequence 11036, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11036
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11036

Query Match 80.9%; Score 38; DB 2; Length 569;
Best Local Similarity 80.0%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAESLYQSK 10
Db 355 AAESWYQTK 364
|||||:|

RESULT 15

US-09-620-405B-487
; Sequence 487, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 487
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-620-405B-487

Query Match 78.7%; Score 37; DB 2; Length 235;
Best Local Similarity 80.0%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAESLYQSK 10
Db 21 AAESWYRSK 30
|||||:|

Search completed: July 5, 2006, 19:24:26
Job time : 22.5243 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 19:09:18 ; Search time 10.9223 Seconds
(without alignments)
79.283 Million cell updates/sec

Title: US-10-774-928A-8

Perfect score: 45

Sequence: 1 ATNAENEFV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.*

1: Piri:*

2: Piri2:*

3: Piri3:*

4: Piri4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	91.1	581	1 KRMS2	keratin, type II c
2	41	91.1	643	1 KRHU2	keratin 1, type II
3	36	80.0	324	2 A81894	probable fructose-
4	36	80.0	324	2 F81126	fructose-1,6-bisph
5	36	80.0	553	2 I59009	epidermal keratin
6	36	80.0	583	2 G81412	aspartate-tRNA lig
7	35	77.8	390	2 A60093	cytokeatin, type
8	35	77.8	480	2 A56694	keratin, type II,
9	35	77.8	513	2 S08381	keratin, 58K type
10	35	77.8	590	2 A29904	keratin 5, type II
11	34	75.6	341	2 B86792	hypothetical prote
12	34	75.6	659	1 A64228	DNA ligase (NAD) (
13	33	73.3	350	2 F71144	probable galactoki
14	33	73.3	384	2 I61769	keratin 6d, type I
15	33	73.3	461	2 A43782	keratin, type II -
16	33	73.3	469	2 S05602	keratin K7, type I
17	33	73.3	489	2 B24177	keratin, 55K type
18	33	73.3	502	2 D95855	probable ABC trans
19	33	73.3	564	1 KRHUEB	keratin 6a, type I
20	33	73.3	564	1 KRHUEB	keratin 6b, type I
21	33	73.3	564	2 I61770	keratin 6e, type I
22	33	73.3	564	2 I61768	keratin 6c, type I
23	33	73.3	564	2 I61771	keratin 6f, type I
24	33	73.3	629	2 A29666	keratin, 65K type
25	33	73.3	629	2 A29629	keratin K3 - rabbi
26	33	73.3	638	2 I53169	cytokeatin 2 - hu
27	33	73.3	1524	2 G84721	hypothetical prote
28	33	73.3	1750	2 G84649	hypothetical prote
29	32	71.1	217	2 S45023	GNP-binding protei

ALIGNMENTS

RESULT 1

KRMS2

keratin, type II cytoskeletal - mouse (fragment)

N;Alternate names: 67-kDa type II keratin

C;Species: Mus musculus (house mouse)

C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004

C;Accession: A02951

R;Steinert, P.M.; Parry, D.A.D.; Idler, W.W.; Johnson, L.D.; Steven, A.C.; Roop, D.R.

J. Biol. Chem. 260, 7142-7149, 1985

A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67,000

ate filament subunits.

A;Reference number: A92535; MUID:85207740; PMID:2581964

A;Accession: A02951

A;Molecule type: mRNA

A;Residues: 1-581 <STE>

A;Cross-references: UNIPROT:P04104; UNIPARC:UPI0000173D5B; GB:M10937; NID:gl98622; PID:9

C;Superfamily: Cytoskeletal keratin

C;Keywords: coiled coil; intermediate filament

F;1-106/Domain: head (fragment) <HED>

F;1-70/Region: V1 subdomain (fragment)

F;71-106/Region: H1 subdomain

F;107-419/Domain: rod <ROD>

F;107-141/Region: coil 1A

F;142-153/Region: linker 1

F;154-254/Region: coil 1B

F;255-271/Region: linker 12

F;272-290/Region: coil 2A

F;291-298/Region: linker 2

F;299-419/Region: coil 2B

F;357/Region: stutter

F;420-581/Domain: tail <END>

F;420-439/Region: H2 subdomain

F;440-581/Region: V2 and E2 subdomains

Query Match 91.1%; Score 41; DB 1; Length 581;

Best Local Similarity 100.0%; Pred. No. 1.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNAENEFV 9

|||||

Db 204 TNAENEFV 211

RESULT 2

KRHU2

keratin-1, type II, cytoskeletal - human

N;Alternate names: 67K type II epidermal keratin; cytokeatin 1

C;Species: Homo sapiens (man)

C;Date: 04-Dec-1986 #sequence_revision 22-Oct-1999 #text_change 10-Dec-1999

C;Accession: A22940; A02950; A43342

R;Johnson, L.D.; Idler, W.W.; Zhou, X.M.; Roop, D.R.; Steinert, P.M.

Proc. Natl. Acad. Sci. U.S.A. 82, 1896-1900, 1985

GNP-binding protei
hypothetical prote
cytochrome-c oxida
cytochrome-c oxida
thioredoxine reduc
probable type I re
keratin, 64K type
keratin, 64K type
gamma-aminobutyrat
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
GNP-binding protei
GNP-binding protei

A:Reference number: A22940; MUID:85166239; PMID:2580302
A:Accession: A22940
A:Molecule type: DNA
A:Residues: 1-643 <OH>
A:Cross-references: UNIPARC:UPI0000173D59; GB:M98776; GB:M11215; GB:M11845; GB:M11846; N
A>Note: translation of initiator Met is not shown
R:Steinert, P.M.; Parry, D.A.D.; Idler, W.W.; Johnson, L.D.; Steven, A.C.; Roop, D.R.
J. Biol. Chem. 260, 7142-7149, 1985
A:Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67,000
late filament subunits
A:Reference number: A92535; MUID:85207740; PMID:2581964
A:Accession: A02950
A:Molecule type: mRNA
A:Residues: 151-183, 'K', 185-199, 'M', 201-204, 'K', 206-236, 'S', 238-239, 'R', 241-356, 'Y', 358-
'S', 638-643 <STE>
A:Cross-references: UNIPARC:UPI000016ABD0; GB:M10338; NID:gl86787; PIDN:AAA36153.1; PID:
'S', 638-643 <STE>
A:Experimental source: tissue neonatal foreskin
A>Note: the authors translated the codon CUG for residue 476 as Met
R:Chipev, C.C.; Korge, B.P.; Markova, N.; Bale, S.J.; Digiovanna, J.J.; Compton, J.G.; S
Cell 70, 821-828, 1992
A:Title: A leucine---proline mutation in the H1 subdomain of keratin 1 causes epidermol
A:Reference number: A43342; MUID:92386601; PMID:1381288
A:Accession: A43342
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 144-146, 'P', 148-159, 'P', 161-183, 'K', 185-186 <CHI>
A:Residues: 144-146, 'P', 148-159, 'P', 161-183, 'K', 185-186 <CHI>
A:Cross-references: UNIPARC:UPI0000173D5A; GB:M98776; GB:M11215; GB:M11845; GB:M11846; N
A>Note: sequence extracted from NCBI backbone (NCBI:112784)
C:Comment: The cytoskeletal and microfibrillar keratins are classified into two types, b
atin I protein subunit appears to be a heterotetramer of two type I and two type II pro
C:Comment: Keratin 1 is expressed in terminally differentiating epidermis.
C:Genetics:
A:Gene: GDB:KRT1
A:Cross-references: GDB:128198; OMIM:139350
A:Map position: 12ql1-12ql3
A>Note: defects in this gene may result in epidermolytic hyperkeratosis
C:Complex: heterotetramer of two type I, usually keratin 10 (see FIR:KRHU0), and two typ
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; heterotetramer; intermediate filament
F:4-179/Domain: head <HD>
F:4-179/Region: E1 and V1 subdomains
F:14-179/Region: H1 subdomain
F:180-492/Domain: rod <ROD>
F:180-214/Region: coil 1A
F:215-226/Region: linker 1
F:227-327/Region: coil 1B
F:328-344/Region: linker 12
F:345-363/Region: coil 2A
F:364-371/Region: linker 2
F:372-492/Region: coil 2B
F:430/Region: stutter
F:493-643/Domain: tail <END>
F:493-512/Region: H2 subdomain
F:513-643/Region: V2 and E2 subdomains

Query Match 91.1%; Score 41; DB 1; Length 643;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNAENEFV 9
|||||||

DB 277 TNAENEFV 284

RESULT 3
A:Accession: A81894
A:Title: probable fructose-bisphosphatase (EC 3.1.3.11) NMA1259 [imported] - Neisseria meningitidis
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: A81894
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: A81894
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-324 <PAR>
A:Cross-references: UNIPROT:Q9JUL6; UNIPARC:UPI00000C4B5F; GB:AL162755; GB:AL157959; NID:
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: fbp; NMA1259
A:Superfamily: fructose-1,6-bisphosphatase
C:Keywords: phosphoric monoester hydrolase

Query Match 80.0%; Score 36; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NAENEFV 9
|||||||

DB 175 NAENEFV 181

RESULT 4
F81126
fructose-1,6-bisphosphatase NMB1060 [imported] - Neisseria meningitidis (strain MC58 sero
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: F81126
R:Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.;
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: F81126
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-324 <TET>
A:Cross-references: UNIPROT:Q9JZH1; UNIPARC:UPI00000C4630; GB:AE002456; GB:AE002098; NID:
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1060
C:Superfamily: fructose-1,6-bisphosphatase

Query Match 80.0%; Score 36; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NAENEFV 9
|||||||

DB 175 NAENEFV 181

RESULT 5
I59009
epidermal keratin subunit II - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I59009; A61205
R:Steinert, P.M.; Parry, D.A.D.; Racoosin, E.L.; Idler, W.W.; Steven, A.C.; Trus, B.L.; F
Proc. Natl. Acad. Sci. U.S.A. 81, 5709-5713, 1984
A:Title: The complete cDNA and deduced amino acid sequence of a type II mouse epidermal
A:Reference number: I59009; MUID:85014838; PMID:6207530
A:Accession: I59009
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-553 <RES>
A:Cross-references: UNIPROT:P50446; UNIPARC:UPI000016CE87; GB:K02108; NID:G198634; PIDN:
R:Finch, J.; Andrews, K.; Krieg, P.; Fuerstenberger, G.; Slaga, T.; Ootsuyama, A.; Tanoo
Carcinogenesis 12, 1519-1522, 1991
A:Title: Identification of a cloned sequence activated during multi-stage carcinogenesis
A:Reference number: A61205; MUID:91316763; PMID:1713533

A;Accession: A61205
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 528-553 <FIN>
A;Cross-references: UNIPARC:UPI00001774C8
C;Genetics:
A;Gene: KER2
C;Superfamily: cytoskeletal keratin

Query Match 80.0%; Score 36; DB 2; Length 553;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNAENEFV 9
|:|||||
DB 250 TDAENEFV 257

RESULT 6

G81412
aspartate-tRNA ligase (EC 6.1.1.12) Cj0640c [imported] - Campylobacter jejuni (strain NC
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: G81412
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketlev, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: G81412
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-583 <PAR>
A;Cross-references: UNIPROT:Q9PHM7; UNIPARC:UPI000013638A; GB:AL1139075; GB:AL111168; NID
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: aspS; Cj0640c
C;Superfamily: lysine-tRNA ligase
C;Keywords: ligase

Query Match 80.0%; Score 36; DB 2; Length 583;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATNAENEFV 9
|:|||||
DB 61 ASNARNEFV 69

RESULT 7

A60093
cytokeratin, type II, early ectodermal - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993
C;Accession: A60093
R;Charlebois, T.S.; Spencer, D.H.; Tarkington, S.K.; Henry, J.J.; Grainger, R.M.
Development 108, 33-45, 1990
A;Title: Isolation of a chick cytokeratin cDNA clone indicative of regional specialization
A;Reference number: A60093; MUID:90276238; PMID:1693557
A;Accession: A60093
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-390 <CHA>
A;Cross-references: UNIPARC:UPI00001774C6
C;Superfamily: cytoskeletal keratin
C;Keywords: intermediate filament

Query Match 77.8%; Score 35; DB 2; Length 390;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TNAENEFV 9
|:|||||

Db 108 TTAENEFV 115

RESULT 8

A56694
keratin, type II, KRT2.13 - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
C;Accession: A56694
R;Powell, B.C.; Crocker, L.A.; Rogers, G.E.
DNA Seq. 3, 401-405, 1993
A;Title: Complete sequence of a hair-like intermediate filament type II keratin gene.
A;Reference number: A56694; MUID:94033628; PMID:7693053
A;Accession: A56694
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-480 <POW>
A;Cross-references: UNIPROT:Q06018; UNIPARC:UPI0000088521; GB:X72379; NID:g297105; PIDN:
C;Genetics:
A;Gene: KRT2.13
A;Introns: 140/3; 210/2; 230/3; 262/3; 317/3; 359/3; 433/2; 444/1
C;Superfamily: cytoskeletal keratin

Query Match 77.8%; Score 35; DB 2; Length 480;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TNAENEFV 9
|:|||||

Db 219 TTAENEFV 226

RESULT 9

S08381
keratin, 58K type II, cytoskeletal (clone pXenCK55(5/6)) - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
C;Accession: S08381
R;Fouquet, B.; Herrmann, H.; Franz, J.K.; Franke, W.W.
Development 104, 533-548, 1988
A;Title: Expression of intermediate filament proteins during development of Xenopus lae
A;Reference number: S08381; MUID:90032362; PMID:2478354
A;Accession: S08381
A;Molecule type: mRNA
A;Residues: 1-513 <FOU>
A;Cross-references: UNIPROT:P16879; UNIPARC:UPI000017151D; EMBL:X14427; NID:g64625; PIDN:
C;Superfamily: cytoskeletal keratin

Query Match 77.8%; Score 35; DB 2; Length 513;
Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TNAENEFV 9
|:|||||

Db 225 TGAENEFV 232

RESULT 10

A29904
keratin 5, type II, epidermal - human
N;Alternate names: 58K type II keratin; cytokeratin 5; K5
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: A29904; A60865; A32568; A27679; I58080
R;Eckert, R.L.; Rorke, E.A.
DNA 7, 337-345, 1988
A;Title: The sequence of the human epidermal 58-kD (5) type II keratin reveals an absen
A;Reference number: A29904; MUID:88296082; PMID:2456903
A;Accession: A29904
A;Molecule type: DNA; mRNA
A;Residues: 1-590 <ECK>
A;Cross-references: UNIPROT:P13647; UNIPARC:UPI000012DB0D; GB:M21389; NID:g186697; PIDN:
R;Galup, C.; Darmon, M.Y.

Query Match 77.8%; Score 35; DB 2; Length 390;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TNAENEFV 9
|:|||||

J. Invest. Dermatol. 91, 39-42, 1988
A:Title: Isolation and characterization of a cDNA clone coding for human epidermal keratin
A:Reference number: A60865; MUID:88258089; PMID:2455002
A:Accession: A60865
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 348-374, 'E', 376-386, 'S', 388-436, 438-542, 'S', 544-590 <GAL>
A:Cross-references: UNIPARC:UPI00001774BD
R:Lersch, R.; Stellmach, V.; Stocks, C.; Gludice, G.; Fuchs, E.
Mol. Cell. Biol. 9, 3685-3697, 1989
A:Title: Isolation, sequence, and expression of a human keratin K5 gene: transcriptional
A:Reference number: A32568; MUID:89384595; PMID:2476664
A:Accession: A32568
A:Molecule type: DNA
A:Residues: 2-8, 'SGA', 12-36, 'GP', 39-78, 'S', 80-196, 'E', 198-260, 'Q', 262-270, 'H', 272-386, 'S'
A:Cross-references: UNIPARC:UPI00001774BE; GB:M28496; NID:g186728
A>Note: the authors translated the codon CGT for residue 15 as Pro and GAG for residue 2
A>Note: this translation is not annotated in GenBank entry HUMKERK5X, release 111.0
R:Lersch, R.; Fuchs, E.
Mol. Cell. Biol. 8, 486-493, 1988
A:Title: Sequence and expression of a type II keratin, K5, in human epidermal cells.
A:Reference number: A27679; MUID:88094424; PMID:2447486
A:Accession: A27679
A:Molecule type: mRNA
A:Residues: 83-196, 'E', 198-260, 'Q', 262-270, 'H', 272-386, 'S', 388-557, 'S', 559-590 <LE2>
A:Cross-references: UNIPARC:UPI000016ABA6; GB:M19723; NID:g186726; PIDN:AAA36145.1; PID:
R:Lane, E.B.; Rugg, E.L.; Navsaria, H.; Leigh, I.M.; Heagerty, A.H.M.; Ishida-Yamamoto,
Nature 356, 244-246, 1992
A:Title: A mutation in the conserved helix termination peptide of keratin 5 in hereditary
A:Reference number: I58080; MUID:92204232; PMID:1372711
A:Accession: I58080
A>Status: translated from GB/EMBL/DDBT
A:Molecule type: mRNA
A:Residues: 467-474, 'G', 476-481 <LAN>
A:Cross-references: UNIPARC:UPI000011F7CB; GB:S90014; NID:g247707; PIDN:AAB21859.1; PID:
C:Comment: This type II keratin is expressed together with the type I keratin 14 in the
C:Genetics:
A:Gene: GDB:KRT5; EBS2
A:Cross-references: GDB:128110; OMIM:148040
A:Map position: 12q11-12q13
A:Introns: 185/3; 257/2; 277/3; 309/3; 364/3; 406/3; 480/2; 492/1
A>Note: defects in this gene may result in Dowling-Meara type epidermolysis bullosa sim
C:Complex: heterotetramer of two type I, usually keratin 14 (see PIR:KRHUE), and two typ
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; cytoskeleton; epidermis; heterotetramer

Query Match 77.8%; Score 35; DB 2; Length 590;
Best Local Similarity 87.5%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TNAENEFFV 9
Db 266 TTAENEFFV 273

RESULT 11
B86792
hypothetical protein gpda (imported) - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 05-Oct-2004
C:Accession: B86792
R:Boletín, A.; Mincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: B86792
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-341 <STO>
A:Cross-references: UNIPROT:Q9CFX6; UNIPARC:UPI000012B98F; GB:AE005176; PID:g12724320; H
C:Experimental source: strain IL1403
C:Genetics:
A:Gene: gpda

C:Superfamily: glycerol-3-phosphate dehydrogenase (NAD)

Query Match 75.6%; Score 34; DB 2; Length 341;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TNAENEFFV 9
Db 331 TRAENEFFI 338

RESULT 12

A64228

DNA ligase (NAD) (EC 6.5.1.2) - Mycoplasma genitalium

C:Species: Mycoplasma genitalium

C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 31-Dec-2004

C:Accession: A64228

R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;

M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.N.

; C.A.; Venter, J.C.

Science 270, 397-403, 1995

A:Title: The minimal gene complement of Mycoplasma genitalium.

A:Reference number: A64200; MUID:96026346; PMID:7569993

A:Accession: A64228

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-659 <TIGR>

A:Cross-references: UNIPROT:P47496; UNIPARC:UPI0000129683; GB:U39703; GB:I43967; NID:g104

A:Experimental source: strain G-37

C:Genetics:

A:Genetic code: SGC3

A:Start codon: GTG

C:Superfamily: DNA ligase (NAD), Liga type

C:Keywords: ligase; NAD

Query Match 75.6%; Score 34; DB 1; Length 659;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNAENEFFV 9
Db 102 TNSKNEFFV 109

RESULT 13

F71144

probable galactokinase - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Oct-2004

C:Accession: F71144

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hino, Y.; Yamamoto, S.; Sekine,

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic ar

A:Reference number: A71000; MUID:98344137; PMID:9679194

A:Accession: F71144

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-350 <KAW>

A:Cross-references: UNIPROT:O58107; UNIPARC:UPI000012B05F; GB:AP000002; NID:g3236129; PFI

A:Experimental source: strain OT3

A>Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A:Gene: PH0369

C:Superfamily: galactokinase

Query Match 73.3%; Score 33; DB 2; Length 350;
Best Local Similarity 77.8%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATNAENEFFV 9
Db 133 AKKAENEFFV 141

RESULT 14

I61769
keratin 6d, type II - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: I61769
R:Takahashi, K.; Paladini, R.D.; Coulombe, P.A.
J. Biol. Chem. 270, 18581-18592, 1995
A:Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
A:Reference number: A57398; MUID:95355491; PMID:7543104
A:Accession: I61769
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-384 <RES>
A:Cross-references: UNIPROT:P48667; UNIPARC:UPI000012DB17; GB:L42602; NID:g914823; GB:L4
28; GB:L42608; NID:g914829; GB:L42609; NID:g914830; GB:L42610; NID:g1488252; PIDN:AAB606
C:Genetics:
A:Gene: KRT6D
A:Introns: 72/2; 92/3; 124/3; 179/3; 221/3; 295/2; 307/1
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil

Query Match 73.3%; Score 33; DB 2; Length 384;
Best Local Similarity 87.5%; Pred.No. 38;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TNAENEFV 9

Db 81 TAAENEFV 88

RESULT 15

A43782
keratin, type II - eastern newt (fragment)
C:Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C>Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C:Accession: A43782
R:Ferretti, P.; Brookes, J.P.; Brown, R.
Development 111, 497-507, 1991
A:Title: A new type II keratin restricted to normal and regenerating limbs and tails is
A:Reference number: A43782; MUID:91372147; PMID:1716554
A:Accession: A43782
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <PER>
A:Cross-references: UNIPROT:O42435; UNIPARC:UPI00001774C4; GB:X57671
C:Superfamily: cytoskeletal keratin

Query Match 73.3%; Score 33; DB 2; Length 461;
Best Local Similarity 87.5%; Pred.No. 46;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TNAENEFV 9

Db 142 TAAENEFV 149

Search completed: July 5, 2006, 19:20:29
Job time : 11.9223 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: July 5, 2006, 18:28:56 ; Search time 92.0971 Seconds
(without alignments)
90.395 Million cell updates/sec

Title: US-10-774-928A-8
Perfect score: 45
Sequence: 1 ATNAENEFV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	91.1	619	2	Q6E1Y9_CANFA
2	41	91.1	625	2	Q6IMF3_RAT
3	41	91.1	627	1	K2C1_MOUSE
4	41	91.1	637	2	Q9D2K8_MOUSE
5	41	91.1	643	1	K2C1_HUMAN
6	38	84.4	222	2	Q4L0E7_MOUSE
7	38	84.4	224	2	Q678L1_MOUSE
8	38	84.4	572	1	K2C1B_MOUSE
9	38	84.4	869	2	Q63ER5_BACCCZ
10	38	84.4	869	2	Q81U13_BACAN
11	36	80.0	207	2	Q5H887_NEIGO
12	36	80.0	324	2	Q9JUL6_NEIMA
13	36	80.0	324	2	Q9ZH1_NEIMEB
14	36	80.0	324	2	Q5F8C3_NEIGI
15	36	80.0	529	2	Q919P5_RANCA
16	36	80.0	557	2	Q6IG07_RAT
17	36	80.0	580	2	Q98UJ3_XENLA
18	36	80.0	583	1	SYD_CAMJF
19	36	80.0	583	1	SYD_CAMJR
20	36	80.0	590	2	Q5XGR4_XENLA
21	36	80.0	598	2	Q701L6_HUMAN
22	36	80.0	600	1	KRHB4_HUMAN
23	36	80.0	600	2	Q6ISB0_HUMAN
24	36	80.0	603	1	KRHB4_MOUSE
25	35	77.8	241	2	Q4Y317_PLACH
26	35	77.8	375	2	Q2UTZ4_ASPOR
27	35	77.8	381	2	Q32MB2_HUMAN
28	35	77.8	480	2	Q06018_SHEEP
29	35	77.8	492	1	K2CO_CHICK
30	35	77.8	512	1	K2C5_XENLA
31	35	77.8	519	1	K2C1E_RAT

32	35	77.8	529	2	Q86V45_HUMAN	Q86V45 homo sapien
33	35	77.8	539	2	Q6NXH9_MOUSE	Q6NXH9 mus musculus
34	35	77.8	540	2	Q86Y46_HUMAN	Q86Y46 homo sapien
35	35	77.8	543	2	Q7RTS7_HUMAN	Q7RTS7 homo sapien
36	35	77.8	553	2	Q6IG03_RAT	Q6IG03 rattus norv
37	35	77.8	554	2	Q3UV11_MOUSE	Q3UV11 mus musculus
38	35	77.8	561	1	K2C6B_MOUSE	Q2331 mus musculus
39	35	77.8	576	1	K2C5_RAT	Q6P6Q2 rattus norv
40	35	77.8	580	1	K2C5_MOUSE	Q922U2 mus musculus
41	35	77.8	581	2	Q6IFZ5_RAT	Q6IFZ5 rattus norv
42	35	77.8	590	1	K2C5_HUMAN	P13647 homo sapien
43	35	77.8	599	2	Q6PVZ5_CHICK	Q6PVZ5 gallus gall
44	35	77.8	601	1	K2C5_BOVIN	Q5XQD5 bos taurus
45	35	77.8	606	2	Q32P04_MOUSE	Q32P04 mus musculus

ALIGNMENTS

RESULT 1

Q6E1Y9_CANFA
ID Q6E1Y9_CANFA PRELIMINARY; PRT; 619 AA.
AC Q6E1Y9;
DT 16-AUG-2004, integrated into UniProtKB/TREMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Epithelial keratin 1.
GN Name=Ker1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15627753; DOI=10.1159/000081527;
RA Credille K.M., Guyon R., Andre C., Murphy K., Tucker K.,
RA Barnhart K.F., Dunstan R.W.;
RT "Comparative sequence analysis and radiation hybrid mapping of two
epidermal type II keratin genes in the dog: keratin I and keratin
2e.";
RL CytoGenet. Genome Res. 108:328-332(2005).
CC -1- SIMILARITY: Belongs to the intermediate filament family.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs License

CC EMBL; AV318945; AAQ83910.1; -; mRNA.
DR Ensembl; ENSCAFG00000007212; Canis familiaris.
DR GO; GO:0005982; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin I.
DR InterPro; IPR003054; Keratin II.
DR PANTHER; PTHR18893.SP5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PRO1248; TYPE1KERATIN.
DR PRINTS; PRO1276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
SQ SEQUENCE 619 AA; 63790 MW; B45AB709AD0909F CRC64;

Query Match 91.1%; Score 41; DB 2; Length 619;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNAENEFV 9

Db 279 TNAENEFV 286

RESULT 2

Q6IMF3_RAT

```
ID O6IME3_RAT PRELIMINARY; PRT; 625 AA.
AC O6IME3;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Type II keratin Kbl.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=23257644; PubMed=15085952; DOI=10.1078/0171-9335-00354;
RA Hesse M., Zimek A., Weber K., Magin T.M.;
RT "Comprehensive analysis of keratin gene clusters in humans and
rodents.";
RL Eur. J. Cell Biol. 83:19-26(2004).
CC -|- MISCELLANEOUS: The sequence shown here is derived from an
EMBL/GenBank/DBJ third party annotation (TPA) entry.
CC -|- SIMILARITY: Belongs to the intermediate filament family.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BK001580; DAA02055.1; -; mRNA.
DR Ensembl; ENSRNOG0000028996; Rattus norvegicus.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin I.
DR PANTHER; PTHR1893:SP5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
SQ SEQUENCE 625 AA; 64831 MW; 790AAC59E2A2707B CRC64;

Query Match 91.1%; Score 41; DB 2; Length 625;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNAENEVF 9
Db 277 TNAENEVF 284
|||||

RESULT 3
K2C1_MOUSE STANDARD; PRT; 627 AA.
AC P04104;
DT 01-NOV-1986, integrated into UniProtKB/Swiss-Prot.
DT 30-MAY-2000, sequence version 2.
DT 07-FEB-2006, entry version 50.
DE Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1)
DE (K1) (67 kDa cytokeatin)
DE Name=Krt1; Synonyms=Krt2-1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=85207740; PubMed=2581964;
RA Steiner P.M., Parry D.A.D., Idler W.W., Johnson L.D., Steven A.C.,
RA Roop D.R.;
RT "Amino acid sequences of mouse and human epidermal type II keratins of
Mr 67,000 provide a systematic basis for the structural and functional
diversity of the end domains of keratin intermediate filament
subunits";
```

```
RL J. Biol. Chem. 260:7142-7149(1985).
RN [2]
RP SEQUENCE REVISION.
RA Roop D.R.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -|- SUBUNIT: Heterotrimer of two type I and two type II keratins.
CC -|- PTM: Undergoes deamination of some arginine residues
(citrullination) (By similarity).
CC -|- MISCELLANEOUS: There are two types of cytoskeletal and
microfibrillar keratin, I (acidic) and II (neutral to basic) (40-
55 and 56-70 kilodaltons, respectively).
CC -|- SIMILARITY: Belongs to the intermediate filament family.
CC -----
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CC -----
DR EMBL; M10937; AAD05191.1; -; mRNA.
DR PIR; A02951; KRMS2.
DR HSSP; P08670; 1GK7.
DR SWISS-2DPAGE; P04104; MOUSE.
DR Ensembl; ENSMUSG00000046834; Mus musculus.
DR MGI; MGI:96698; Krt2-1.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin I.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893:SP5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Citrullination; Coiled coil; Intermediate filament; Keratin.
FT INIT MET 0 0
FT CHAIN 1 627
FT REGION 1 186
FT REGION 187 496
FT REGION 187 222
FT REGION 187 222
FT REGION 223 242
FT REGION 243 333
FT REGION 334 357
FT REGION 358 496
FT REGION 497 627
FT SITE 451 451
FT SITE 451 451
SQ SEQUENCE 627 AA; 65092 MW; EF7E848654539578 CRC64;

Query Match 91.1%; Score 41; DB 1; Length 627;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNAENEVF 9
Db 285 TNAENEVF 292
|||||

RESULT 4
Q9D2K8_MOUSE PRELIMINARY; PRT; 637 AA.
ID Q9D2K8_MOUSE
AC Q9D2K8;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 23.
DE 0 day neonate head cDNA, RIKEN full-length enriched library,
DE clone:4833436C19 product:keratin complex 2, basic, gene 1, full insert
DE sequence.
DE Name=Krt2-1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=C57BL/6J; TISSUE=Head;
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RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Head;
RC PubMed=16141072; DOI=10.1126/science.1112014;
RX Oyama K., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aldinis V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Atualiya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA Di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
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RL Science 309:1559-1563(2005).
[3]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Head;
RC PubMed=16141073; DOI=10.1126/science.1112009;
RX RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
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RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
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RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[5]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
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RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
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RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
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RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
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RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[6]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RX Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[7]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
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RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[8]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Head;
RC Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
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RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejina Y., Tova T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: AK019521; BAB31776.1; -; mRNA.
DR HSSP: P08670; 1GK7.
DR Ensemble: ENSMUSG0000046834; Mus musculus.
DR MGI: MGI:96698; Krt2-1.
DR GO: GO:0005982; C:intermediate filament; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR001664; IF.
DR InterPro: IPR002957; Keratin I.
DR InterPro: IPR003054; Keratin II.
DR PANTHER: PTHR18993:SP5; Keratin_II; 1.
DR Pfam: PF00038; Filament; 1.
DR PRINTS: PR01248; TYPE1KERATIN.
DR PRINTS: PR01276; TYPE2KERATIN.
DR PROSITE: PS00226; IF; 1.
KW Intermediate filament; Keratin.
SQ SEQUENCE 637 AA; 65627 MW; D6344FDD0468ECA7 CRC64;

Query Match 91.1%; Score 41; DB 2; Length 637;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNAENFV 9
DB 286 TNAENFV 293
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RESULT 5
K2C1 HUMAN
ID K2C1 HUMAN STANDARD; PRT; 643 AA.
AC P04264; Q14720; Q6GSJ0; Q9H298;
DT 20-MAR-1987, integrated into UniProtKB/Swiss-Prot.
DT 01-FEB-1996, sequence version 4.
DE 07-FEB-2006, entry version 76.
DE Keratin, type II cytoskeletal 1 (Cytokeratin-1) (Keratin-1)
DE (K1) (67 kDa cytokearatin) (Hair alpha protein).
GN Name=kRT1; Synonyms=KRTA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=85166239; PubMed=2580302;
RA Johnson L.D., Idler W.W., Zhou X.-M., Roop D.R., Steinert P.M.;
RA "Structure of a gene for the human epidermal 67-kDa keratin.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:1896-1900(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Whitlock N.V., Eady R.A.J., McGrath J.A.;
RA "Genomic organization of the human keratin 1 gene.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Hatzel S.J., Eady R.A.J., Wennerstrand L., Dopping-Hepenstal P.J.,
RA Leigh I.M., Munro C., Kelsell D.P.;
RA "Novel splice site mutation in keratin 1 underlies mild epidermolytic
RA palmoplantar keratoderma in three kindreds.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT TYR-357.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP PRELIMINARY NUCLEOTIDE SEQUENCE [MRNA] OF 151-643.
RX MEDLINE=85207740; PubMed=2581964;
RA Steinert P.M., Parry D.A.D., Idler W.W., Johnson L.D., Steven A.C.,
RA Roop D.R.;
RT "Amino acid sequences of mouse and human epidermal type II keratins of
RT Mr 67,000 provide a systematic basis for the structural and functional
RT diversity of the end domains of keratin intermediate filament
RT subunits.";
RL J. Biol. Chem. 260:7142-7149(1985).
RN [6]
RP PROTEIN SEQUENCE OF 1-7.
RC TISSUE=Platelet;
RX MEDLINE=22608298; PubMed=12655801; DOI=10.1038/nbt810;
RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
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RT spectrometric identification of sorted N-terminal peptides.";
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RN [7]
RP CITRULLINATION
RX MEDLINE=96374388; PubMed=8780679; DOI=10.1006/bbrc.1996.1240;
RA Senshu T., Kan S., Ogawa H., Manabe M., Asaga H.;
RT "Preferential delamination of keratin K1 and filaggrin during the
RT terminal differentiation of human epidermis.";
RL Biochem. Biophys. Res. Commun. 225:712-719(1996).
RN [8]
RP VARIANT EHK PRO-160.
RX MEDLINE=92386601; PubMed=1381288; DOI=10.1016/0092-8674(92)90315-4;
RA Chipav C.C., Korge B.P., Markova N., Bale S.J., Digiovanna J.J.,
RA Compton J.G., Steinert P.M.;
RT "A leucine-->proline mutation in the H1 subdomain of keratin 1 causes
RT epidermolytic hyperkeratosis.";
RL Cell 70:821-828(1992).
RN [9]
RP VARIANT ALLELE 1B 559-GLY--TYR-565 DEL.
RX MEDLINE=93107743; PubMed=1281859; DOI=10.1111/1523-1747.epi2614149;
RA Korge B.P., Compton J.G., Steinert P.M., Mischke D.;
RT "The two size alleles of human keratin 1 are due to a deletion in the
RT glycine-rich carboxyl-terminal V2 subdomain.";
RL J. Invest. Dermatol. 99:697-702(1992).
RN [10]
RP VARIANT EHK GLN-489.
RX MEDLINE=92376531; PubMed=1380725;
RA Rothnagel J.A., Dominy A.M., Dempsey L.D., Longley M.A.,
RA Greenhalgh D.A., Gagne T.A., Huber M., Frenk E., Hohl D., Roop D.R.;
RT "Mutations in the rod domains of keratins 1 and 10 in epidermolytic
RT hyperkeratosis.";
RL Science 257:1128-1130(1992).
RN [11]
RP VARIANT EHK CYS-481.
RX MEDLINE=94216497; PubMed=7512983;
RA Syder A.J., Yu Q.-C., Paller A.S., Giudice G., Pearson R., Fuchs E.;
RT "Genetic mutations in the K1 and K10 genes of patients with

RT epidermolytic hyperkeratosis. Correlation between location and disease
RT severity.";
RL J. Clin. Invest. 93:1533-1542(1994).
RN [12]
RP VARIANTS EHK GLY-154; SER-187 AND PRO-192.
RX MEDLINE=94117869; PubMed=7507151; DOI=10.1111/1523-1747.ep12371725;
RA Yang J.-M., Chipev C.C., Digiovanna J.J., Bale S.J., Marekov L.N.,
RA Steinert P.M., Compton J.G. and J.G. domains in the keratin 1 gene in
RT "Mutations in the H1 and J1 domains in the keratin 1 gene in
RT epidermolytic hyperkeratosis";
RL J. Invest. Dermatol. 102:17-23(1994).
RN [13]
RP VARIANTS EHK PRO-185 AND SER-187.
RX MEDLINE=94117870; PubMed=7507152; DOI=10.1111/1523-1747.ep12371726;
RA McLean W.H.I., Eady R.A.J., Dopping-Hepenstal P.J.C., McMillan J.R.,
RA Leigh I.M., Navsaria H.A., Higgins C., Harper J.I., Paige D.G.,
RA Morley S.M.;
RT "Mutations in the rod 1A domain of keratins 1 and 10 in bullous
RT congenital ichthyosiform erythroderma (BCIE)";
RL J. Invest. Dermatol. 102:24-30(1994).
RN [14]
RP VARIANTS NEPPK ILE-73.
RX MEDLINE=95096501; PubMed=7528239; DOI=10.1111/1523-1747.ep12412771;
RA Kimonis V., Digiovanna J.J., Yang J.-M., Doyle S.Z., Bale S.J.,
RA Compton J.G.;
RT "A mutation in the V1 end domain of keratin 1 in non-epidermolytic
RT palmar-plantar keratoderma";
RL J. Invest. Dermatol. 103:764-769(1994).
RN [15]
RP VARIANTS EHK VAL-339.
RX MEDLINE=95072666; PubMed=9856846;
RX DOI=10.1046/j.1523-1747.1998.00389.x;
RA Kremer H., Lavrijssen A.P., McLean W.H.I., Lane E.B., Melchers D.,
RA Rutter D.J., Mariman E.C., Steijlen P.M.;
RT "An atypical form of bullous congenital ichthyosiform erythroderma is
RT caused by a mutation in the L12 linker region of keratin 1";
RL J. Invest. Dermatol. 111:1224-1226(1998).
RN [16]
RP VARIANTS AEI PHE-478 AND THR-478.
RX MEDLINE=99162195; PubMed=10053007;
RA Sybert V.P., Francis J.S., Corden L.D., Smith L.T., Weaver M.,
RA Stephens K., McLean W.H.I.;
RT "Cyclic ichthyosis with epidermolytic hyperkeratosis: a phenotype
RT conferred by mutations in the 2B domain of keratin K1";
RL Am. J. Hum. Genet. 64:732-738(1999).
RN [17]
RP VARIANTS EHK THR-187.
RX MEDLINE=99247363; PubMed=10232403;
RA Arin M.J., Longley M.A., Kuster W., Huber M., Hohl D., Rothnagel J.A.,
RA Roop D.R.;
RT "An asparagine to threonine substitution in the 1A domain of keratin
RT 1: a novel mutation that causes epidermolytic hyperkeratosis";
RL Exp. Dermatol. 8:124-127(1999).
RN [18]
RP VARIANTS AEI PHE-478.
RX MEDLINE=20062276; PubMed=10597140;
RA Michael E.J., Schneiderman P., Grossman M.E., Christiano A.M.;
RT "Epidermolytic hyperkeratosis with polycyclic psoriasiform plaques
RT resulting from a mutation in the keratin 1 gene";
RL Exp. Dermatol. 8:501-503(1999).
RN [19]
RP VARIANTS EHK PRO-213.
RX MEDLINE=20305470; PubMed=10844506;
RX DOI=10.1046/j.1365-2230.2000.00625.x;
RA Cserhalmi-Friedman P.B., Squeo R., Gordon D., Garzon M.,
RA Schneiderman P., Grossman M.E., Christiano A.M.;
RT "Epidermolytic hyperkeratosis in a Hispanic family resulting from a
RT mutation in the keratin 1 gene";
RL Clin. Exp. Dermatol. 25:241-243(2000).
RN [20]
RP VARIANTS EHK THR-478.
RX MEDLINE=20151078; PubMed=10688370;
RX DOI=10.1034/j.1600-0625.2000.009001016.x;

RA Arin M.J., Longley M.A., Epstein E.H. Jr., Rothnagel J.A., Roop D.R.;
RT "Identification of a novel mutation in keratin 1 in a family with
RT epidermolytic hyperkeratosis";
RL Exp. Dermatol. 9:16-19(2000).
RN [21]
RP VARIANTS EHK ASP-154.
RX MEDLINE=21423058; PubMed=11531804;
RX DOI=10.1046/j.1365-2133.2001.04327.x;
RA Whittock N.V., Ashton G.H.S., Griffiths W.A.D., Eady R.A.J.,
RA McGrath J.A.;
RT "New mutations in keratin 1 that cause bullous congenital
RT ichthyosiform erythroderma and keratin 2e that cause ichthyosis
RT bullosa of Siemens";
RL Br. J. Dermatol. 145:330-335(2001).
RN [22]
RP INVOLVEMENT IN IHCM.
RX MEDLINE=211184521; PubMed=11286616;
RX DOI=10.1046/j.1523-1747.2001.01292.x;

Query Match 91.1%; Score 41; DB 1; Length 643;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TNAENFV 9
Db 277 TNAENFV 284

RESULT 6
Q4L0E7 MOUSE
ID Q4L0E7 MOUSE PRELIMINARY; PRT; 222 AA.
AC Q4L0E7;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Type II cytokeratin Kb39 (Fragment).
GN Name=4732484G22Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NMRI; TISSUE=Tail skin;
RA Zimek A., Hesse M.;
RT "Cornea-specific cytochrome Kb3 seems to be absent in the rodent
RT lineage";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL: AY651826; AAV85505.1; -; mRNA.
DR MGI: 3588209; 4732484G22Rik.
DR GO: GO:0005882; C:intermediate filament; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR002957; Keratin I.
DR InterPro: PTHR1893.SF5; Keratin II.
DR PANTHER: PTHR1893.SF5; Keratin II; 1.
DR Pfam: PF00038; Filament; 1.
DR PRINTS: PR01248; TYPE1KERATIN.
DR PRINTS: PR01276; TYPE2KERATIN.
KW Keratin.
FT NON_TER 1 222
SQ SEQUENCE 222 AA; 25801 MW; 483B4F5890332C1D1 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 222;
Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TNAENFV 9

```

Db          78 TNAENDFV 85
|||||:|
RESULT 7
Q678L1_MOUSE
ID Q678L1_MOUSE PRELIMINARY; PRT; 224 AA.
AC Q678L1_MOUSE PRELIMINARY; PRT; 224 AA.
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 12.
DE Keratin 1b (Fragment).
GN Names=4732484G22Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NMRI; TISSUE=Tail skin;
RA Zimek A., Hesse M., Magin T., Weber K.;
RT "Homologies between the human, mouse and rat keratin-clusters.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; AY379112; AAR23390.1; -; mRNA.
DR Ensembl; ENSMUSG0000067594; Mus musculus.
DR MGI; MGI:3588209; 4732484G22Rik.
DR GO; GO:0005982; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR18893:SF5; Keratin_II; 1.
DR PRINTS; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
KW Keratin.
FT NON TER 1 1
FT NON TER 224 224
SQ SEQUENCE 224 AA; 25995 MW; DD6F783B4F589032 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 224;
Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNAENEFV 9
|||||:|
Db 78 TNAENDFV 85

RESULT 8
K2C1B_MOUSE
ID K2C1B_MOUSE STANDARD; PRT; 572 AA.
AC Q61F26;
DT 24-MAY-2005, integrated into UniProtKB/Swiss-Prot.
DT 05-JUL-2004, sequence version 1.
DE Keratin, type II cytoskeletal 1b.
DE Keratin, type II cytoskeletal 1b (Type II keratin Kb39) (Embryonic
DE type II keratin-1).
GN Name=Krt1b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG The mouse genome sequencing consortium;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

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RN [2]
RP PARTIAL PROTEIN SEQUENCE, IDENTIFICATION, AND CITRULLINATION.
RC STRAIN=C57BL/6; TISSUE=Epidermis;
RX PubMed=15619433; DOI=10.1016/j.jdermsci.2004.07.003;
RA Senzhu T., Ishida-Yamamoto A., Takahashi H., Iizuka H.;
RT "Prediction of a coding sequence for a novel type II keratin from N-
RT terminal sequences of mouse epidermal proteins site-specifically
RT deaminated in embryonic development.";
RL J. Dermatol. Sci. 37:41-48(2005).
RN [3]
RP IDENTIFICATION, AND TISSUE SPECIFICITY.
RX MEDLINE=23257644; PubMed=15085952; DOI=10.1078/0171-9335-00354;
RA Hesse M., Zimek A., Weber K., Magin T.M.;
RT "Comprehensive analysis of keratin gene clusters in humans and
RT rodents.";
RL Eur. J. Cell Biol. 83:19-26(2004).
CC -!- TISSUE SPECIFICITY: Expressed in stratified epithelia.
CC -!- PTM: Undergoes deamination of some arginine residues
CC (citrullination).
CC -!- MISCELLANEOUS: There are two types of cytoskeletal and
CC microfibrillar keratin: I (acidic; 40-55 kDa) [K9 to K20] and II
CC (neutral to basic; 56-70 kDa) [K1 to K8].
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----
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CC -----
DR EMBL; CAAA01098975; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR EMBL; CAAA01098987; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR EMBL; BK005256; DAA05633.1; -; mRNA.
DR EMBL; BK003993; DAA02234.1; -; mRNA.
DR MGI; MGI:3588209; 4732484G22Rik.
DR InterPro; IPR001664; IF.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR18893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Citrullination; Coiled coil; Direct protein sequencing;
KW Intermediate filament; Keratin; Phosphorylation.
FT CHAIN 1 572
FT Keratin, type II cytoskeletal 1b.
FT /FTID=PRO_0000063712.
FT REGION 1 166
FT REGION 167 476
FT REGION 167 476 Rod.
FT REGION 203 221 Coiled 1A.
FT REGION 203 221 Linker 1.
FT REGION 222 313 Coiled 1B.
FT REGION 314 337 Linker 12.
FT REGION 338 476 Coiled 2.
FT REGION 477 568 Tail.
FT SITE 420 420 Stutter.
FT MOD_RES 55 55 Phosphoserine (By similarity).
SQ SEQUENCE 572 AA; 61359 MW; 4D6A8BEC8E250096 CRC64;

Query Match 84.4%; Score 38; DB 1; Length 572;
Best Local Similarity 87.5%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNAENEFV 9
|||||:|
Db 265 TNAENDFV 272

RESULT 9
Q63ER5_BACCCZ
ID Q63ER5_BACCCZ PRELIMINARY; PRT; 869 AA.
AC Q63ER5;
DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Hypothetical protein yhgE.
DE Names=yhgE; OrderedLocustNames=BCE33L0996;
GN Bacillus cereus (strain ZK / E33L).

```



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OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=28661;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Brettn T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; CP000001; AAU19250.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 869 AA; 92188 MW; 1B8C5CFD50572342 CRC64;

Query Match      84.4%; Score 38; DB 2; Length 869;
Best Local Similarity 87.5%; Pred. No. 81;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 TNAENEFV 9
Db 483 TNAQNEFV 490
|||||

RESULT 10
O81U13 BACAN
ID O81U13 BACAN PRELIMINARY; PRT; 869 AA.
AC O81U13; 061298; 06KW31.
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Hypothetical protein.
DE OrderedLocusNames=BA1081, BAS1009, GBAA1081; ORFNames=BA_1081;
GN Bacillus anthracis.
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Ostad O.A., Helgason E., Rillstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Raunio D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RA "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86 (2003).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Ames ancestor;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Stearie;
RA Brettn T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus anthracis Sterne.";

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RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AE016879; AAP25060.1; -; Genomic DNA.
DR EMBL; AE017334; AAT30181.1; -; Genomic DNA.
DR EMBL; AE017225; AAT53333.1; -; Genomic DNA.
DR TIGR; BAI081; -.
DR TIGR; GBAA1081; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 869 AA; 92270 MW; 1466959BF791FA41 CRC64;

Query Match      84.4%; Score 38; DB 2; Length 869;
Best Local Similarity 87.5%; Pred. No. 81;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 TNAENEFV 9
Db 483 TNAQNEFV 490
|||||

RESULT 11
O5H887 NEIGO
ID O5H887 NEIGO PRELIMINARY; PRT; 207 AA.
AC O5H887;
DT 01-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Fructose-1,6-bisphosphatase (Fragment).
DE Name=fbp;
GN Neisseria gonorrhoeae.
OS Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NID103;
RA Takahashi H., Watanabe H.;
RT "The pseudogenes highly homologous to Neisseria meningitidis ggt gene
RT encoding gamma-glutamyl aminopeptidase in the related species:
RT Implication for the molecular evolution of the meningococcal ggt
RT gene";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AB175034; BAD89030.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0042578; F:phosphoric ester hydrolase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR000146; In_Fb_phptase.
DR Pfam; PF00316; FBPase; I.
DR PRINTS; PR00115; FBPHTASE.
DR PRINTS; PR00377; INFBPHPTASE.
DR ProDom; PD001491; In_Fb_phptase; 1.
KW Carbohydrate metabolism; Hydrolase.
FT NON TER 1
SQ SEQUENCE 207 AA; 23183 MW; F57B82163CA7FC24 CRC64;

Query Match      80.0%; Score 36; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 NAENEFV 9
Db 58 NAENEFV 64
|||||

RESULT 12
O9JUL6 NEIMA
ID O9JUL6 NEIMA PRELIMINARY; PRT; 324 AA.

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AC Q9JUL6;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 21-FEB-2006, entry version 26.
DE Putative fructose-1,6-bisphosphatase (EC 3.1.3.11).
GN Name=fbp; OrderedLocusNames=NMA1259;
OS Neisseria meningitidis serogroup A.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;

RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=22491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Felwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajadream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis 22491."
RL Nature 404:502-506(2000).
CC -----
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CC -----
DR EMBL; AL162755; CAB84514.1; -; Genomic_DNA.
DR PIR; A81894; A81894.
DR HSSP; P46275; 1DBZ.
DR BioCyc; NMEN65699:NMA1259-MONOMER; -.
DR GO; GO:0042132; F:fructose-bisphosphatase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0043578; F:phosphoric ester hydrolase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR000146; In_FBP_phptase.
DR Pfam; PF00316; FBPase; 1.
DR PRINTS; PR00115; FBPHPTASE.
DR PRINTS; PR00377; INFBPHPTASE.
DR ProDom; PD001491; In_FBP_phptase; 1.
DR Carbohydrate metabolism; Complete proteome; Hydrolase.
KW Carbohydrate metabolism; Complete proteome; Hydrolase.
SQ SEQUENCE 324 AA; 35551 MW; 5F148C8C4AF4B4A9 CRC64;

Query Match 80.0%; Score 36; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NAENEFV 9
DB 175 NAENEFV 181

RESULT 13
Q9JZH1 NEIMB Q9JZH1 NEIMB PRELIMINARY; PRT; 324 AA.
AC Q9JZH1;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 21-FEB-2006, entry version 25.
DE Fructose-1,6-bisphosphatase (EC 3.1.3.11).
GN Name=fbp; OrderedLocusNames=NMB1060;
OS Neisseria meningitidis serogroup B.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;

RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=WC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Eden J.F.,
RA Dodson R.G., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,

AC Q9JUL6;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 21-FEB-2006, entry version 26.
DE Putative fructose-1,6-bisphosphatase (EC 3.1.3.11).
GN Name=fbp; OrderedLocusNames=NMA1259;
OS Neisseria meningitidis serogroup A.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;

RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=22491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Felwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajadream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis 22491."
RL Nature 404:502-506(2000).
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CC -----
DR EMBL; AL162755; CAB84514.1; -; Genomic_DNA.
DR PIR; A81894; A81894.
DR HSSP; P46275; 1DBZ.
DR BioCyc; NMEN65699:NMA1259-MONOMER; -.
DR GO; GO:0042132; F:fructose-bisphosphatase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0043578; F:phosphoric ester hydrolase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR000146; In_FBP_phptase.
DR Pfam; PF00316; FBPase; 1.
DR PRINTS; PR00115; FBPHPTASE.
DR PRINTS; PR00377; INFBPHPTASE.
DR ProDom; PD001491; In_FBP_phptase; 1.
DR Carbohydrate metabolism; Complete proteome; Hydrolase.
KW Carbohydrate metabolism; Complete proteome; Hydrolase.
SQ SEQUENCE 324 AA; 35551 MW; 5F148C8C4AF4B4A9 CRC64;

Query Match 80.0%; Score 36; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NAENEFV 9
DB 175 NAENEFV 181

RESULT 14
Q5F8C3 NEIG1 Q5F8C3 NEIG1 PRELIMINARY; PRT; 324 AA.
AC Q5F8C3;
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 15-MAR-2005, sequence version 1.
DT 07-MAR-2006, entry version 9.
DE Putative fructose-bisphosphatase (EC 3.1.3.11).
GN OrderedLocusNames=NGO0862;
OS Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=24231;

RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Lewis L.A., Gillaspay A.F., McLaughlin R.E., Gibson M., Ducey T.F.,
RA Ownbey T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,
RA Song L., Lin S., Yuan X., Najjar F., Zhan M., Ren Q., Zhu H., Qi S.,
RA Kenton S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;
RT "The complete genome sequence of Neisseria gonorrhoeae."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AE004969; AAW9564.1; -; Genomic_DNA.
DR GenomeReviews; AE004969_GR; NGO0862.
DR GO; GO:0042132; F:fructose-bisphosphatase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0043578; F:phosphoric ester hydrolase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR000146; In_FBP_phptase.
DR Pfam; PF00316; FBPase; 1.

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DR PIRSF: PIRSF000904; FBPTase_SBPase; 1.
DR PRINTS; PRO0115; FBPHPTASE.
DR PRINTS; PRO0377; INFBPHPTASE.
DR ProDom; PD001491; In_FB_phptase; 1.
KW Carbohydrate metabolism; Complete proteome; Hydrolase.
SQ SEQUENCE 324 AA; 35474 MW; 013500A67852B411 CRC64;

Query Match 80.0%; Score 36; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NAENEV 9
Db 175 NAENEV 181

RESULT 15
Q919P5 RANCA
ID Q919P5 RANCA PRELIMINARY; PRT; 529 AA.
AC Q919P5
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Inner-ear cytokesterin.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;
OC Aquarana.
OX NCBI_TaxID=8400;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Inner-ear;
RX MEDLINE=20243794; PubMed=10758152; DOI=10.1073/pnas.070050797;
RA Cyr J.L., Bell A.M., Hudspeth A.J.;
RT "Identification with a recombinant antibody of an inner-ear
cytokesterin, a marker for hair-cell differentiation.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4908-4913(2000).
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----
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CC -----
DR EMBL; AF229168; AAF34720.1; -; mRNA.
DR HSSP; P08670; ICK7.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin I.
DR InterPro; IPR003054; Keratin II.
DR PANTHER; PTHR18893.SFS; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PRO1248; TYPE1KERATIN.
DR PRINTS; PRO1276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament.
SQ SEQUENCE 529 AA; 56619 MW; 3B6125D4AAEC108E CRC64;

Query Match 80.0%; Score 36; DB 2; Length 529;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSAENEV 9
Db 230 TSAENEV 237

Search completed: July 5, 2006, 19:01:30
Job time : 93.1971 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 18:28:26 ; Search time 78.2039 Seconds

(without alignments)
52.618 Million cell updates/sec

Title: US-10-774-928A-8

Perfect score: 45

Sequence: 1 ATNAENEFV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq 8:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

9: Geneseqp2005s:*

10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	6	AAO26388 Psoriasis
2	45	100.0	9	9	ADV04413 Leishmani
3	41	91.1	11	6	ABG74868 Human cyt
4	41	91.1	113	6	ABG74871 Human cyt
5	41	91.1	628	8	ADG85115 Mouse ato
6	41	91.1	643	6	ABG74869 Human cyt
7	41	91.1	644	8	ADQ17549 Human sof
8	41	91.1	644	9	AEA15501 Human pol
9	36	80.0	11	4	AAU28642 DPI tript
10	36	80.0	11	4	AAU26290 Depressio
11	36	80.0	324	8	ADJ49030 Oil-asso
12	36	80.0	324	8	ADJ50324 Oil-asso
13	36	80.0	395	6	ABP79368 N. gonorr
14	36	80.0	583	6	ABU26459 Protein e
15	36	80.0	600	9	AEA15488 Human pol
16	35	77.8	11	4	AAU68144 Human Bre
17	35	77.8	11	4	AAU68118 Human Bre
18	35	77.8	11	4	AAU68063 Human Bre
19	35	77.8	11	4	AAU68448 Human Bre
20	35	77.8	20	9	AED42280 Human str
21	35	77.8	342	7	ADE15641 Human the
22	35	77.8	508	8	ADS10914 Human the
23	35	77.8	521	5	ABG94649 Human NOV

24	35	77.8	521	7	ADL36002 Human NOV
25	35	77.8	526	5	ABJ04655 Protein o
26	35	77.8	529	5	ABB83482 Human cyt
27	35	77.8	529	9	AEA15497 Human pol
28	35	77.8	536	5	ABJ04646 Protein o
29	35	77.8	540	9	AEA15499 Human pol
30	35	77.8	543	9	AEA20229 Novel hum
31	35	77.8	567	7	ADB5618 Human pro
32	35	77.8	590	7	ADB70328 Keratin 5
33	35	77.8	590	7	ADB75394 Prostate
34	35	77.8	590	8	ADJ37107 Human mal
35	35	77.8	590	8	ADR99136 Keratin 5
36	35	77.8	590	9	AEA15495 Human pol
37	35	77.8	590	9	AE887738 Human cyt
38	35	77.8	601	8	ADM07163 Bos tauru
39	35	77.8	602	6	ABR41632 Human DIT
40	34	75.6	271	5	AAU96118 Ehrlichia
41	34	75.6	341	5	ABB54677 Lactococc
42	34	75.6	341	8	ADS29399 Bacterial
43	34	75.6	659	6	ABU35613 Protein e
44	34	75.6	872	6	ABP76774 N. gonorr
45	34	75.6	886	6	ABP79007 N. gonorr

ALIGNMENTS

RESULT 1

AAO26388

ID AAO26388 standard; peptide; 9 AA.

AC AAO26388;

XX 30-JAN-2003 (first entry)

XX Psoriasis treating immunotherapeutic peptide, SEQ ID No 8.

XX Antipsoriatic; immunostimulant; gene therapy; pharmaceutical composition;

KW vaccine; immunogenic variant; immunotherapeutic agent; psoriasis;

KW gene therapy.

XX Leishmania sp.

XX OS

XX WO200274239-A2.

XX 26-SEP-2002.

XX 04-MAR-2002; 2002WO-US006496.

XX 16-MAR-2001; 2001US-00809003.

PR (AKIV-) AKIVA LLC.

XX O'daly JA;

XX WPI; 2003-018763/01.

XX New polypeptide and immunogenic variants comprising amino acid sequences

PT of particulate antigens, useful for the treatment and clinical remission

PT of psoriasis.

XX Claim 1; Page 43; 56pp; English.

XX The invention relates to a polypeptide comprising an isolated amino acid

CC sequence or immunogenic variants selected from any of 14 fully defined

CC sequences of 7-16 amino acids, given in the specification. The

CC immunotherapeutic agents and a pharmaceutical compositions comprising

CC polynucleotides and vectors of the invention are useful for the treatment

CC and clinical remission of psoriasis. The isolated nucleic acids are

CC useful as probes. The sequences of the invention can be used in the

CC treatment of disorders by gene therapy. This sequence represents one of

CC the 14 immunotherapeutic peptides of the invention

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 45; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATNAINEFV 9
 |||||

Db 1 ATNAINEFV 9

RESULT 2

ADV04413
 ID ADV04413 standard; peptide; 9 AA.

XX ADV04413;

XX 24-FEB-2005 (first entry)

DE Leishmania immunotherapeutic peptide SEQ ID NO:8.

XX T-lymphocyte; immunogenicity; antigen; antiprosoratic; immunostimulant;
 psoriasis.

OS Leishmania sp.

XX US2004241168-A1.

XX 02-DEC-2004.

XX 09-FEB-2004; 2004US-00774928.

XX 16-MAR-2001; 2001US-00809003.

PR 17-OCT-2003; 2003US-00687892.

XX (ODAL/) ODALY J A.

PA Odaly JA;

XX WPI; 2005-011563/01.

DR Inhibiting selectively T-cell rolling in human, by administering compound
 PT interfering with cutaneous lymphocyte antigen-E selectin interaction and
 PT leukocyte function associated antigen-1 interaction.

XX Claim 18; SEQ ID NO 8; 21pp; English.

XX The invention relates to a novel method for selectively inhibiting T-cell
 CC rolling in a human host, comprising administering a compound that
 CC selectively interferes with the cutaneous lymphocyte antigen (CLA)-E
 CC selectin interaction and leukocyte function associated antigen (LFA)-
 CC 1/intercellular adhesion molecule (ICAM) and very late antigen
 CC (VLA)/vascular cell adhesion molecule (VCAM) interactions. The compound
 CC includes an immunotherapeutic agent, which comprises a purified protein
 CC extract that is isolated by diethylaminoethyl Sephadex chromatography of
 CC a Nonidet P-40 insoluble particulate antigen fraction derived from
 CC isolated killed cells of amastigotes from one or more species of the
 CC Leishmania genus, where the particulate antigen fraction is solubilized
 CC with 8M urea and 0.025 M Tris(hydroxymethyl)aminomethane pH 8.3 applied
 CC to diethylaminoethyl Sephadex and is eluted with a solution comprising
 CC 0.1 M sodium chloride, 8 M urea and 0.025 M
 CC Tris(hydroxymethyl)aminomethane pH 8.3, and the purified protein extract
 CC includes polypeptides having apparent molecular weights of 73, 80 and 82
 CC kDa, after total reduction and alkylation. The species is L. amazonensis ,
 CC L. venezuelensis , L. brasiliensis and/or L. chagasi. A compound of the
 CC invention has antiprosoratic and immunostimulant activity, and inhibits T-
 CC cell rolling by interfering with CLA-E selectin interaction and LFA-
 CC 1/ICAM and VLA/VCAM interactions. The method is useful for selectively
 CC inhibiting T-cell rolling in a human host, and for treating psoriasis.
 CC The present sequence represents a Leishmania peptide used in the
 CC invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 45; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATNAINEFV 9
 |||||

Db 1 ATNAINEFV 9

RESULT 3

ABG74868
 ID ABG74868 standard; peptide; 11 AA.

XX AC ABG74868;

XX 19-JUN-2003 (first entry)

DE Human cytokeraatin-1 associated peptide SEQ ID 2.

XX Cytokeratin-1; inflammation; infection; soluble; sepsis; veterinary;
 KW sepsis-like systemic infection; human.

XX Homo sapiens.

XX WO2003002600-A1.

XX 09-JAN-2003.

XX 12-JUN-2002; 2002WO-EP006473.

XX 27-JUN-2001; 2001DE-01030985.

PA (BRAH-) BRAHMS AG.

XX Bergmann A, Struck J, Uehlein M;

XX WPI; 2003-201491/19.

XX New use of soluble cytokeraatin-1 fragments from body fluid are tissue as
 PT marker peptides or to provide therapeutics for the diagnosis, prognosis
 PT and treatment of inflammatory disease and infection, including systemic
 PT inflammation.

XX Disclosure; Page 38; 51pp; German.

XX This invention describes a novel use of soluble cytokeraatin-1 fragments
 CC from body fluid or tissue as marker peptides for the detection, prognosis
 CC and control of inflammation and infection or as a therapeutic target for
 CC inflammation and infection. The invention also describes a method of
 CC producing a soluble cytokeraatin-1 fragment in rich or pure form from a
 CC human material rich in cytokeraatin-1 by enzymatically splitting the
 CC cytokeraatin-1 with endoprotease to obtain the hydrolysis products and
 CC purifying the resulting fragments. The novel cytokeraatin fragments are
 CC useful for the differential diagnosis, early recognition and prognosis,
 CC evaluation of severity of sepsis and heavy infection, particularly sepsis
 CC -like systemic infection. The fragments are used in human and veterinary
 CC therapy, particularly the fragment or it's specific antibody is used to
 CC treat inflammatory disease or infection. This sequence represents a
 CC cytokeraatin-1 associated peptide described in the disclosure of the
 CC invention

XX Sequence 11 AA;

Query Match 91.1%; Score 41; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNAINEFV 9
 |||||

Db 1 TNAINEFV 8

RESULT 4

ABG74871
ID ABG74871 standard; protein; 113 AA.

XX AC ABG74871;

XX DT 19-JUN-2003 (first entry)

XX DE Human cytokerin-1 protein fragment.

XX KW Cytokeratin-1; inflammation; infection; soluble; sepsis; veterinary;
XX KW sepsis-like systemic infection; human.

XX OS Homo sapiens.

XX PN WO2003002600-A1.

XX PD 09-JAN-2003.

XX PF 12-JUN-2002; 2002WO-EP006473.

XX PR 27-JUN-2001; 2001DE-01030985.

XX PA (BRAH-) BRAHMS AG.

XX PI Bergmann A, Struck J, Uehlein M;

XX DR WPI; 2003-201491/19.

XX PS New use of soluble cytokerin-1 fragments from body fluid are tissue as
XX PT marker peptides or to provide therapeutics for the diagnosis, prognosis
XX PT and treatment of inflammatory disease and infection, including systemic
XX PT inflammation.

XX Claim 4; Page 41; 51pp; German.

XX CC This invention describes a novel use of soluble cytokerin-1 fragments
XX CC from body fluid or tissue as marker peptides for the detection, prognosis
XX CC and control of inflammation and infection or as a therapeutic target for
XX CC inflammation and infection. The invention also describes a method of
XX CC producing a soluble cytokerin-1 fragment in rich or pure form from a
XX CC human material rich in cytokerin-1 by enzymatically splitting the
XX CC cytokerin-1 with endoprotease to obtain the hydrolysis products and
XX CC purifying the resulting fragments. The novel cytokerin fragments are
XX CC useful for the differential diagnosis, early recognition and prognosis,
XX CC evaluation of severity of sepsis and heavy infection, particularly sepsis
XX CC -like systemic infection. The fragments are used in human and veterinary
XX CC therapy, particularly the fragment or its specific antibody is used to
XX CC treat inflammatory disease or infection. This sequence represents the
XX CC human cytokerin-1 protein fragment described in the disclosure of the
XX CC invention

XX SQ Sequence 113 AA;

Query Match 91.1%; Score 41; DB 6; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.1;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNAENEFV 9

DB 93 TNAENEFV 100
|||||

RESULT 5

AD85115
ID AD85115 standard; protein; 628 AA.

XX AC AD85115;

XX DT 18-NOV-2004 (first entry)

XX DE Mouse atopic dermatitis-related protein sequence SeqID117.

KW atopic dermatitis; gene expression level; skin; inflammation; rash;
KW dermatological; antiinflammatory; antipsoriatic; psoriasis; mouse;
KW murine.

XX OS Mus musculus.

XX PN WO2004031386-A1.

XX PD 15-APR-2004.

XX PF 01-AUG-2003; 2003WO-JP009808.

XX PR 06-AUG-2002; 2002JP-00229318.

XX PR 14-MAY-2003; 2003JP-00136543.

XX PA (GENO-) GENOX RES INC.

XX PA (UYJU-) UNIV JUNTENDO.

XX PI Itoh M, Ogawa K, Shinagawa A, Sudo H, Ogawa H, Ra C;

XX PI Mitsuishi K,

XX DR WPI; 2004-330185/30.

XX DR N-PSDB; ADS85114.

XX PT Determination of difference in expression level of specified genes in
XX PT inflamed and non-inflamed skin sites for diagnosis and examination of
XX PT atopic dermatitis and psoriasis.

XX Example 1; SEQ ID NO 117; 611pp; Japanese.

XX CC This invention relates to a novel method for the examination of atopic
XX CC dermatitis in which the expression level of specified genes in specimens
XX CC of skin taken from inflamed (rash) areas and non-inflamed areas is
XX CC compared and the presence of increased or reduced expression in the
XX CC inflamed areas determined. The invention may be useful for the
XX CC development of compounds with a dermatological, antiinflammatory or
XX CC antipsoriatic activity acting as inhibitors and stimulators of genes
XX CC involved in atopic dermatitis and psoriasis. The invention may be useful
XX CC for treatment, prevention, diagnosis and assessment of atopic dermatitis
XX CC and psoriasis. The present sequence is that of an atopic dermatitis-
XX CC related protein which was used in the exemplification of the invention.

XX SQ Sequence 628 AA;

Query Match 91.1%; Score 41; DB 8; Length 628;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNAENEFV 9

DB 286 TNAENEFV 293
|||||

RESULT 6

ABG74869

ID ABG74869 standard; protein; 643 AA.

XX AC ABG74869;

XX DT 19-JUN-2003 (first entry)

XX DE Human cytokerin-1 protein.

XX KW Cytokeratin-1; inflammation; infection; soluble; sepsis; veterinary;
XX KW sepsis-like systemic infection; human.

XX OS Homo sapiens.

XX PN WO2003002600-A1.

XX PD 09-JAN-2003.

XX PF 12-JUN-2002; 2002WO-EP006473.

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XX 27-JUN-2001; 2001DE-01030985.
XX (BRAH-) BRAHMS AG.
XX Bergmann A, Struck J, Uehlein M;
XX WPI; 2003-201491/19.
XX New use of soluble cytokeratin-1 fragments from body fluid are tissue as
XX marker peptides or to provide therapeutics for the diagnosis, prognosis
XX and treatment of inflammatory disease and infection, including systemic
XX inflammation.
XX Claim 3; Page 38-40; 51pp; German.
XX This invention describes a novel use of soluble cytokeratin-1 fragments
XX from body fluid or tissue as marker peptides for the detection, prognosis
XX and control of inflammation and infection or as a therapeutic target for
XX inflammation and infection. The invention also describes a method of
XX producing a soluble cytokeratin-1 fragment in rich or pure form from a
XX human material rich in cytokeratin-1 by enzymatically splitting the
XX cytokeratin-1 with endoprotease to obtain the hydrolysis products and
XX purifying the resulting fragments. The novel cytokeratin fragments are
XX useful for the differential diagnosis, early recognition and prognosis,
XX evaluation of severity of sepsis and heavy infection, particularly sepsis
XX -like systemic infection. The fragments are used in human and veterinary
XX therapy, particularly the fragment or it's specific antibody is used to
XX treat inflammatory disease or infection. This sequence represents the
XX human cytokeratin-1 protein described in the disclosure of the invention
XX
XX Sequence 643 AA;
XX
Query Match          91.1%; Score 41; DB 6; Length 643;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TNAENEV 9
Db      277 TNAENEV 284
      |||||
RESULT 7
ID ADQ17549 standard; protein; 644 AA.
XX
XX ADQ17549;
AC
XX
XX ADQ17549;
XX
XX 26-AUG-2004 (first entry)
XX Human soft tissue sarcoma-upregulated protein - SEQ ID 366.
XX
XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX
XX Homo sapiens.
XX
XX WO2004048938-A2.
XX
XX 10-JUN-2004.
XX
XX 26-NOV-2003; 2003WO-US038193.
XX
XX 26-NOV-2002; 2002US-0429739P.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Aziz N, Ginsburg WM, Zlotnik A;
XX
XX WPI; 2004-441208/41.
XX
XX Early detection of soft tissue sarcoma comprises determining expression
XX of a gene in a first soft tissue sample and a normal soft tissue sample
XX and comparing the gene expression, also useful in treating soft tissue
XX
XX sarcoma.
XX Example 2; SEQ ID NO 366; 210pp; English.
XX
XX The invention relates to a novel method for detecting soft tissue sarcoma
XX which comprises obtaining a first soft tissue sample from an individual,
XX and a normal soft tissue sample from the same or different individual,
XX determining the expression of a gene in both samples and comparing the
XX expression of the gene in both soft tissue samples, where a higher level
XX of protein expression in the first soft tissue sample indicates the
XX presence of soft tissue sarcoma. The method of the invention has
XX cytostatic applications and may be useful for detecting soft tissue
XX sarcoma, possibly via gene therapy or vaccine production. The nucleic
XX acid sequences may be useful in diagnostic and screening applications.
XX The current sequence is that of a human soft tissue sarcoma-upregulated
XX protein of the invention. The current sequence is not shown within the
XX specification per se but was submitted in CD format by the inventor.
XX
XX Sequence 644 AA;
XX
Query Match          91.1%; Score 41; DB 8; Length 644;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TNAENEV 9
Db      278 TNAENEV 285
      |||||
RESULT 8
ID AEA15501 standard; protein; 644 AA.
XX
XX AEA15501;
AC
XX
XX 28-JUL-2005 (first entry)
XX Human polypeptide #120.
XX
XX Diagnosis; prognosis; cancer; breast tumor; ovary tumor; stomach tumor;
XX colon tumor; esophagus tumor; bladder tumor; non-small-cell lung cancer;
XX cytostatic; neoplasm.
XX
XX Homo sapiens.
XX
XX WO2005047534-A2.
XX
XX 26-MAY-2005.
XX
XX 15-OCT-2004; 2004WO-EP011599.
XX
XX 28-OCT-2003; 2003EP-00024565.
XX
XX (FARB ) BAYER HEALTHCARE AG.
XX
XX Wirtz R, Munnes M;
XX
XX WPI; 2005-372393/38.
XX
XX N-PSDB; AEA15423.
XX
XX Predicting a response to cancer treatment by detecting at least 2
XX markers, which are genes or genomic nucleic acid sequences that are
XX located on one chromosomal region, which is altered in malignant
XX neoplasia. The invention also relates to a method for the prediction,
XX diagnosis or prognosis of malignant neoplasia, methods for detecting
XX
XX Claim 7; SEQ ID NO 463; 464pp; English.
XX
XX The invention relates to a method of predicting response to cancer
XX treatment comprising detection of at least 2 markers, where the markers
XX are genes and fragments or genomic nucleic acid sequences that are
XX located on one chromosomal region, which is altered in malignant
XX neoplasia. The invention also relates to a method for the prediction,
XX diagnosis or prognosis of malignant neoplasia, methods for detecting
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CC deregulations in malignant neoplasia and breast cancer, a method of
 CC determining the phenotype of a cell or tissue, a method for identifying
 CC genomic regions which are altered on the chromosomal level and encode
 CC genes that are linked by function and are differentially expressed in
 CC malignant neoplasia and breast cancer, methods of screening for agents
 CC which regulate the activity of a polypeptide or a polynucleotide and
 CC antibodies that specifically bind to a full length or partial
 CC polypeptide. The method is useful for predicting response to cancer
 CC treatment. The methods and compositions are useful for predicting,
 CC diagnosing, prognosing, preventing or treating malignant neoplasia
 CC including breast cancer, ovarian cancer, gastric cancer, colon cancer,
 CC esophageal cancer, mesenchymal cancer, bladder cancer or non-small-cell
 CC lung cancer. This sequence represents a human polypeptide used in the
 CC scope of the invention.

XX Sequence 644 AA;

Query Match 91.1%; Score 41; DB 9; Length 644;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNAENEFV 9
 |||||
 Db 278 TNAENEFV 285

RESULT 9
 AAU28642
 ID AAU28642 standard; peptide; 11 AA.

XX

AC AAU28642;

XX 03-JAN-2002 (first entry)

XX DPI tryptic digest peptide #239.

XX Human; depression associated protein isoform; tryptic digest peptide;
 XX DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
 XX neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
 XX maniac-depressive illness; schizoaffective disorder.

XX Homo sapiens.

XX WO200162787-A1.

XX 30-AUG-2001.

XX 23-FEB-2001; 2001WO-GB000786.

XX 24-FEB-2000; 2000GB-00004412.

XX 08-DEC-2000; 2000GB-00030050.

XX 12-DEC-2000; 2000US-0254830P.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Herath HMAc, Parekh RB, Rohlf C, Terrett JA, Tyson KL;

XX WPI; 2001-570626/64.

XX Novel nucleic acid encoding a protein associated with bipolar affective
 PT disorder, which is used for diagnosis, prophylaxis and therapy of
 PT neuropsychiatric disorders, such as bipolar affective disorder.

XX Disclosure; Page 36; 153pp; English.

XX The present invention relates to the identification of depression
 CC associated protein isoforms (DPIs), particularly the tryptic digest
 CC peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)
 CC described are decreased in the cerebrospinal fluid (CSF) of BAD (bipolar
 CC affective disorder) subjects, whilst other DPIs (AAU28626-AAU28887) are
 CC increased in BAD subjects. Also described are peptide sequences
 CC identified from DPI-45 and DPI-213 and the nucleic acid sequence they are
 CC encoded by. The sequences of the invention are useful for clinical

CC screening, diagnosis, prognosis, therapy and prophylaxis of
 CC neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder,
 CC BP), maniac-depressive illnesses, attention deficit disorders,
 CC schizoaffective disorders, and unipolar affective disorders. The present
 CC sequence represents one of the DPI tryptic digest peptides of the present
 CC invention

XX Sequence 11 AA;

Query Match 80.0%; Score 36; DB 4; Length 11;
 Best Local Similarity 87.5%; Pred. No. 1.9;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNAENEFV 9
 |||||
 Db 1 TDAENEFV 8

RESULT 10

AAU26290
 ID AAU26290 standard; peptide; 11 AA.

XX

AC AAU26290;

XX 18-DEC-2001 (first entry)

XX Depression-Associated Protein isoform DPI-60.

XX Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;
 KW DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;
 KW CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;
 KW attention deficient disorder; schizoaffective disorder;
 KW unipolar affective disorder.

XX Homo sapiens.

XX WO200163294-A2.

XX 30-AUG-2001.

XX 23-FEB-2001; 2001WO-GB000791.

XX 24-FEB-2000; 2000GB-00004412.

XX 08-DEC-2000; 2000GB-00030050.

XX 12-DEC-2000; 2000US-0254830P.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Herath HMAc, Parekh RB, Rohlf C;

XX WPI; 2001-582081/65.

XX Preparation for diagnosing or treating bipolar affected disorder (BAD) or
 PT unipolar depression, or for screening for modulators, comprises a BAD-
 PT associated protein isoform.

XX Claim 8; Page 36; 163pp; English.

XX The invention relates to a preparation comprising an isolated Bipolar
 CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are
 CC used to screen, diagnose or prognosis of BAD or unipolar depression,
 CC determine the stage or severity of BAD or unipolar depression, identify a
 CC subject at risk of developing BAD or unipolar depression, or monitor the
 CC effect of therapy in a subject. They are also used to screen for or
 CC identify agents that interact with a DPI. These agents, antibodies
 CC against the DPIs, and nucleic acids encoding the DPIs are used to treat
 CC or prevent BAD or unipolar depression. Diseases that can be treated are
 CC attention deficient disorder, a schizoaffective disorder, a bipolar or a
 CC unipolar affective disorder. The DPIs are used in proteomics. The
 CC proteomic approach of using DPIs for screening, diagnosis or prognosis of
 CC BAD or unipolar depression overcomes the problems of using gene
 CC expression analysis, such as not being able to obtain central nervous
 CC system (CNS) tissue from a living patient under normal circumstances. The

CC present sequence is a DIP increased in the CSF (cerebro-spinal fluid) of
CC subjects having BAD

XX Sequence 11 AA;

Query Match 80.0%; Score 36; DB 4; Length 11;
Best Local Similarity 87.5%; Pred. No. 1.9;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNAENEFV 9
|:|||||
Db 1 TDAENEFV 8

RESULT 11

ADJ49030
ID ADJ49030 standard; protein; 324 AA.

XX AC ADJ49030;

XX DT 06-MAY-2004 (first entry)

XX DE Oil-associated gene related protein #530.

XX KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.

XX OS Unidentified.

XX PN US2004025202-A1.

XX PD 05-FEB-2004.

XX PF 14-MAR-2003; 2003US-00389566.

XX PR 15-MAR-2002; 2002US-0365301P.

XX PR 26-JUN-2002; 2002US-0391786P.

XX PR 26-JUN-2002; 2002US-0392018P.

XX PA (LAUR/) LAURIE C C.

XX PA (RAVA/) RAVANELLO M.

XX PA (SAVA/) SAVAGE T.

XX PA (LEDE/) LEDEAUX J R.

XX PA (ROGE/) ROGERS J A.

XX PI Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;

XX DR WPI; 2004-142683/14.

XX PT Novel recombinant DNA construct comprising a promoter functional in

XX plants operably linked to an oil-associated gene for producing transgenic

XX plant seed.

XX PS Example 3; SEQ ID NO 1034; 22pp; English.

XX CC The invention relates to a recombinant DNA construct comprising a

XX promoter functional in plants operably linked to an oil-associated gene.

XX CC The construct is useful for transgenic plant seed which has in its genome

XX the construct, that is functional in the plant to transcribe the oil-

XX associated gene. The transgenic plant seed grows into a plant having

XX enhanced seed oil as compared to wild type. The construct is useful for

XX CC producing hybrid maize seed. The transgenic plant seed is useful for

XX CC producing vegetable oil. The present sequence represents the amino acid

XX sequence of an oil-associated gene related protein.

XX Sequence 324 AA;

Query Match 80.0%; Score 36; DB 8; Length 324;

Best Local Similarity 100.0%; Pred. No. 67;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NAENEFV 9

|||||

Db 175 NAENEFV 181

RESULT 12

ADJ50324
ID ADJ50324 standard; protein; 324 AA.

XX AC ADJ50324;

XX DT 06-MAY-2004 (first entry)

XX DE Oil-associated gene related protein #1824.

XX KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.

XX OS Unidentified.

XX PN US2004025202-A1.

XX PD 05-FEB-2004.

XX PF 14-MAR-2003; 2003US-00389566.

XX PR 15-MAR-2002; 2002US-0365301P.

XX PR 26-JUN-2002; 2002US-0391786P.

XX PR 26-JUN-2002; 2002US-0392018P.

XX PA (LAUR/) LAURIE C C.

XX PA (RAVA/) RAVANELLO M.

XX PA (SAVA/) SAVAGE T.

XX PA (LEDE/) LEDEAUX J R.

XX PA (ROGE/) ROGERS J A.

XX PI Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;

XX DR WPI; 2004-142683/14.

XX PT Novel recombinant DNA construct comprising a promoter functional in

XX plants operably linked to an oil-associated gene for producing transgenic

XX plant seed.

XX PS Example 3; SEQ ID NO 2328; 22pp; English.

XX CC The invention relates to a recombinant DNA construct comprising a

XX promoter functional in plants operably linked to an oil-associated gene.

XX CC The construct is useful for transgenic plant seed which has in its genome

XX the construct, that is functional in the plant to transcribe the oil-

XX associated gene. The transgenic plant seed grows into a plant having

XX enhanced seed oil as compared to wild type. The construct is useful for

XX CC producing hybrid maize seed. The transgenic plant seed is useful for

XX CC producing vegetable oil. The present sequence represents the amino acid

XX sequence of an oil-associated gene related protein.

XX Sequence 324 AA;

Query Match 80.0%; Score 36; DB 8; Length 324;

Best Local Similarity 100.0%; Pred. No. 67;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NAENEFV 9

|||||

Db 175 NAENEFV 181

RESULT 13

ABP79368
ID ABP79368 standard; protein; 395 AA.

XX AC ABP79368;

XX DT 07-MAR-2003 (first entry)

XX DE N. gonorrhoeae amino acid sequence SEQ ID 5266.

XX Antibacterial; infection; vaccine; gene therapy.
XX Neisseria gonorrhoeae.
XX WO200279243-A2.
XX 10-OCT-2002.
XX 12-FEB-2002; 2002WO-IB002069.
XX 12-FEB-2001; 2001GB-00003424.
XX (CHIR-) CHIRON SPA.
XX Fontana MR, Pizza M, Massignani V, Monaci E;
XX WPI; 2003-058415/05.
XX N-PSDB; ABZ40338.
XX New protein from Neisseria gonorrhoeae, useful for the manufacture of a
PT medicament for treating or preventing N. gonorrhoeae infection.
XX Disclosure; Page 574; 815pp; English.
XX The present invention relates to proteins from Neisseria gonorrhoeae.
XX Also disclosed are the nucleic acid molecules encoding the proteins and
XX antibodies that specifically bind to the proteins. The composition
XX comprising the protein, nucleic acid or antibody is useful for the
XX manufacture of a medicament for treating or preventing N. gonorrhoeae
XX infection, this may be in the form of a vaccine or gene therapy.
XX Sequences given in records ABP76736-ABP81046 represent nucleic acid
XX molecules of the invention
XX
SQ Sequence 395 AA;
Query Match 80.0%; Score 36; DB 6; Length 395;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 NAENEV 9
Db 246 NAENEV 252
|||||
RESULT 14
ABU26459
ID ABU26459 standard; protein; 583 AA.
XX
XX AC ABU26459;
XX 19-JUN-2003 (first entry)
XX Protein encoded by Prokaryotic essential gene #11986.
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX Campylobacter jejuni.
XX WO200277183-A2.
XX 03-OCT-2002.
XX 21-MAR-2002; 2002WO-US009107.
XX 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948993.
XX 25-OCT-2001; 2001US-0342923P.
XX 08-FEB-2002; 2002US-00072851.
XX 06-MAR-2002; 2002US-0362699P.
XX (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Antibacterial; infection; vaccine; gene therapy.
XX Neisseria gonorrhoeae.
XX WO200279243-A2.
XX 10-OCT-2002.
XX 12-FEB-2002; 2002WO-IB002069.
XX 12-FEB-2001; 2001GB-00003424.
XX (CHIR-) CHIRON SPA.
XX Fontana MR, Pizza M, Massignani V, Monaci E;
XX WPI; 2003-058415/05.
XX N-PSDB; ABZ40338.
XX New protein from Neisseria gonorrhoeae, useful for the manufacture of a
PT medicament for treating or preventing N. gonorrhoeae infection.
XX Disclosure; Page 574; 815pp; English.
XX The present invention relates to proteins from Neisseria gonorrhoeae.
XX Also disclosed are the nucleic acid molecules encoding the proteins and
XX antibodies that specifically bind to the proteins. The composition
XX comprising the protein, nucleic acid or antibody is useful for the
XX manufacture of a medicament for treating or preventing N. gonorrhoeae
XX infection, this may be in the form of a vaccine or gene therapy.
XX Sequences given in records ABP76736-ABP81046 represent nucleic acid
XX molecules of the invention
XX
SQ Sequence 395 AA;
Query Match 80.0%; Score 36; DB 6; Length 395;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 NAENEV 9
Db 246 NAENEV 252
|||||
RESULT 14
ABU26459
ID ABU26459 standard; protein; 583 AA.
XX
XX AC ABU26459;
XX 19-JUN-2003 (first entry)
XX Protein encoded by Prokaryotic essential gene #11986.
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX Campylobacter jejuni.
XX WO200277183-A2.
XX 03-OCT-2002.
XX 21-MAR-2002; 2002WO-US009107.
XX 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948993.
XX 25-OCT-2001; 2001US-0342923P.
XX 08-FEB-2002; 2002US-00072851.
XX 06-MAR-2002; 2002US-0362699P.
XX (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Antibacterial; infection; vaccine; gene therapy.
XX Neisseria gonorrhoeae.
XX WO200279243-A2.
XX 10-OCT-2002.
XX 12-FEB-2002; 2002WO-IB002069.
XX 12-FEB-2001; 2001GB-00003424.
XX (CHIR-) CHIRON SPA.
XX Fontana MR, Pizza M, Massignani V, Monaci E;
XX WPI; 2003-058415/05.
XX N-PSDB; ABZ40338.
XX New protein from Neisseria gonorrhoeae, useful for the manufacture of a
PT medicament for treating or preventing N. gonorrhoeae infection.
XX Disclosure; Page 574; 815pp; English.
XX The present invention relates to proteins from Neisseria gonorrhoeae.
XX Also disclosed are the nucleic acid molecules encoding the proteins and
XX antibodies that specifically bind to the proteins. The composition
XX comprising the protein, nucleic acid or antibody is useful for the
XX manufacture of a medicament for treating or preventing N. gonorrhoeae
XX infection, this may be in the form of a vaccine or gene therapy.
XX Sequences given in records ABP76736-ABP81046 represent nucleic acid
XX molecules of the invention
XX
SQ Sequence 395 AA;
Query Match 80.0%; Score 36; DB 6; Length 583;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATNAENEV 9
Db 61 ASARNEV 69
|:|||||
RESULT 15
AEA15488
ID AEA15488 standard; protein; 600 AA.
XX
XX AC AEA15488;
XX 28-JUL-2005 (first entry)
XX Human polypeptide #107.
XX Diagnosis; prognosis; cancer; breast tumor; ovary tumor; stomach tumor;
XX colon tumor; esophagus tumor; bladder tumor; non-small-cell lung cancer;
XX cytostatic; neoplasm.
XX Homo sapiens.
XX WO2005047534-A2.
XX 26-MAY-2005.
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
XX N-PSDB; ACA30329.
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.
XX Claim 25; SEQ ID NO 54383; 1766pp; English.
XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX proliferation; (7) identifying a compound that influences the activity of
XX the gene product or that has an activity against a biological pathway
XX required for proliferation, or that inhibits cellular proliferation; (8)
XX identifying a gene required for cellular proliferation or the biological
XX pathway in which a proliferation-required gene or its gene product lies
XX on a gene on which the test compound that inhibits proliferation of an
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX compound's activity; (11) a culture comprising strains in which the gene
XX product is overexpressed or underexpressed; (12) determining the extent
XX to which each of the strains is present in a culture or collection of
XX strains; or (13) identifying the target of a compound that inhibits the
XX proliferation of an organism. The antisense nucleic acids are useful for
XX identifying proteins or screening for homologous nucleic acids required
XX for cellular proliferation to isolate candidate molecules for rational
XX drug discovery programs, or for screening homologous nucleic acids
XX K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
XX the target prokaryotic essential genes. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 583 AA;

```

XX 15-OCT-2004; 2004WO-EF011599.
PF
XX
XX 28-OCT-2003; 2003EP-00024565.
PR
XX
XX (FARB ) BAYER HEALTHCARE AG.
PA
XX
XX Wirtz R, Munnes M;
PI
XX
XX WPI; 2005-372393/38.
DR
XX N-PSDB; AEA15410.
DR
XX
PT Predicting a response to cancer treatment by detecting at least 2
PT markers, which are genes or genomic nucleic acid sequences that are
PT located on one chromosomal region, which is altered in malignant
PT neoplasia.
XX
XX Claim 7; SEQ ID NO 450; 464pp; English.
PS
XX
CC The invention relates to a method of predicting response to cancer
CC treatment comprising detection of at least 2 markers, where the markers
CC are genes and fragments or genomic nucleic acid sequences that are
CC located on one chromosomal region, which is altered in malignant
CC neoplasia. The invention also relates to a method for the prediction,
CC diagnosis or prognosis of malignant neoplasia, methods for detecting
CC deregulations in malignant neoplasia and breast cancer, a method of
CC determining the phenotype of a cell or tissue, a method for identifying
CC genomic regions which are altered on the chromosomal level and encode
CC genes that are linked by function and are differentially expressed in
CC malignant neoplasia and breast cancer, methods of screening for agents
CC which regulate the activity of a polypeptide or a polynucleotide and
CC antibodies that specifically bind to a full length or partial
CC polypeptide. The method is useful for predicting response to cancer
CC treatment. The methods and compositions are useful for predicting,
CC diagnosing, prognosing, preventing or treating malignant neoplasia
CC including breast cancer, ovarian cancer, gastric cancer, colon cancer,
CC esophageal cancer, mesenchymal cancer, bladder cancer or non-small-cell
CC lung cancer. This sequence represents a human polypeptide used in the
CC scope of the invention.
XX
SQ Sequence 600 AA;
Query Match 80.0%; Score 36; DB 9; Length 600;
Best Local Similarity 100.0%; Pred No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 NAENEV 9
Db 262 NAENEV 268
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Search completed: July 5, 2006, 18:43:51
Job time : 80.2039 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 20:38:52 ; Search time 65.8835 Seconds
(without alignments)
63.277 Million cell updates/sec

Title: US-10-774-928A-8

Perfect score: 45

Sequence: 1 ATNAENEFV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	5	US-10-774-928-8
2	41	91.1	11	5	US-10-480-848A-2
3	41	91.1	11	5	US-10-480-848A-5
4	41	91.1	643	5	US-10-480-848A-3
5	41	91.1	644	5	US-10-723-860-366
6	36	80.0	11	3	US-09-791-393-170
7	36	80.0	11	3	US-09-791-389-170
8	36	80.0	324	4	US-10-389-566-1034
9	36	80.0	324	4	US-10-389-566-2328
10	36	80.0	324	5	US-10-732-923-17878
11	36	80.0	324	5	US-10-732-923-17879
12	36	80.0	324	6	US-11-188-298-3960
13	36	80.0	324	6	US-11-188-298-15864
14	36	80.0	395	5	US-10-467-657-5266
15	36	80.0	583	4	US-10-282-122A-54383
16	35	77.8	11	3	US-09-988-493-41
17	35	77.8	20	6	US-11-075-234-346
18	35	77.8	222	4	US-10-231-913-263
19	35	77.8	315	4	US-10-231-913-259
20	35	77.8	318	4	US-10-231-913-261
21	35	77.8	521	4	US-10-015-115-48
22	35	77.8	526	4	US-10-231-913-32
23	35	77.8	529	4	US-10-250-613-11
24	35	77.8	529	6	US-11-124-368A-182
25	35	77.8	536	4	US-10-231-913-14
26	35	77.8	567	4	US-10-104-047-3772
27	35	77.8	567	6	US-11-072-512-3772

Sequence 218, Appl
Sequence 20, Appl
Sequence 142, App
Sequence 218, App
Sequence 8, Appli
Sequence 46, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 18432, A
Sequence 63537, A
Sequence 78, Appl
Sequence 4544, Ap
Sequence 199521,
Sequence 14, Appl
Sequence 66, Appl

28 35 77.8 590 4 US-10-205-823-218
29 35 77.8 590 4 US-10-236-031B-20
30 35 77.8 590 4 US-10-788-792-142
31 35 77.8 590 6 US-11-051-454-218
32 35 77.8 590 6 US-11-037-713-8
33 34 75.6 271 3 US-09-811-007-46
34 34 75.6 271 4 US-10-062-624-46
35 34 75.6 271 4 US-10-062-051-46
36 34 75.6 271 4 US-10-062-920-46
37 34 75.6 271 4 US-10-680-349-46
38 34 75.6 271 5 US-10-731-554-46
39 34 75.6 341 4 US-10-369-493-18432
40 34 75.6 659 4 US-10-282-122A-63537
41 34 75.6 872 5 US-10-467-657-78
42 34 75.6 886 5 US-10-467-657-4544
43 34 75.6 1336 4 US-10-437-963-199521
44 33 73.3 11 3 US-09-988-493-14
45 33 73.3 11 3 US-09-988-493-66

ALIGNMENTS

RESULT 1

US-10-774-928-8

; Sequence 8, Application US/10774928

; Publication No. US20040241168A1

; GENERAL INFORMATION:

; APPLICANT: O'Daly, Jose

; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission

; TITLE OF INVENTION: Psoriasis

; FILE REFERENCE: 302178

; CURRENT APPLICATION NUMBER: US/10/774,928

; CURRENT FILING DATE: 2004-02-09

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 8

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Leishmania

US-10-774-928-8

Query Match 100.0%; Score 45; DB 5; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.9e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATNAENEFV 9

Db 1 ATNAENEFV 9

RESULT 2

US-10-480-848A-2

; Sequence 2, Application US/10480848A

; Publication No. US20040219597A1

; GENERAL INFORMATION:

; APPLICANT: B.R.A.H.M.S Aktiengesellschaft

; TITLE OF INVENTION: Use of soluble cytochrome 1 fragments in diagnosis and

; FILE REFERENCE: 3537PCTNAT

; CURRENT APPLICATION NUMBER: US/10/480,848A

; CURRENT FILING DATE: 2003-12-15

; PRIOR APPLICATION NUMBER: DE 101 30 985.6

; PRIOR FILING DATE: 2001-06-27

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Primat (Pavian)

US-10-480-848A-2

Query Match 91.1%; Score 41; DB 5; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNAENEV 9
| | | | |
Db 1 TNAENEV 8

RESULT 3

US-10-480-848A-5
; Sequence 5, Application US/10480848A
; Publication No. US20040219597A1
; GENERAL INFORMATION:
; APPLICANT: B.R.A.H.M.S Aktiengesellschaft
; TITLE OF INVENTION: Use of soluble cytokeatin 1 fragments in diagnosis and
; TITLE OF INVENTION: therapy
; FILE REFERENCE: 3537PCTNAT
; CURRENT APPLICATION NUMBER: US/10/480,848A
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: DE 101 30 985.6
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-480-848A-5

Query Match 91.1%; Score 41; DB 5; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNAENEV 9
| | | | |
Db 93 TNAENEV 100

RESULT 4

US-10-480-848A-3
; Sequence 3, Application US/10480848A
; Publication No. US20040219597A1
; GENERAL INFORMATION:
; APPLICANT: B.R.A.H.M.S Aktiengesellschaft
; TITLE OF INVENTION: Use of soluble cytokeatin 1 fragments in diagnosis and
; TITLE OF INVENTION: therapy
; FILE REFERENCE: 3537PCTNAT
; CURRENT APPLICATION NUMBER: US/10/480,848A
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: DE 101 30 985.6
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; TITLE: L.Johnson et al., Structure of a gene for the human
; TITLE: epidermal 67-kDa keratin
; JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
; VOLUME: 1985
; ISSUE: 82
; PAGES: 1896-1900
US-10-480-848A-3

Query Match 91.1%; Score 41; DB 5; Length 643;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNAENEV 9
| | | | |
Db 277 TNAENEV 284

RESULT 5

US-10-723-860-366
; Sequence 366, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nataeba
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 366
; LENGTH: 644
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-366

Query Match 91.1%; Score 41; DB 5; Length 644;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNAENEV 9
| | | | |
Db 278 TNAENEV 285

RESULT 6

US-09-791-393-170
; Sequence 170, Application US/09791393
; Publication No. US20030032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 170
; LENGTH: 11
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-393-170

Query Match 80.0%; Score 36; DB 3; Length 11;
Best Local Similarity 87.5%; Pred. No. 3.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNAENEV 9
| | | | |
Db 1 TDAENEV 8

RESULT 7

US-09-791-389-170

```
; Sequence 170, Application US/09791389
; Publication No. US2003003273A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 0030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 170
; LENGTH: 11
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-170
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```
Query Match 80.0%; Score 36; DB 3; Length 11;
Best Local Similarity 87.5%; Pred. No. 3.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 2 TNAENEFV 9
Db 1 TDAENEFV 8
```

```
RESULT 8
US-10-389-566-1034
; Sequence 1034, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1034
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-389-566-1034
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Query Match 80.0%; Score 36; DB 4; Length 324;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 3 NAENEFV 9
Db 175 NAENEFV 181
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RESULT 9
US-10-389-566-2328
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; Sequence 2328, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2328
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-389-566-2328
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Query Match 80.0%; Score 36; DB 4; Length 324;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 3 NAENEFV 9
Db 175 NAENEFV 181
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RESULT 10
US-10-732-923-17878
; Sequence 17878, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 17878
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Neisseria meningitidis MC58
US-10-732-923-17878
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Query Match 80.0%; Score 36; DB 5; Length 324;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 3 NAENEFV 9
Db 175 NAENEFV 181
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RESULT 11
US-10-732-923-17879
; Sequence 17879, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
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; SEQ ID NO 17879
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Neisseria meningitidis Z2491
US-10-732-923-17879

Query Match
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NAENEVF 9
Db 175 NAENEVF 181

RESULT 12
US-11-188-298-3960
; Sequence 3960, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 3960
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Neisseria meningitidis MC58
US-11-188-298-3960

Query Match
Best Local Similarity 80.0%; Score 36; DB 6; Length 324;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NAENEVF 9
Db 175 NAENEVF 181

RESULT 13
US-11-188-298-15864
; Sequence 15864, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 15864
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Neisseria meningitidis Z2491
US-11-188-298-15864

Query Match
Best Local Similarity 80.0%; Score 36; DB 6; Length 324;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NAENEVF 9
Db 175 NAENEVF 181

RESULT 14
US-10-467-657-5266
; Sequence 5266, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwinn99, version 1.04
; SEQ ID NO 5266
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5266

Query Match
Best Local Similarity 80.0%; Score 36; DB 5; Length 395;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NAENEVF 9
Db 246 NAENEVF 252

RESULT 15
US-10-282-122A-54383
; Sequence 54383, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Cart, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File wrapper or PALM.
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; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54383
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
US-10-282-122A-54383
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Query Match 80.0%; Score 36; DB 4; Length 583;
Best Local Similarity 77.8%; Pred. No. 2.3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 ATNAENEV 9
|:|:|:|:|
Db 61 ASNARNEV 69
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OM protein - protein search, using sw model

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Title: US-10-774-928A-8

Perfect score: 45

Sequence: 1 ATNAENEFF 9

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Searched: 112942 seqs, 26832045 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
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- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pap.*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	75.6	153	6	US-10-449-902-35066
2	34	75.6	943	6	US-10-449-902-55109
3	33	73.3	469	6	US-10-505-328-457
4	32	71.1	327	6	US-10-471-571A-4214
5	32	71.1	328	6	US-10-449-902-42678
6	31	68.9	98	6	US-10-449-902-30269
7	31	68.9	221	6	US-10-449-902-30681
8	31	68.9	416	6	US-10-471-571A-4782
9	31	68.9	1019	6	US-10-449-902-53317
10	31	68.9	1186	7	US-11-121-154-172
11	30	66.7	170	6	US-10-449-902-46868
12	30	66.7	401	7	US-11-168-010-6
13	30	66.7	401	7	US-11-168-130-6
14	30	66.7	414	6	US-10-449-902-38632
15	30	66.7	424	7	US-11-168-010-5
16	30	66.7	424	7	US-11-168-130-5
17	30	66.7	460	6	US-10-449-902-30876
18	30	66.7	471	6	US-10-511-937-2582
19	30	66.7	471	7	US-11-105-233-67
20	30	66.7	483	7	US-11-105-233-180
21	30	66.7	569	6	US-10-449-902-50324
22	29.5	65.6	357	6	US-10-953-349-13122
23	29.5	65.6	375	6	US-10-953-349-13121
24	29	64.4	23	7	US-11-134-871-2119
25	29	64.4	153	6	US-10-449-902-47002

26	29	64.4	220	6	US-10-953-349-20575	Sequence 20575, A
27	29	64.4	303	6	US-10-953-349-1993	Sequence 1993, Ap
28	29	64.4	322	6	US-10-471-571A-3888	Sequence 3888, Ap
29	29	64.4	344	6	US-10-449-902-37534	Sequence 37534, A
30	29	64.4	377	6	US-10-953-349-1992	Sequence 1992, Ap
31	29	64.4	382	6	US-10-953-349-1991	Sequence 1991, Ap
32	29	64.4	423	6	US-10-449-902-43160	Sequence 43160, A
33	28	62.2	95	6	US-10-953-349-35135	Sequence 35135, A
34	28	62.2	214	6	US-10-953-349-2848	Sequence 2848, Ap
35	28	62.2	217	6	US-10-449-902-44464	Sequence 44464, A
36	28	62.2	220	6	US-10-449-902-30877	Sequence 30877, A
37	28	62.2	220	6	US-10-449-902-33167	Sequence 33167, A
38	28	62.2	232	6	US-10-449-902-41670	Sequence 41670, A
39	28	62.2	242	7	US-11-251-208-190	Sequence 190, App
40	28	62.2	262	7	US-11-174-307B-3930	Sequence 3930, Ap
41	28	62.2	302	6	US-10-953-349-16065	Sequence 16065, A
42	28	62.2	314	6	US-10-471-571A-4458	Sequence 4458, Ap
43	28	62.2	316	6	US-10-953-349-16064	Sequence 16064, A
44	28	62.2	331	6	US-10-471-571A-1962	Sequence 1962, Ap
45	28	62.2	343	6	US-10-953-349-16063	Sequence 16063, A

ALIGNMENTS

RESULT 1
US-10-449-902-35066
; Sequence 35066, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35066
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-35066

Query Match 75.6%; Score 34; DB 6; Length 153;
Best Local Similarity 75.0%; Pred. No. 3.3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATNAENEFF 8
||| |||:
Db 48 ATNGENDF 55

RESULT 2
US-10-449-902-55109
; Sequence 55109, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269

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; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55109
; LENGTH: 943
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-55109

Query Match      75.6%; Score 34; DB 6; Length 943;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 ATNAENEF 8
Db      838 ATNGENDF 845

RESULT 3
US-10-505-928-457
; Sequence 457, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 457
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-457

Query Match      73.3%; Score 33; DB 6; Length 469;
Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      2 TNAENEF 9
Db      188 TAAENEFV 195

RESULT 4
US-10-471-571A-4214
; Sequence 4214, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927NO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4214
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(327)
; OTHER INFORMATION: thioredoxine reductase
US-10-471-571A-4214

Query Match      68.9%; Score 31; DB 6; Length 98;
Best Local Similarity 75.0%; Pred. No. 8.4;
Matches 6; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY      1 ATNAENEF 8

Query Match      71.1%; Score 32; DB 6; Length 327;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 ATNAENEFV 9
Db      121 AVNKENDFV 129

RESULT 5
US-10-449-902-42678
; Sequence 42678, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42678
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-42678

Query Match      71.1%; Score 32; DB 6; Length 328;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 ATNAENEFV 9
Db      190 ATNAENNAV 198

RESULT 6
US-10-449-902-30269
; Sequence 30269, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30269
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-30269

Query Match      68.9%; Score 31; DB 6; Length 98;
Best Local Similarity 75.0%; Pred. No. 8.4;
Matches 6; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY      1 ATNAENEF 8
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Db 39 ATNVENAF 46
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RESULT 7

US-10-449-902-30681
; Sequence 30681, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30681
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-30681

Query Match 68.9%; Score 31; DB 6; Length 221;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATNAENEV 8
||| || |

Db 165 ATNVENAF 172

RESULT 8

US-10-471-571A-4782
; Sequence 4782, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927W0
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4782
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(416)
; OTHER INFORMATION: signal recognition particle
US-10-471-571A-4782

Query Match 68.9%; Score 31; DB 6; Length 416;
Best Local Similarity 77.8%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATNAENEV 9
||| ||| |

Db 12 ATNKENEV 20

RESULT 9

US-10-449-902-53317

; Sequence 53317, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53317
; LENGTH: 1019
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-53317

Query Match 68.9%; Score 31; DB 6; Length 1019;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATNAENEV 9
||| || |

Db 297 AVNAENPFL 305

RESULT 10

US-11-121-154-172
; Sequence 172, Application US/111211154
; Publication No. US20060105914A1
; GENERAL INFORMATION:
; APPLICANT: TAYLOR, LARRY EDMUND
; APPLICANT: WEINER, RONALD M.
; APPLICANT: HUTCHESON, STEVEN WAYNE
; APPLICANT: EKBORG, NATHAN A.
; APPLICANT: HOWARD, MICHAEL
; TITLE OF INVENTION: PLANT WALL DEGRADATIVE COMPOUNDS AND SYSTEMS
; FILE REFERENCE: 108172-00121
; CURRENT APPLICATION NUMBER: US/11/121,154
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,971
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 172
; LENGTH: 1186
; TYPE: PRT
; ORGANISM: Microbulbifer degradans
US-11-121-154-172

Query Match 68.9%; Score 31; DB 7; Length 1186;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TNAENEV 8
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Db 406 TNAANEF 412

RESULT 11

US-10-449-902-46868
; Sequence 46868, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 46868

; LENGTH: 170

; TYPE: PRT

; ORGANISM: Oryza sativa

; US-10-449-902-46868

Query Match 66.7%; Score 30; DB 6; Length 170;

Best Local Similarity 66.7%; Pred. No. 26;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATNAENEV 9

||: |||||

DB 48 ATSGEGEV 56

RESULT 12

US-11-168-010-6

; Sequence 6, Application US/11168010

; Publication No. US20060104962A1

; GENERAL INFORMATION:

; APPLICANT: The Scripps Research Institute

; APPLICANT: Friedlander, Martin

; APPLICANT: Otani, Atsushi

; APPLICANT: Dasilva, Karen

; APPLICANT: Moreno, Stacey (Hanekamp)

; TITLE OF INVENTION: TRANSFECTED HEMATOPOIETIC STEM CELLS AND

; FILE REFERENCE: TSRI-988.3

; CURRENT APPLICATION NUMBER: US/11/168,010

; CURRENT FILING DATE: 2005-06-28

; PRIOR APPLICATION NUMBER: 10/833,743

; PRIOR FILING DATE: 2004-04-28

; PRIOR APPLICATION NUMBER: 10/628,783

; PRIOR FILING DATE: 2003-07-25

; PRIOR APPLICATION NUMBER: 60/467,051

; PRIOR FILING DATE: 2003-05-02

; PRIOR APPLICATION NUMBER: 60/398,522

; PRIOR FILING DATE: 2002-07-25

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 401

; TYPE: PRT

; ORGANISM: homo sapiens

; US-11-168-010-6

Query Match 66.7%; Score 30; DB 7; Length 401;

Best Local Similarity 66.7%; Pred. No. 70;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATNAENEV 9

||: |||||

DB 7 ATEAEEDFV 15

RESULT 13

US-11-168-130-6

; Sequence 6, Application US/11168010

; Publication No. US20060104963A1

; GENERAL INFORMATION:

; APPLICANT: The Scripps Research Institute

; APPLICANT: Friedlander, Martin

; APPLICANT: Otani, Atsushi
; APPLICANT: Dasilva, Karen
; APPLICANT: Moreno, Stacey (Hanekamp)
; TITLE OF INVENTION: TREATMENT OF CONE CELL DEGENERATION WITH
; FILE REFERENCE: TSRI-988.4
; CURRENT APPLICATION NUMBER: US/11/168,130
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 10/933,634
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/833,743
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 10/628,783
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/467,051
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 60/398,522
; PRIOR FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 401
; TYPE: PRT
; ORGANISM: homo sapiens
; US-11-168-130-6

Query Match 66.7%; Score 30; DB 7; Length 401;

Best Local Similarity 66.7%; Pred. No. 70;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATNAENEV 9

||: |||||

DB 7 ATEAEEDFV 15

RESULT 14

US-10-449-902-38632

; Sequence 38632, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 38632

; LENGTH: 414

; TYPE: PRT

; ORGANISM: Oryza sativa

; US-10-449-902-38632

Query Match 66.7%; Score 30; DB 6; Length 414;

Best Local Similarity 66.7%; Pred. No. 72;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATNAENEV 9

||: |||||

DB 191 ALRAENDFV 199

RESULT 15

US-11-168-010-5

; Sequence 5, Application US/11168010

; Publication No. US20060104962A1

; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Friedlander, Martin
; APPLICANT: Otani, Atsushi
; APPLICANT: DaSilva, Karen
; APPLICANT: Moreno, Stacey (Hanekamp)
; TITLE OF INVENTION: TRANSFECTED HEMATOPOIETIC STEM CELLS AND
; TITLE OF INVENTION: METHODS OF TREATMENT OF NEOVASCULAR EYE DISEASES THEREWITH
; FILE REFERENCE: TSRI-988.3
; CURRENT APPLICATION NUMBER: US/11/168,010
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 10/833,743
; PRIOR FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: 10/628,783
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/467,051
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 60/398,522
; PRIOR FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 424
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-168-010-5

Query Match 66.7%; Score 30; DB 7; Length 424;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATNAENEV 9
||| :||
Db 30 ATAEEDFV 38

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Job time : 6.15534 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 19:18:42 ; Search time 20.2718 Seconds
(without alignments)
38.861 Million cell updates/sec

Title: US-10-774-928A-8

Perfect score: 45

Sequence: 1 ATNAENEV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB.pcp.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pcp.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pcp.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pcp.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PTUS COMB.pcp.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE COMB.pcp.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/baCkfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	2	US-09-809-003A-8
2	41	91.1	637	2	US-09-949-016-8152
3	41	91.1	643	2	US-09-538-092-844
4	35	77.8	567	2	US-10-104-047-3772
5	34	75.6	271	2	US-09-660-587-46
6	34	75.6	271	2	US-09-811-007A-46
7	33	73.3	251	2	US-09-248-796A-17802
8	33	73.3	398	2	US-10-104-047-3388
9	33	73.3	459	2	US-09-489-039A-12641
10	33	73.3	469	2	US-09-077-606-3
11	33	73.3	476	2	US-09-949-016-9096
12	33	73.3	505	3	US-10-116-821-14
13	33	73.3	546	1	US-09-067-351-1
14	33	73.3	546	2	US-09-360-490-1
15	33	73.3	551	1	US-09-067-351-2
16	33	73.3	551	2	US-09-360-490-2
17	33	73.3	564	2	US-09-949-016-6628
18	33	73.3	569	2	US-09-949-016-11035
19	33	73.3	569	2	US-09-949-016-11036
20	32	71.1	327	2	US-08-956-171E-5208
21	32	71.1	327	2	US-08-781-986A-5208
22	32	71.1	432	2	US-09-270-767-43899
23	32	71.1	459	2	US-09-328-352-4523
24	32	71.1	1091	2	US-09-328-352-5758
25	31	68.9	80	2	US-09-248-796A-15929
26	31	68.9	139	2	US-09-248-796A-20474

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27 31 68.9 171 2 US-09-134-001C-3566 Sequence 3566, Ap
28 31 68.9 213 1 US-08-531-525-11 Sequence 11, Appl
29 31 68.9 213 1 US-08-718-270A-11 Sequence 11, Appl
30 31 68.9 229 2 US-09-248-796A-24307 Sequence 24307, A
31 31 68.9 305 2 US-09-248-796A-18731 Sequence 18731, A
32 31 68.9 416 2 US-09-007-476-2 Sequence 2, Appli
33 31 68.9 492 1 US-08-463-090B-10 Sequence 10, Appl
34 31 68.9 506 2 US-09-248-796A-15570 Sequence 15570, A
35 31 68.9 574 2 US-10-104-047-2310 Sequence 2310, Ap
36 31 68.9 693 2 US-09-538-092-534 Sequence 534, App
37 31 68.9 1031 2 US-09-914-259-24 Sequence 24, Appl
38 30 66.7 17 2 US-09-979-672-8 Sequence 8, Appli
39 30 66.7 46 2 US-09-813-718-51 Sequence 51, Appl
40 30 66.7 85 2 US-09-813-718-45 Sequence 45, Appl
41 30 66.7 159 2 US-09-270-767-36313 Sequence 36313, A
42 30 66.7 159 2 US-09-270-767-51530 Sequence 51530, A
43 30 66.7 163 2 US-09-248-796A-27537 Sequence 27537, A
44 30 66.7 254 2 US-09-586-106B-101 Sequence 101, App
45 30 66.7 254 2 US-10-799-870-101 Sequence 101, App

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ALIGNMENTS

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RESULT 1
US-09-809-003A-8
; Sequence 8, Application US/09809003A
; Patent No. 6673351
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 302178
; CURRENT APPLICATION NUMBER: US/09/809,003A
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Leishmania
; US-09-809-003A-8

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Query Match 100.0%; Score 45; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATNAENEV 9
Db 1 ATNAENEV 9

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RESULT 2

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US-09-949-016-8152
; Sequence 8152, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8152
; LENGTH: 637

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; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-8152

Query Match          91.1%; Score 41; DB 2; Length 637;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TNAENEFV 9
Db      243 TTAENEFV 250

RESULT 5
US-09-660-587-46
; Sequence 46, Application US/09660587
; Patent No. 6392023
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; FILE REFERENCE: D6152CIP2
; CURRENT APPLICATION NUMBER: US/09/660,587
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/261,358
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 46
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Ehrlichia canis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. canis p28-9 protein
US-09-660-587-46

Query Match          75.6%; Score 34; DB 2; Length 271;
Best Local Similarity 55.6%; Pred. No. 38;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATNAENEFV 9
Db      141 ATNSDNKFI 149

RESULT 6
US-09-811-007A-46
; Sequence 46, Application US/09811007A
; Patent No. 6660289
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; FILE REFERENCE: D6152CIP2
; CURRENT APPLICATION NUMBER: US/09/811,007A
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 09/660,587
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 46
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Ehrlichia canis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. canis p28-9 protein
US-09-811-007A-46

Query Match          75.6%; Score 34; DB 2; Length 271;
Best Local Similarity 55.6%; Pred. No. 38;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATNAENEFV 9
Db      141 ATNSDNKFI 149

RESULT 7
US-09-248-796A-17802

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; Sequence 17802, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17802
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17802

Query Match      73.3%; Score 33; DB 2; Length 251;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 TNAENEVF 9
Db      198 TNPQNEVF 205

RESULT 8
US-10-104-047-3388
; Sequence 3388, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR FILING DATE:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3388
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3388

Query Match      73.3%; Score 33; DB 2; Length 398;
Best Local Similarity 87.5%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 TNAENEVF 9
Db      110 TAAENEVF 117

RESULT 9
US-09-489-039A-12641
; Sequence 12641, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12641
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; LENGTH: 459
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12641

Query Match      73.3%; Score 33; DB 2; Length 459;
Best Local Similarity 66.7%; Pred. No. 1.le+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ATNAENEVF 9
Db      132 STNADNPFV 140

RESULT 10
US-09-077-606-3
; Sequence 3, Application US/09077606
; Patent No. 6774220
; GENERAL INFORMATION:
; APPLICANT: JIANG, Pan Hong
; APPLICANT: KABA, Aboubacar
; APPLICANT: CHANY-FOURNIER, Francoise
; APPLICANT: CERUTTI, Italina
; APPLICANT: CHANY, Charles
; TITLE OF INVENTION: COMPOUNDS HAVING LECTINIC PROPERTIES AND THEIR
; TITLE OF INVENTION: BIOLOGICAL APPLICATIONS
; FILE REFERENCE: 040388/0113
; CURRENT APPLICATION NUMBER: US/09/077,606
; CURRENT FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: WO PCT/FR96/01937
; EARLIER FILING DATE: 1996-12-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-077-606-3

Query Match      73.3%; Score 33; DB 2; Length 469;
Best Local Similarity 87.5%; Pred. No. 1.le+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 TNAENEVF 9
Db      188 TAAENEVF 195

RESULT 11
US-09-949-016-9096
; Sequence 9096, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 9096
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9096
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Query Match          73.3%; Score 33; DB 2; Length 476;
Best Local Similarity 87.5%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 1;

QY      2 TNAENEVF 9
      | | | | |
Db      195 TAAENEVF 202

RESULT 12
US-10-116-821-14
; Sequence 14, Application US/10116821
; Patent No. 7033804
; GENERAL INFORMATION:
; APPLICANT: Dodge, Timothy C.
; APPLICANT: Valle, Fernando
; TITLE OF INVENTION: Methods for the Production of Products
; FILE REFERENCE: in Host Cells
; FILE REFERENCE: GC620-3
; CURRENT APPLICATION NUMBER: US/10/116,821
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/282,277
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Pantoea citrea
US-10-116-821-14

Query Match          73.3%; Score 33; DB 3; Length 505;
Best Local Similarity 62.5%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 5; Conservative 3; Mismatches 0;

QY      2 TNAENEVF 9
      | | | | |
Db      2 TNAENKVI 9

RESULT 13
US-09-067-351-1
; Sequence 1, Application US/09067351
; Patent No. 5994081
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN KERATINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,351
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0511 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555

QY      2 TNAENEVF 9
      | | | | |
Db      265 TAAENEVF 272

RESULT 14
US-09-360-490-1
; Sequence 1, Application US/09360490
; Patent No. 6221843
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN KERATINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/360,490
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/067,351
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0511 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 546 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PANTUT02
; CLONE: 1467090
US-09-067-351-1

Query Match          73.3%; Score 33; DB 1; Length 546;
Best Local Similarity 87.5%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 1;

QY      2 TNAENEVF 9
      | | | | |
Db      265 TAAENEVF 272

RESULT 15
US-09-360-490-1
; Sequence 1, Application US/09360490
; Patent No. 6221843
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN KERATINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/360,490
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/067,351
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0511 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 546 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PANTUT02
; CLONE: 1467090
US-09-360-490-1

Query Match          73.3%; Score 33; DB 2; Length 546;
Best Local Similarity 87.5%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 1;
```

Qy 2 TNAENEFV 9
| | | | |
Db 265 TAAENEFV 272

RESULT 15

US-09-067-351-2
; Sequence 2, Application US/09067351
; Patent No. 5994081
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN KERATINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,351
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0511 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 551 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KERANOT02
; CLONE: 2029060
; US-09-067-351-2

Query Match 73.3%; Score 33; DB 1; Length 551;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TNAENEFV 9
| | | | |
Db 247 TAAENEFV 254

Search completed: July 5, 2006, 19:24:25
Job time : 21.2718 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 19:09:18 ; Search time 19.4175 Seconds
(without alignments)
79.283 Million cell updates/sec

Title: US-10-774-928A-9

Perfect score: 66

Sequence: 1 XXYSELNRVQLRLSI 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*

1: Pirl:*

2: Pirl2:*

3: Pirl3:*

4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	83.3	643	1 KRHU2	keratin 1, type II
2	52	78.8	581	1 KRMS2	keratin, type II c
3	49	74.2	524	2 A23518	keratin, 57K type
4	47	71.2	384	2 I61769	keratin 6d, type I
5	47	71.2	553	2 I59009	epidermal keratin
6	47	71.2	564	1 KRHUEA	keratin 6a, type I
7	47	71.2	564	1 KRHUEB	keratin 6b, type I
8	47	71.2	564	2 I61770	keratin 6e, type I
9	47	71.2	564	2 I61768	keratin 6c, type I
10	47	71.2	564	2 I61771	keratin 6f, type I
11	47	71.2	645	2 A44861	keratin, 67K type
12	46	69.7	534	2 I37942	keratin 4, type II
13	45	68.2	629	2 A29666	keratin, 65K type
14	45	68.2	638	2 I53169	cytokeatin 2 - hu
15	44	66.7	590	2 A29904	keratin 5, type II
16	44	66.7	629	2 S42629	keratin K3 - rabbi
17	43	65.2	491	2 S05408	keratin, type II,
18	43	65.2	503	2 S29094	keratin, type II,
19	43	65.2	508	1 KRSHU2	keratin type II, m
20	42	63.6	390	2 A60093	cytokeatin, type
21	42	63.6	469	2 S05602	keratin K7, type I
22	42	63.6	489	2 B24177	keratin, 55K type
23	42	63.6	506	2 S58150	hypothetical-prote
24	42	63.6	520	2 J80291	intermediate filam
25	42	63.6	623	2 I49969	keratin, 58K type
26	41	62.1	532	2 S08381	probable membrane
27	41	62.1	532	2 S54571	keratin-like prote
28	40	60.6	257	2 I38025	conserved hypothet
29	40	60.6	352	2 C83451	

ALIGNMENTS

RESULT 1

KRHU2

keratin 1, type II, cytoskeletal - human

N;Alternate names: 67K type II epidermal keratin; cytokeratin 1

C;Species: Homo sapiens (man)

C;Date: 04-Dec-1986 #sequence, revision 22-Oct-1999 #text_change 10-Dec-1999

C;Accession: A22940; A02950; A43342

R;Johnson, L.D.; Idler, W.W.; Zhou, X.M.; Roop, D.R.; Steinert, P.M.

Proc. Natl. Acad. Sci. U.S.A. 82, 1896-1900, 1985

A;Reference number: A22940; MUID:85166239; PMID:2580302

A;Accession: A22940

A;Molecule type: DNA

A;Residues: 1-643 <JOH>

A;Cross-references: UNIPARC:UPI0000173D59; GB:M98776; GB:M11215; GB:M11845; GB:M11846; N

A;Note: translation of initiator Met is not shown

R;Steinert, P.M.; Parry, D.A.D.; Idler, W.W.; Johnson, L.D.; Steven, A.C.; Roop, D.R.

J. Biol. Chem. 260, 7142-7149, 1985

A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67,000

late filament subunits.

A;Reference number: A92535; MUID:85207740; PMID:2581964

A;Accession: A02950

A;Molecule type: mRNA

A;Residues: 151-183, 'K', 185-199, 'M', 201-204, 'K', 206-236, 'S', 238-239, 'R', 241-356, 'Y', 358-

, 'S', 638-643 <STE>

A;Cross-references: UNIPARC:UPI000016ABD0; GB:M10938; NID:g186787; PIDN:AAA36153.1; PID:

A;Experimental source: tissue neonatal foreskin

A;Note: the authors translated the codon CUG for residue 476 as Met

R;Chipev, C.C.; Korge, B.P.; Markova, N.; Bale, S.J.; DiGiovanna, J.J.; Compton, J.G.; S

Cell 70, 821-828, 1992

A;Title: A leucine---proline mutation in the H1 subdomain of keratin 1 causes epidermol

A;Reference number: A43342; MUID:92386601; PMID:1381288

A;Accession: A43342

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 144-146, 'P', 148-159, 'P', 161-183, 'K', 185-186 <CHI>

A;Cross-references: UNIPARC:UPI0000173D5A; GB:M98776; GB:M11215; GB:M11845; GB:M11846; N

A;Note: sequence extracted from NCBI backbone (NCBI:P:112784)

C;Comment: The cytoskeletal and microfibrillar keratins are classified into two types, t

atin IF protein subunit appears to be a heterotetramer of two type I and two type II pro

C;Comment: Keratin 1 is expressed in terminally differentiating epidermis.

C;Genetics:

A;Gene: GDB:KRT1

A;Cross-references: GDB:I128198; OMIM:I139350

A;Map position: 12q11-12q13

A;Note: defects in this gene may result in epidermolytic hyperkeratosis

C;Complex: heterotetramer of two type I, usually keratin 10 (see PIR:KRHU0), and two typ

C;Superfamily: cytoskeletal keratin

C;Keywords: coiled coil; heterotetramer; intermediate filament

F;4-179/Domain: head <HED>

F;4-143/Region: E1 and V1 subdomains

F;14-179/Region: H1 subdomain

F;180-492/Domain: rod <ROD>

hypothetical prote
keratin, 64K type
keratin type II,
keratin, type II,
keratin type II -
hypothetical prote
mucs (AF238304) [i
hypothetical prote
DNA polymerase III
hypothetical prote
hypothetical prote
gonadal protein z6
probable uracil ph
glucose-6-phosphat
guanosine-3',5'-bi
guanosine-3',5'-bi

30 40 60.6 373 2 A71690
31 40 60.6 425 1 KRXL2A
32 40 60.6 479 2 A61368
33 40 60.6 480 2 A56694
34 40 60.6 495 2 I57463
35 40 60.6 532 2 H85035
36 39 59.1 170 2 F97501
37 39 59.1 170 2 AB2720
38 39 59.1 1451 2 D64203
39 38 57.6 47 2 D95156
40 38 57.6 77 2 F95154
41 38 57.6 90 2 A30172
42 38 57.6 360 2 H71324
43 38 57.6 558 2 I48073
44 38 57.6 718 2 B81058
45 38 57.6 725 2 B81819

```
F:180-214/Region: coil 1A
F:215-226/Region: linker 1
F:227-327/Region: coil 1B
F:328-344/Region: linker 12
F:345-363/Region: coil 2A
F:364-371/Region: linker 2
F:372-492/Region: coil 2B
F:430/Region: stutter
F:493-643/Domain: tail <END>
F:493-512/Region: H2 subdomain
F:513-643/Region: V2 and E2 subdomains

Query Match      83.3%; Score 55; DB 1; Length 643;
Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY      4 SELNRVIOQLRS 15
Db      398 SELNRVIOQLRS 409
|||||:|||||

RESULT 2
KRMS2
keratin, type II cytoskeletal - mouse (fragment)
N:Alternate names: 67-kDa type II keratin
C:Species: Mus musculus (house mouse)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C:Accession: A02951
R:Steinert, P.M.; Parry, D.A.D.; Idler, W.W.; Johnson, L.D.; Steven, A.C.; Roop, D.R.
J. Biol. Chem. 260, 7142-7149, 1985
A:Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67,000
       keratin subunits
A:Reference number: A92535; MUID:85207740; PMID:2581964
A:Accession: A02951
A:Molecule type: mRNA
A:Residues: 1-581 <STE>
A:Cross-references: UNIPROT:P04104; UNIPARC:UPI0000173DSB; GB:M10937; NID:g198622; PID:g
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament
F:1-106/Domain: head (fragment) <HED>
F:1-70/Region: V1 subdomain (fragment)
F:71-106/Region: H1 subdomain
F:107-419/Domain: rod <ROD>
F:107-141/Region: coil 1A
F:142-153/Region: linker 1
F:154-254/Region: coil 1B
F:255-271/Region: linker 12
F:272-290/Region: coil 2A
F:291-298/Region: linker 2
F:299-419/Region: coil 2B
F:357/Region: stutter
F:420-581/Domain: tail <END>
F:420-439/Region: H2 subdomain
F:440-581/Region: V2 and E2 subdomains

Query Match      78.8%; Score 52; DB 1; Length 581;
Best Local Similarity 91.7%; Pred. No. 0.41; Indels 0; Gaps 0;
Matches 11; Conservative 1; Mismatches 1;

QY      4 SELNRVIOQLRS 15
Db      325 SELNRVIOQLRS 336
|||||:|||||

RESULT 3
A23518
keratin, 57K type II cytoskeletal - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
C:Accession: A23518
R:Knapp, B.; Rentrop, M.; Schweitzer, J.; Winter, H.
Nucleic Acids Res. 14, 751-763, 1986
A:Title: Nonepidermal members of the keratin multigene family: cDNA sequences and in situ
```

```
A:Reference number: A93640; MUID:86120369; PMID:2418416
A:Accession: A23518
A:Molecule type: mRNA
A:Residues: 1-524 <KNA>
A:Cross-references: UNIPROT:P07744; UNIPARC:UPI00000298E2; GB:X03491; NID:g52784; PIDN:C
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil

Query Match      74.2%; Score 49; DB 2; Length 524;
Best Local Similarity 83.3%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 0;

QY      4 SELNRVIOQLRS 15
Db      365 SELNRVIOQLRA 376
|||||:|||||

RESULT 4
I61769
keratin 6d, type II - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: I61769
R:Takahashi, K.; Paladini, R.D.; Coulombe, P.A.
J. Biol. Chem. 270, 18581-18592, 1995
A:Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
A:Reference number: A57398; MUID:95355491; PMID:7543104
A:Accession: I61769
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-384 <RES>
A:Cross-references: UNIPROT:P48667; UNIPARC:UPI000012DB17; GB:L42602; NID:g914823; GB:L4
28; GB:L42608; NID:g914829; GB:L42609; GB:L42610; NID:g1488252; PIDN:AAB606
C:Genetics:
A:Gene: KRT6D
A:Introns: 72/2; 92/3; 124/3; 179/3; 221/3; 295/2; 307/1
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil

Query Match      71.2%; Score 47; DB 2; Length 384;
Best Local Similarity 75.0%; Pred. No. 1.9; Indels 0; Gaps 0;
Matches 9; Conservative 3; Mismatches 0;

QY      4 SELNRVIOQLRS 15
Db      202 A6INRMIOQLRS 213
|||||:|||||

RESULT 5
I59009
epidermal keratin subunit II - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I59009; A61205
R:Steinert, P.M.; Parry, D.A.D.; Racoosin, E.L.; Idler, W.W.; Steven, A.C.; Trus, B.L.; F
proc. Natl. Acad. Sci. U.S.A. 81, 5709-5713, 1984
A:Title: The complete cDNA and deduced amino acid sequence of a type II mouse epidermal
A:Reference number: I59009; MUID:85014838; PMID:6207530
A:Accession: I59009
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-553 <RES>
A:Cross-references: UNIPROT:P50446; UNIPARC:UPI000016CE87; GB:K02108; NID:g198634; PIDN:
R:Finch, J.; Andrews, K.; Krieg, P.; Fuerstenberger, G.; Slaga, T.; Ootsuyama, A.; Tanook
Carcinogenesis 12, 1519-1522, 1991
A:Title: Identification of a cloned sequence activated during multi-stage carcinogenesis
A:Reference number: A61205; MUID:91316763; PMID:1713533
A:Accession: A61205
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 528-553 <FIN>
A:Cross-references: UNIPARC:UPI00001774C8
C:Genetics:
```


A:Gene: KRT6B
 A:Note: this may not be a distinct gene
 C:Superfamily: cytoskeletal keratin
 C:Keywords: coiled coil

Query Match 71.2%; Score 47; DB 2; Length 564;
 Best Local Similarity 75.0%; Pred. No. 2.9;
 Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVIOQLRS 15

Db 382 AEINRMIOQLRS 393

RESULT 9

161768 .
 keratin 6c, type II - human
 C:Species: Homo sapiens (man)
 C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
 C:Accession: I61768
 R:Takahashi, K.; Paladini, R.D.; Coulombe, P.A.
 J. Biol. Chem. 270, 18581-18592, 1995

A:Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
 A:Reference number: A57398; MUID:95355491; PMID:7543104

A:Accession: I61768

A>Status: translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-564 <RES>

A:Cross-references: UNIPROT:P48666; UNIPARC:UPI0000167E80; GB:L42593; NID:g908791; GB:L42593; GB:L42599; NID:g908797; GB:L42600; NID:g908798; GB:L42601; NID:g908799; PIDN:AAAC4176

C:Genetics:

A:Gene: KRT6C

A:Introns: 180/3; 252/2; 272/3; 304/3; 359/3; 401/3; 475/2; 487/1

C:Superfamily: cytoskeletal keratin

C:Keywords: coiled coil

Query Match 71.2%; Score 47; DB 2; Length 564;
 Best Local Similarity 75.0%; Pred. No. 2.9;
 Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVIOQLRS 15

Db 382 AEINRMIOQLRS 393

RESULT 10

161771
 keratin 6f, type II - human
 C:Species: Homo sapiens (man)
 C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
 C:Accession: I61771
 R:Takahashi, K.; Paladini, R.D.; Coulombe, P.A.
 J. Biol. Chem. 270, 18581-18592, 1995

A:Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
 A:Reference number: A57398; MUID:95355491; PMID:7543104

A:Accession: I61771

A>Status: translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-564 <RES>

A:Cross-references: UNIPROT:P48669; UNIPARC:UPI000013CD50; GB:L42612; NID:g908804; PIDN:161771

C:Genetics:

A:Gene: KRT6F

A:Note: this may not be a distinct gene

C:Superfamily: cytoskeletal keratin

C:Keywords: coiled coil

Query Match 71.2%; Score 47; DB 2; Length 564;
 Best Local Similarity 75.0%; Pred. No. 2.9;
 Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVIOQLRS 15

Db 382 AEINRMIOQLRS 393

RESULT 11

A44861

keratin, 67K type II epidermal - human

N:Alternate names: cytokeratin 2, CK 2; epidermal cytokeratin 2

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: A44861

R:Collin, C.; Moll, R.; Kubicka, S.; Ouhayoun, J.P.; Franke, W.W.

Exp. Cell Res. 202, 132-141, 1992

A:Title: Characterization of human cytokeratin 2, an epidermal cytoskeletal protein synt:

A:Reference number: A44861; MUID:92380238; PMID:1380918

A:Accession: A44861

A:Molecule type: mRNA

A:Residues: 1-645 <COL>

A:Cross-references: UNIPROT:P35908; UNIPARC:UPI000012DB03; GB:S43646

A:Experimental source: epidermis

A:Note: the authors translated the codon GGC for residue 146 as Cys

C:Note: sequence extracted from NCBI backbone (NCBIN:112351)

C:Superfamily: cytoskeletal keratin

C:Keywords: coiled coil; intermediate filament

Query Match 71.2%; Score 47; DB 2; Length 645;
 Best Local Similarity 90.9%; Pred. No. 3.4;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVIOQLR 14

Db 403 SELNRVIOQLQ 413

RESULT 12

I37942

keratin 4, type II, cytoskeletal - human

N:Alternate names: basic cytokeratin; cytokeratin 4

C:Species: Homo sapiens (man)

C:Date: 12-Aug-1996 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004

C:Accession: I37942; S01068; S21884; A30186; S31662

R:Wanner, R.; Forster, H.H.; Tilmans, I.; Mischke, D.

J. Invest. Dermatol. 100, 735-741, 1993

A:Title: Allelic variations of human keratins K4 and K5 provide polymorphic markers withi

A:Reference number: I37942; MUID:93267125; PMID:7684424

A:Accession: I37942

A>Status: translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-127, I', 129-144 <WAN1>

A:Cross-references: UNIPROT:P19013; UNIPARC:UPI000016AB8C; EMBL:X67683; NID:g34020; PIDN:

R:Leube, R.E.; Bader, B.L.; Bosch, F.X.; Zimbelmann, R.; Achtstaetter, T.; Franke, W.W.

J. Cell Biol. 106, 1249-1261, 1988

A:Title: Molecular characterization and expression of the stratification-related cytokerat

A:Reference number: S01068; MUID:88198369; PMID:2452170

A:Accession: S01068

A:Molecule type: mRNA

A:Residues: 'S', 128-534 <LEU>

A:Cross-references: UNIPARC:UPI000016ABA3; EMBL:X07695; NID:g34072; PIDN:CAA30534.1; PID

R:Wanner, R.; Tilmans, I.; Mischke, D.

submitted to the EMBL Data Library, July 1991

A:Reference number: S21884

A:Accession: S21884

A:Molecule type: DNA

A:Residues: 411-534 <WAN2>

A:Cross-references: UNIPARC:UPI000016ABA5; EMBL:X61028; NID:g34076; PIDN:CAA43362.1; PID

A:Experimental source: allele K4a

C:Genetics:

A:Gene: GDB:KRT4; CYK4

A:Cross-references: GDB:120697; OMIM:123940

A:Map position: 12p11.2-12q11

A:Introns: 463/2; 475/1

C:Superfamily: cytoskeletal keratin

C:Keywords: coiled coil; intermediate filament

F;1-152/Domain: head #status predicted <HEA>

F;153-464/Domain: helical rod #status predicted <ROD>

F:465-534/Domain: tail #status predicted <TAI>

Query Match 69.7%; Score 46; DB 2; Length 534;
 Best Local Similarity 75.0%; Pred. No. 4.1;
 Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SELNRVIOQLRS 15
 :||||:|||||
 Db 370 AELNRMIQLRLA 381

RESULT 13

A29666

keratin, 65K type II cytoskeletal - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 20-Apr-2001

C;Accession: A29666

R;Klinge, E.M.; Sylvestre, Y.R.; Freedberg, I.M.; Blumenberg, M.

J. Mol. Evol. 24, 319-329, 1987

A;Title: Evolution of keratin genes: different protein domains evolve by different paths

A;Reference number: A29666; MUID:87254239; PMID:2439698

A;Accession: A29666

A;Molecule type: DNA

A;Residues: 1-629 <KLI>

A;Cross-references: UNIPARC:UPI0000161C35; GB:X05418; NID:934040; PIDN:CAA28991.1; PID:9

92; PIDN:CAA28994.1; PID:91335193; PIDN:CAA28995.1; PID:91335194; GB:X05421; NID:934047;

A;Note: the authors translated the codon AAC for residue 63 as Asp and ACA for residue 2

s mistranslated as a Met initiator codon

C;Genetics:

A;Introns: 215/3; 289/2; 309/3; 341/3; 396/3; 438/3; 512/2; 525/1

A;Superfamily: cytoskeletal keratin

C;Keywords: coiled coil

Query Match

Best Local Similarity 68.2%; Score 45; DB 2; Length 629;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ELNRVIOQLRS 15
 :||||:|||||
 Db 420 ELNRMIQLRLA 430

RESULT 14

I53169

cytokeratin 2 - human

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: I53169

R;Collin, C.; Ouhayoun, J.

Differentiation 51, 137-148, 1992

A;Title: Suprabasal marker proteins distinguishing keratinizing squamous epithelia: Cyt

A;Reference number: I53169; MUID:93114504; PMID:1282112

A;Accession: I53169

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-638 <RES>

A;Cross-references: UNIPROT:Q01546; UNIPARC:UPI000012DB04; GB:M99063; NID:9181389; PIDN:

C;Superfamily: cytoskeletal keratin

Query Match

Best Local Similarity 68.2%; Score 45; DB 2; Length 638;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ELNRVIOQLRS 15
 :||||:|||||
 Db 403 ELNRMIQLRLA 413

RESULT 15

A29904

keratin 5, type II, epidermal - human

N;Alternate names: 58K type II keratin; cytokeratin 5; K5

C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
 C;Accession: A29904; A60865; A32568; A27679; I58080
 R;Eckert, R.L.; Rorke, E.A.
 DNA 7, 337-345, 1988

A;Title: The sequence of the human epidermal 58-kD (S) type II keratin reveals an absenc
 A;Reference number: A29904; MUID:88296082; PMID:2456903

A;Accession: A29904

A;Molecule type: DNA; mRNA

A;Residues: 1-590 <ECK>

A;Cross-references: UNIPROT:PI3647; UNIPARC:UPI000012DB0D; GB:M21389; NID:9186697; PIDN:

R;Galup, C.; Darmon, M.Y.

J. Invest. Dermatol. 91, 39-42, 1988

A;Title: Isolation and characterization of a cDNA clone coding for human epidermal kerat

A;Reference number: A60865; MUID:88258089; PMID:2455002

A;Accession: A60865

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 348-374, 'E', 376-386, 'S', 388-436, 438-542, 'S', 544-590 <GAL>

A;Cross-references: UNIPARC:UPI00001774BD

R;Lersch, R.; Stellmach, V.; Stocks, C.; Giudice, G.; Fuchs, E.

Mol. Cell. Biol. 9, 3685-3697, 1989

A;Title: Isolation, sequence, and expression of a human keratin K5 gene: transcriptional

A;Reference number: A32568; MUID:99384595; PMID:2476664

A;Accession: A32568

A;Molecule type: DNA

A;Residues: 2-8, 'SGA', 12-36, 'GP', 39-78, 'S', 80-196, 'E', 198-260, 'Q', 262-270, 'H', 272-386, 'S'

A;Cross-references: UNIPARC:UPI00001774BB; GB:M28496; NID:9186728

A;Note: the authors translated the codon CGT for residue 15 as Pro and GAG for residue 2

A;Note: this translation is not annotated in GenBank entry HUMKERK5X, release 111.0

R;Lersch, R.; Fuchs, E.

Mol. Cell. Biol. 8, 486-493, 1988

A;Title: Sequence and expression of a type II keratin, K5, in human epidermal cells.

A;Reference number: A27679; MUID:88094424; PMID:2447486

A;Accession: A27679

A;Molecule type: mRNA

A;Residues: 83-196, 'E', 198-260, 'Q', 262-270, 'H', 272-386, 'S', 388-557, 'S', 559-590 <LE2>

A;Cross-references: UNIPARC:UPI000016ABA6; GB:M19723; NID:9186726; PIDN:AAA36145.1; PID:

R;Lane, E.B.; Rugg, E.L.; Navsaria, H.; Leigh, I.M.; Heagerty, A.H.W.; Ishida-Yamamoto,

Nature 356, 244-246, 1992

A;Title: A mutation in the conserved helix termination peptide of keratin 5 in hereditar

A;Reference number: I58080; MUID:92204232; PMID:1372711

A;Accession: I58080

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 467-474, 'G', 476-481 <LAN>

A;Cross-references: UNIPARC:UPI000011F7CB; GB:S90014; NID:9247707; PIDN:AAB21859.1; PID:

C;Comment: This type II keratin is expressed together with the type I keratin 14 in the

C;Genetics:

A;Gene: GDB:KRT5; EBS2

A;Cross-references: GDB:128110; OMIM:148040

A;Map position: 12q11-12q13

A;Introns: 185/3; 257/2; 277/3; 309/3; 364/3; 406/3; 480/2; 492/1

A;Note: defects in this gene may result in Dowling-Meara type epidermolysis bullosa simp

C;Complex: heterotetramer of two type I, usually keratin 14 (see PIR:KGHE), and two type

C;Superfamily: cytoskeletal keratin

C;Keywords: coiled coil; cytoskeleton; epidermis; heterotetramer

Query Match

Best Local Similarity 66.7%; Score 44; DB 2; Length 590;

Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SELNRVIOQLRS 15
 :||||:|||||
 Db 387 TENRMIQLRLA 398

Search completed: July 5, 2006, 19:20:32

Job time : 20.4175 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 18:28:56 ; Search time 163.728 Seconds
(without alignments)
90.395 Million cell updates/sec

Title: US-10-774-928A-9

Perfect score: 66

Sequence: 1 XXYSELNRVQLRLRSI 16

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	83.3	625	Q6IMF3_RAT	Q6imf3 rattus norv
2	55	83.3	643	1 K2C1_HUMAN	P04264 homo sapien
3	52	78.8	627	1 K2C1_MOUSE	P04104 mus musculu
4	52	78.8	637	2 Q9D2R8_MOUSE	Q9d2k8 mus musculu
5	50	75.8	79	2 Q63280_RAT	Q63280 rattus norv
6	50	75.8	381	2 Q99MH7_MOUSE	Q99mh7 mus musculu
7	50	75.8	398	2 Q8NA87_HUMAN	Q8na87 homo sapien
8	50	75.8	510	2 Q8WWZ0_HUMAN	Q8wwz0 homo sapien
9	50	75.8	511	2 Q8WWY9_HUMAN	Q8wwy9 homo sapien
10	50	75.8	536	1 K2C4_RAT	Q6ig00 rattus norv
11	50	75.8	551	2 Q8BGZ7_MOUSE	Q8bgz7 m 10 days n
12	50	75.8	552	2 Q4FZU2_RAT	Q4fzu2 rattus norv
13	50	75.8	573	2 Q6IG05_RAT	Q6ig05 rattus norv
14	50	75.8	576	1 K2C5_RAT	Q9p6q2 rattus norv
15	50	75.8	580	1 K2C5_MOUSE	Q92tu2 mus musculu
16	50	75.8	601	1 K2C5_BOVIN	Q5xqns bos taurus
17	50	75.8	606	2 Q32P04_MOUSE	Q32p04 mus musculu
18	50	75.8	619	2 Q6E1Y9_CANFA	Q6e1y9 canis fami
19	49	74.2	525	1 K2C4_MOUSE	P07744 mus musculu
20	48	72.7	532	2 Q6IFZ4_RAT	Q6ifz4 rattus norv
21	48	72.7	538	2 Q8BIS2_MOUSE	Q8bis2 mus musculu
22	47	71.2	203	2 Q9CV13_MOUSE	Q9cv13 mus musculu
23	47	71.2	278	2 Q9CV72_MOUSE	Q9cv72 mus musculu
24	47	71.2	384	1 K2C6D_HUMAN	P48667 homo sapien
25	47	71.2	551	2 Q95678_HUMAN	Q95678 homo sapien
26	47	71.2	551	2 Q9NSA9_HUMAN	Q9nsa9 homo sapien
27	47	71.2	552	1 K2C6A_MOUSE	P50446 mus musculu
28	47	71.2	552	2 Q6IFZ8_MOUSE	Q6ifz8 mus musculu
29	47	71.2	554	2 Q3UV11_MOUSE	Q3uv11 mus musculu
30	47	71.2	561	1 K2C6B_MOUSE	Q9z331 mus musculu
31	47	71.2	563	1 K2C6A_HUMAN	P02536 homo sapien

32	47	71.2	563	1 K2C6B_HUMAN	P04259 homo sapien
33	47	71.2	563	1 K2C6C_HUMAN	P48666 homo sapien
34	47	71.2	563	1 K2C6E_HUMAN	P48668 homo sapien
35	47	71.2	564	2 Q2TAZ9_HUMAN	Q2ta29 homo sapien
36	47	71.2	590	1 K2C5_HUMAN	P13647 homo sapien
37	47	71.2	590	2 Q5XGT4_XENLA	Q5xgt4 xenopus lae
38	47	71.2	639	2 Q4VAQ2_HUMAN	Q4vaq2 homo sapien
39	47	71.2	645	1 K22E_HUMAN	P35908 homo sapien
40	46	69.7	381	2 Q32MB2_HUMAN	Q32mb2 homo sapien
41	46	69.7	534	1 K2C4_HUMAN	P19013 homo sapien
42	46	69.7	539	2 Q6NXH9_MOUSE	Q6nxh9 mus musculu
43	46	69.7	540	2 Q86Y46_HUMAN	Q86y46 homo sapien
44	46	69.7	553	2 Q6IG03_RAT	Q6ig03 rattus norv
45	46	69.7	599	2 Q6PVZ5_CHICK	Q6pvz5 gallus gall

ALIGNMENTS

RESULT 1

Q6IMF3_RAT ID Q6IMF3_RAT PRELIMINARY; PRT; 625 AA.
AC Q6IMF3;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Type II keratin Kbl.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=23257644; PubMed=15085952; DOI=10.1078/0171-9335-00354;
RA Hesse M., Zimek A., Weber K., Magin T.M.;
RT "Comprehensive analysis of keratin gene clusters in humans and rodents.";
RL Eur. J. Cell Biol. 83:19-26(2004).
CC -!- MISCELLANEOUS: The sequence shown here is derived from an EMBL/GenBank/DBJ third party annotation (TPA) entry.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; BK001580; DAA02055.1; -; mRNA.
CC Ensembl; ENSRNOC0000028996; Rattus norvegicus.
CC GO; GO:0005982; C:intermediate filament; IEA.
CC GO; GO:0005198; F:structural molecule activity; IEA.
CC InterPro; IPR001664; IF.
CC InterPro; IPR002957; Keratin I.
CC InterPro; IPR003054; Keratin II.
CC PANTHER; PTHR1893.SF5; Keratin_II; 1.
CC Pfam; PF00038; Filament; 1.
CC PRINTS; PR01248; TYPE1KERATIN.
CC PRINTS; PR01276; TYPE2KERATIN.
CC PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
SQ SEQUENCE 625 AA; 64831 MW; 790AAC59E2A2707B CRC64;

Query Match 83.3%; Score 55; DB 2; Length 625;

Best Local Similarity 100.0%; Pred. No. 0.92;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SELNRVQLRLRS 15

DB 398 SELNRVQLRLRS 409

RESULT 2

K2C1_HUMAN ID K2C1_HUMAN STANDARD; PRT; 643 AA.

AC P04264; Q14720; O6GSJ0; Q9H298;
 DT 20-MAR-1987, integrated into UniProtKB/Swiss-Prot.
 DT 01-FEB-1996, sequence version 4.
 DT 07-FEB-2006, entry version 16.
 DE Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1)
 GN [K1] (67 kDa cytokeratin) (Hair alpha protein).
 GN Names=KRT1; Synonyms=KRTA;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX MEDLINE=85166239; PubMed=2580302;
 RA Johnson L.D., Idler W.W., Zhou X.-M., Roop D.R., Steinert P.M.;
 RT "Structure of a gene for the human epidermal 67-kDa keratin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:1896-1900(1985).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RA Whitlock N.V., Eady R.A.J., McGrath J.A.;
 RT "Genomic organization of the human keratin 1 gene.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RA Hatsell S.J., Eady R.A.J., Wennerstrand L., Dopping-Hepenstal P.J.,
 RA Leigh I.M., Munro C., Kelsell D.P.;
 RT "Novel splice site mutation in keratin 1 underlies mild epidermolytic
 RT palmoplantar keratoderma in three kindreds.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP TISSUE=skin;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mulláhy S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP PRELIMINARY NUCLEOTIDE SEQUENCE [MRNA] OF 151-643.
 RX MEDLINE=85207740; PubMed=2581964;
 RA Steinert P.M., Parry D.A.D., Idler W.W., Johnson L.D., Steven A.C.,
 RA Roop D.R.;
 RT "Amino acid sequences of mouse and human epidermal type II keratins of
 RT Mr 67,000 provide a systematic basis for the structural and functional
 RT diversity of the end domains of keratin intermediate filament
 RT subunits.";
 RL J. Biol. Chem. 260:7142-7149(1985).
 RN [6]
 RP PROTEIN SEQUENCE OF 1-7.
 RC TISSUE=platelet;
 RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;
 RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
 RA Thomas G.R., Vandekerckhove J.;
 RT "Exploring proteomes and analyzing protein processing by mass
 RT spectrometric identification of sorted N-terminal peptides.";
 RL Nat. Biotechnol. 21:566-569(2003).
 RN [7]
 RP CITRULLINATION
 RX MEDLINE=96374388; PubMed=8780679; DOI=10.1006/bbrc.1996.1240;
 RA Senshu T., Kan S., Ogawa H., Manabe M., Asaga H.;
 RT "Preferential demination of keratin K1 and filaggrin during the
 RT terminal differentiation of human epidermis.";
 RL Biochem. Biophys. Res. Commun. 225:712-719(1996).
 RN [8]
 RP VARIANT EHK PRO-160.
 RX MEDLINE=92386601; PubMed=1381288; DOI=10.1016/0092-8674(92)90315-4;
 RA Chipev C.C., Korge B.P., Markova N., Bale S.J., Digiovanna J.J.,
 RA Compton J.G., Steinert P.M.;
 RT "A leucine-->proline mutation in the H1 subdomain of keratin 1 causes
 RT epidermolytic hyperkeratosis.";
 RL Cell 70:821-828(1992).
 RN [9]
 RP VARIANT ALLELE 1B 559-GLY--TYR-565 DEL.
 RX MEDLINE=93107743; PubMed=1281859; DOI=10.1111/1523-1747.ep12614149;
 RA Korge B.P., Compton J.G., Steinert P.M., Mischke D.;
 RT "The two size alleles of human keratin 1 are due to a deletion in the
 RT glycine-rich carboxyl-terminal V2 subdomain.";
 RL J. Invest. Dermatol. 99:697-702(1992).
 RN [10]
 RP VARIANT EHK GLN-489.
 RX MEDLINE=92376531; PubMed=1380725;
 RA Rothnagel J.A., Dominey A.M., Dempsey L.D., Longley M.A.,
 RA Greenhalgh D.A., Gagne T.A., Huber M., Frenk E., Hohl D., Roop D.R.;
 RT "Mutations in the rod domains of keratins 1 and 10 in epidermolytic
 RT hyperkeratosis.";
 RL Science 257:1128-1130(1992).
 RN [11]
 RP VARIANT EHK CYS-481.
 RX MEDLINE=94216497; PubMed=7512983;
 RA Syder A.J., Yu Q.-C., Paller A.S., Giudice G., Pearson R., Fuchs E.;
 RT "Genetic mutations in the K1 and K10 genes of patients with
 RT epidermolytic hyperkeratosis. Correlation between location and disease
 RT severity.";
 RL J. Clin. Invest. 93:1533-1542(1994).
 RN [12]
 RP VARIANTS EHK GLY-154; SER-187 AND PRO-192.
 RX MEDLINE=94117869; PubMed=7507151; DOI=10.1111/1523-1747.ep12371725;
 RA Yang J.-M., Chipev C.C., Digiovanna J.J., Bale S.J., Marekov L.N.,
 RA Steinert P.M., Compton J.G.;
 RT "Mutations in the H1 and 1A domains in the keratin 1 gene in
 RT epidermolytic hyperkeratosis.";
 RL J. Invest. Dermatol. 102:17-23(1994).
 RN [13]
 RP VARIANTS EHK PRO-185 AND SER-187.
 RX MEDLINE=94117870; PubMed=7507152; DOI=10.1111/1523-1747.ep12371726;
 RA McLean W.H.I., Eady R.A.J., Dopping-Hepenstal P.J.C., McMillan J.R.,
 RA Leigh I.M., Navsaria H.A., Higgins C., Harper J.I., Paige D.G.,
 RA Morley S.M.;
 RT "Mutations in the rod 1A domain of keratins 1 and 10 in bullous
 RT congenital ichthyosiform erythroderma (BCIE).";
 RL J. Invest. Dermatol. 102:24-30(1994).
 RN [14]
 RP VARIANT NEPPK ILE-73.
 RX MEDLINE=95096501; PubMed=7528239; DOI=10.1111/1523-1747.ep12412771;
 RA Kimonis V., Digiovanna J.J., Yang J.-M., Doyle S.Z., Bale S.J.,
 RA Compton J.G.;
 RT "A mutation in the V1 end domain of keratin 1 in non-epidermolytic
 RT palmar-plantar keratoderma.";
 RL J. Invest. Dermatol. 103:764-769(1994).
 RN [15]
 RP VARIANT EHK VAL-339.
 RX MEDLINE=99072666; PubMed=9856846;
 RX DOI=10.1046/j.1523-1747.1998.00389.x;
 RA Kremer H., Lavrijssen A.P., McLean W.H.I., Lane E.B., Melchers D.,
 RA Ruiter D.J., Marman E.C., Steijlen P.M.;
 RT "An atypical form of bullous congenital ichthyosiform erythroderma is
 RT caused by a mutation in the L12 linker region of keratin 1.";
 RL J. Invest. Dermatol. 111:1224-1226(1998).
 RN [16]

```
RP VARIANTS AEI PHE-478 AND THR-478.
RX MEDLINE=99162195; PubMed=10053007;
RA Sybert V.P., Francis J.S., Corden L.D., Smith L.T., Weaver M.,
RA Stephens K., McLean W.H.I.;
RT "Cyclic ichthyosis with epidermolytic hyperkeratosis: a phenotype
RT conferred by mutations in the 2B domain of keratin K1.",
RL Am. J. Hum. Genet. 64:732-738(1999).
RN [17]
RP VARIANT EHK THR-187.
RX MEDLINE=99247363; PubMed=10232403;
RA Arin M.J., Longley M.A., Kuster W., Huber M., Hohl D., Rothnagel J.A.,
RA Roop D.R.;
RT "An asparagine to threonine substitution in the 1A domain of keratin
RT 1: a novel mutation that causes epidermolytic hyperkeratosis.",
RL Exp. Dermatol. 8:124-127(1999).
RN [18]
RP VARIANT AEI PHE-478.
RX MEDLINE=2062276; PubMed=10597140;
RA Michael E.J., Schneiderman P., Grossman M.E., Christiano A.M.;
RT "Epidermolytic hyperkeratosis with polycyclic psoriasiform plaques
RT resulting from a mutation in the keratin 1 gene.",
RL Exp. Dermatol. 8:501-503(1999).
RN [19]
RP VARIANT EHK PRO-213.
RX MEDLINE=20305470; PubMed=10844506;
RA DOI=10.1046/j.1365-2230.2000.00625.x;
RA Csernaimi-Friedman P.B., Squeo R., Gordon D., Garzon M.,
RA Schneiderman P., Grossman M.E., Christiano A.M.;
RT "Epidermolytic hyperkeratosis in a Hispanic family resulting from a
RT mutation in the keratin 1 gene.",
RL Clin. Exp. Dermatol. 25:241-243(2000).
RN [20]
RP VARIANT EHK THR-478.
RX MEDLINE=20151078; PubMed=10688370;
RA DOI=10.1034/j.1600-0625.2000.009001016.x;
RA Arin M.J., Longley M.A., Epstein E.H. Jr., Rothnagel J.A., Roop D.R.;
RT "Identification of a novel mutation in keratin 1 in a family with
RT epidermolytic hyperkeratosis.",
RL Exp. Dermatol. 9:16-19(2000).
RN [21]
RP VARIANT EHK ASP-154.
RX MEDLINE=21423058; PubMed=11531804;
RA DOI=10.1046/j.1365-2133.2001.04327.x;
RA Whittock N.V., Ashton G.H.S., Griffiths W.A.D., Eady R.A.J.,
RA McGrath J.A.;
RT "New mutations in keratin 1 that cause bullous congenital
RT ichthyosiform erythroderma and keratin 2e that cause ichthyosis
RT bullosa of Siemens.",
RL Br. J. Dermatol. 145:330-335(2001).
RN [22]
RP INVOLVEMENT IN IHCM.
RX MEDLINE=21184521; PubMed=11286616;
RA DOI=10.1046/j.1523-1747.2001.01292.x;

Query Match 83.3%; Score 55; DB 1; Length 643;
Best Local Similarity 100.0%; Pred. No. 0.95; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY 4 SELNRVQLRLS 15
Db 398 SELNRVQLRLS 409
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RESULT 3
K2C1 MOUSE STANDARD; PRT; 627 AA.
AC P04104;
DT 01-NOV-1986, integrated into UniProtKB/Swiss-Prot.
DT 30-MAY-2000, sequence version 2.
DE 07-FEB-2006, entry version 50.
DE Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1)
DE (K1) (67 kDa cytokeratin).
GN Name=Krt1; Synonyms=Krt2-1;
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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=85207740; PubMed=2581964;
RA Steinert P.M., Parry D.A.D., Idler W.W., Johnson L.D., Steven A.C.,
RA Roop D.R.;
RT "Amino acid sequences of mouse and human epidermal type II keratins of
RT Mr 67,000 provide a systematic basis for the structural and functional
RT diversity of the end domains of keratin intermediate filament
RT subunits.",
RL J. Biol. Chem. 260:7142-7149(1985).
RN [2]
RP SEQUENCE REVISION.
RA Roop D.R.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBUNIT: Heterotetramer of two type I and two type II keratins.
CC -1- PTM: Undergoes deamination of some arginine residues
CC (citrullination) (By similarity).
CC -1- MISCELLANEOUS: There are two types of cytoskeletal and
CC microfibrillar keratin, I (acidic) and II (neutral to basic) (40-
CC 55 and 56-70 kilodaltons, respectively).
CC -1- SIMILARITY: Belongs to the intermediate filament family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: M10937; AAD05191.1; -; mRNA.
DR PIR: A02951; KEMS2.
DR HSP; P08670; IGK7.
DR SWISS-2DPAGE; P04104; MOUSE.
DR Ensembl: ENSMUSG00000046834; Mus musculus.
DR MGI: MGI:96698; Krt2-1.
DR InterPro: IPR001664; IF.
DR InterPro: IPR002957; Keratin_I.
DR InterPro: IPR003054; Keratin_II.
DR PANTHER: PTHR1893:SP5; Keratin_II; 1.
DR Pfam: PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Citrullination; Coiled coil; Intermediate filament; Keratin.
FT INIT MET 0 0 By similarity.
FT CHAIN 1 627 Keratin, type II cytoskeletal 1.
FT /FTID=PRO_0000063710.
FT REGION 1 186 Head.
FT REGION 187 496 Rod.
FT REGION 187 222 Coil 1A.
FT REGION 223 242 Linker 1.
FT REGION 243 333 Coil 1B.
FT REGION 334 357 Linker 12.
FT REGION 358 496 Coil 2.
FT REGION 497 627 Tail.
FT SITE 451 451 Stutter.
SQ SEQUENCE 627 AA; 65092 MW; EF7E848654539578 CRC64;

Query Match 78.8%; Score 52; DB 1; Length 627;
Best Local Similarity 91.7%; Pred. No. 3-2;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVQLRLS 15
Db 406 SELNRVQLRLS 417
|||||:|||||

RESULT 4
Q9D2K8 MOUSE
ID Q9D2K8_MOUSE PRELIMINARY; PRT; 637 AA.
AC Q9D2K8;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
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DT 01-JUN-2001, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE 0 day neonate head cDNA, RIKEN full-length enriched library,
 DE clone:4833436c19 product:keratin complex 2, basic, gene 1, full insert
 DE sequence.
 GN Name=Krt2-1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX NCSTR=10090;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Banael M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA Di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Heminger P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Humaneck L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarovic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
 RA Nakazaki Y., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
 RA Petrovsky N., Piazza S., Reid J.C., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Vezardo R., Wei C.L., Yagi K.,
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashina T., Kohjima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Dragani T.A., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shinada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Iwama H., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bash G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20330913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
RN [8]

CC NUCLEOTIDE SEQUENCE.
CC STRAIN=C57BL/6J; TISSUE=Head;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami T., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Belongs to the intermediate filament family.

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CC -----
CC

DR EMBL; AK019521; ICK7

DR HSSP; P08670; ICK7

DR Ensembl; ENSMUSG00000046834; Mus musculus.

DR MGI; MGI:96698; Krt2-1.

DR GO; GO:0005882; C:intermediate filament; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR001664; IF.

DR InterPro; IPR002957; Keratin I.

DR InterPro; IPR003054; Keratin II.

DR PANTHER; PTHR1893:SF5; Keratin_II; 1.

DR Pfam; PF00038; Filament; 1.

DR PRINTS; PR01248; TYPE1KERATIN.

DR PRINTS; PR01276; TYPE2KERATIN.

DR PROSITE; PS00226; IF; 1.

KW Intermediate filament; Keratin.

SQ SEQUENCE 637 AA; 65627 MW; D6344FDD0468EAC7 CRC64;

Query Match 78.8%; Score 52; DB 2; Length 637;

Best Local Similarity 91.7%; Pred. No. 3.2;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVQLRLS 15

|||||:|||||

Db 407 SELNRMIQLRLS 418

RESULT 5

ID Q63280 RAT PRELIMINARY; PRT; 79 AA.

AC Q63280;

DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.

DT 01-NOV-1996, sequence version 1.

DT 07-FEB-2006, entry version 21.

DE Keratin K5 (fragment).

GN Name=keratin K5;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidae; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

[1]

CC NUCLEOTIDE SEQUENCE.

CC STRAIN=Dark agouti; TISSUE=Mammary;

CC MEDLINE=93046184; PubMed=1384967;

RA Paine M.L., Gibbins J.R., Chew K.E., Demetrious A., Kefferd R.F.;

RT "Loss of keratin expression in anaplastic carcinoma cells due to

posttranscriptional down-regulation acting in trans."

Cancer Res. 52:6603-6611(1992).

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CC -----
CC

DR EMBL; M89644; AAA99993.1; -; Genomic DNA.

DR GO; GO:0005882; C:intermediate filament; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR001664; IF.

DR InterPro; IPR003054; Keratin II.

DR PANTHER; PTHR1893:SF5; Keratin_II; 1.

DR Pfam; PF00038; Filament; 1.

KW Keratin.

FT NON TER 1 1

FT NON TER 79 79

SQ SEQUENCE 79 AA; 9395 MW; 92786203021AE926 CRC64;

Query Match 75.8%; Score 50; DB 2; Length 79;

Best Local Similarity 83.3%; Pred. No. 0.8;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVQLRLS 15

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Db 60 SELNRMIQLRLS 71

RESULT 6

Q99MH7 MOUSE

ID Q99MH7 MOUSE PRELIMINARY; PRT; 381 AA.

AC Q99MH7;

DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.

DT 01-JUN-2001, sequence version 1.

DT 07-FEB-2006, entry version 20.

DE Cytochrome KRT2-6HF (Fragment).

GN Name=Krtcap1; Synonyms=Krt2-6hf;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidae; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

[1]

CC NUCLEOTIDE SEQUENCE.

CC STRAIN=C3H/HeN;

CC MEDLINE=2286385; PubMed=1239393;

RA Polster C., Yoshiki A., Fujiwara K., Guenet J.-L., Kusakabe M.;

RT "Hague (Hag): a new mouse hair mutation with an unstable semidominant

allele."

Genetics 162:831-840(2002).

CC -1- SIMILARITY: Belongs to the intermediate filament family.

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CC -----
CC

DR EMBL; AF343088; AAK17206.1; -; mRNA.

DR HSSP; P08670; ICK4.

DR Ensembl; ENSMUSG00000022986; Mus musculus.

DR MGI; MGI:1923500; Krtcap1.

DR GO; GO:0005882; C:intermediate filament; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR001664; IF.

DR InterPro; IPR002957; Keratin I.

DR InterPro; IPR003054; Keratin II.

DR PANTHER; PTHR1893:SF5; Keratin_II; 1.

DR Pfam; PF00038; Filament; 1.

DR PRINTS; PR01248; TYPE1KERATIN.

DR PRINTS; PR01276; TYPE2KERATIN.

DR PROSITE; PS00226; IF; 1.

KW Intermediate filament; Keratin.

FT NON TER 1 1

SQ SEQUENCE 381 AA; 42383 MW; 4143A882F7F6E9A1 CRC64;

Query Match 75.8%; Score 50; DB 2; Length 381;

Best Local Similarity 83.3%; Pred. No. 4.2;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVQLRLS 15

[illegible]

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RP NUCLEOTIDE SEQUENCE.
RA McLean W.H.I.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the intermediate filament family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY033496; AAK55109.1; -; Genomic_DNA.
DR HSPSP; P08670; ICK7.
DR Ensemble; ENSG00000170486; Homo sapiens.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR18993:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
SQ SEQUENCE 511 AA; 55977 MW; 61E830C382063731 CRC64;

Query Match 75.8%; Score 50; DB 2; Length 511;
Best Local Similarity 83.3%; Pred. No. 5.8;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SELNRVQLRLRS 15
Db 344 SELNRQLRLRS 355
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|||||:|||||

RESULT 10
K2C4_RAT STANDARD; PRT; 536 AA.
AC Q6IG00;
DT 22-NOV-2005, integrated into UniProtKB/Swiss-Prot.
DT 05-JUL-2004, sequence version 1.
DT 07-MAR-2006, entry version 14.
DE Keratin, type II cytoskeletal 4 (Cytokeratin-4) (CK-4) (Keratin-4)
DE (K4) (Type II keratin K4).
GN Name=Krt4; Synonyms=Kb4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Brown Norway;
RX PubMed=15057822; DOI=10.1038/nature02426;
RA Gibbs R.A., Weinstock G.M., Metzker M.L., Muzny D.M., Sodergren E.J.,
RA Scherer S., Scott G., Steffen D., Worley K.C., Burch P.E., Okwuonu G.,
RA Hines S., Lewis L., Deramo C., Delgado O., Dugan-Rocha S., Miner G.,
RA Morgan M., Hawes A., Gill R., Holt R.A., Adams M.D., Amanatides P.G.,
RA Baden-Tillson H., Barnstead M., Chin S., Evans C.A., Ferriera S.,
RA Poser C., Gloddek A., Gu Z., Jennings D., Kraft C.L., Nguyen T.,
RA Prannkoch C.M., Sitter C., Sutton G.G., Venter J.C., Woodage T.,
RA Smith D., Lee H.M., Gustafson E., Cahill P., Kana A.,
RA Doucette-Stamm L., Weinstock K., Fechtel K., Weiss R.J., Osogawa K.,
RA Green E.D., Blakesley R.W., Bouffard G.G., De Jong P.J., Jones S.,
RA Zhu B., Marra M., Schein J., Bosdet I., Fjell C., Jones S.,
RA Krzywinski M., Mathewson C., Siddiqui A., Wye N., McPherson J.,
RA Zhao S., Fraser C.M., Shetty J., Shatsman S., Geer K., Chen Y.,
RA Abramson S., Nierman W.C., Havlak P.H., Chen R., Durbin K.J., Egan A.,
RA Ren Y., Song X.Z., Li B., Liu X., Cawley S., Cooney A.J.,
RA D'Souza L.M., Martin K., Wu J.Q., Gonzalez-Garay M.L., Jackson A.R.,
RA Kalafus K.J., McLeod M.P., Milosavljevic A., Virk D., Volkov A.,
RA Wheeler D.A., Zhang Z., Bailey J.A., Eichler E.E., Tuzun E.,
RA Birney E., Mongin E., Ureka-Vidal A., Woodmark C., Zdobnov E.,
RA Bork P., Suyama M., Torrents D., Alexandersson M., Trask B.J.,
RA Young J.M., Huang H., Wang H., Xing H., Daniels S., Gietzen D.,
RA Schmidt J., Stevens K., Vitt U., Wingrove J., Camara F., Mar Alba M.,
RA Abril J.F., Guigo R., Smit A., Dubchak I., Rubin E.M., Couronne O.,

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RA Poliakov A., Hubner N., Ganten D., Goesele C., Hummel O., Kreitler T.,
RA Lee Y.A., Monti J., Schulz H., Zimdahl H., Himmelbauer H., Lehrach H.,
RA Jacob H.J., Bromberg S., Gullings-Handley J., Jensen-Seaman M.I.,
RA Kwitek A.E., Lazar J., Pasko D., Tonellato P.J., Twigger S.,
RA Ponting C.P., Duarte J.M., Rice S., Goodstadt L., Beaton S.A.,
RA Enes R.D., Winter E.E., Webber C., Brandt P., Nyakatura G.,
RA Adetobi M., Charomonte F., Elnitski L., Eswara P., Hardison R.C.,
RA Hou M., Kolbe D., Makova K., Miller W., Nekrutenko A., Riemer C.,
RA Schwartz S., Taylor J., Yang S., Zhang Y., Lindpaintner K.,
RA Andrews T.D., Caccamo M., Clamp M., Clarke L., Curwen V., Durbin R.,
RA Eyras E., Searle S.M., Cooper G.M., Batzoglou S., Brudno M., Sidow A.,
RA Stone E.A., Payseur B.A., Bourque G., Lopez-Otin C., Puente X.S.,
RA Chakrabarti K., Chatterji S., Dewey C., Pachter L., Bray N., Yap V.B.,
RA Caspi A., Tesler G., Pevzner P.A., Haussler D., Roskin K.M.,
RA Baertsch R., Clawson H., Furey T.S., Hinrichs A.S., Karolchik D.,
RA Kent W.J., Rosenbloom K.R., Trumbower H., Weirauch M., Cooper D.N.,
RA Stenson P.D., Ma B., Brent M., Arumugam M., Shteynberg D.,
RA Copley R.R., Taylor M.S., Riethman H., Mudunuri U., Peterson J.,
RA Guyer M., Felsenfeld A., Old S., Mockrin S., Collins F.,
RT "Genome sequence of the Brown Norway rat yields insights into
mammalian evolution.";
RL Nature 428:493-521 (2004).
RN [2]
RN IDENTIFICATION.
RP MEDLINE=23257644; PubMed=15085952; DOI=10.1078/0171-9335-00354;
RX Hesse M., Zimek A., Weber K., Magin T.M.;
RA "Comprehensive analysis of keratin gene clusters in humans and
rodents.";
RT Rur. J. Cell Biol. 83:19-26(2004).
CC -1- SUBUNIT: Heterotetramer of two type I and two type II keratins.
CC Keratin 4 is generally associated with keratin 13.
CC -1- MISCELLANEOUS: There are two types of cytoskeletal and
microfibrillar keratin: I (acidic; 40-55 kDa) [K9 to K20] and II
(neutral to basic; 56-70 kDa) [K1 to K8].
CC -1- SIMILARITY: Belongs to the intermediate filament family.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AABR03057015; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR EMBL; BK003985; DAA02230.1; -; mRNA.
DR Ensembl; ENSRNCG00000032332; Rattus norvegicus.
DR RGD; 1359272; Kb4.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR18993:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PROSITE; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Coiled coil; Intermediate filament; Keratin; Phosphorylation.
FT Keratin, type II cytoskeletal 4.
FT /FTid=PRO_0000063724.
CHAIN 1 536
REGION 1 145 Head.
REGION 146 454 Rod.
REGION 146 181 Coil 1A.
REGION 182 200 Linker 1.
REGION 200 293 Coil 1B.
REGION 294 316 Linker 12.
REGION 317 454 Coil 2.
REGION 455 524 Tail.
REGION 524 511 Gly-rich.
FT COMPBias 471 511 Gly-rich.
FT COMPBias 395 395 Stutter.
FT SITE 51 Phosphoserine (By similarity).
FT MOD RES 51 51 Phosphoserine (By similarity).
SQ SEQUENCE 536 AA; 57667 MW; 5D1AC47FA0477DB4 CRC64;

Query Match 75.8%; Score 50; DB 1; Length 536;
Best Local Similarity 83.3%; Pred. No. 6.1;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SELNRVQLRLRS 15

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365 SELNRMQIRRS 376

DB
RESULT 11
Q8BG27 MOUSE
AC Q8BG27 MOUSE PRELIMINARY; PRT; 551 AA.
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE 10 days neonate skin cDNA, RIKEN full-length enriched library,
DE clone:4732475I03 product:CYTOKERATIN homolog (6 days neonate skin
DE cDNA, RIKEN full-length enriched library, clone:A030012D14
DE product:CYTOKERATIN homolog) (10 days neonate skin cDNA, RIKEN full-
DE length enriched library, clone:4732468K03 product:CYTOKERATIN TYPE II
DE homolog).
DE Names:Krtcap1;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Oyama R., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Carninci P., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Adinolfi V., Allen J.E.,
RA Ambei-Imbato A., Apeil R.W., Bersano T., Aturaliya R.N., Bailey T.L.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernhar D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Gleicher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Sempile C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nieuwen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashina T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563 (2005).
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RT (Genome Network Core Team) and the FANTOM Consortium;
RL "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nika I., Oatso N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarrelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKensie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yashinashi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nika I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli K., Barsh G.,
RA Blake J., Okello D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Schor K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
CC Murioidea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN
RP NUCLEOTIDE SEQUENCE
RX MEDLINE=23257644; PubMed=15085952; DOI=10.1078/0171-9335-00354;
RA Hesse M., Zimek A., Weber K., Magin T.M.;
RT "Comprehensive analysis of keratin gene clusters in humans and
rodents";
RL Eur. J. Cell Biol. 83:19-26(2004).
CC -!- MSCELLANEUS: The sequence shown here is derived from an
EMBL/GenBank/DBSJ third party annotation (TPA) entry.
CC -!- SIMILARITY: Belongs to the intermediate filament family.

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CC
CC
CC EMBL; BK003980; DAA02225.1; -; mRNA.
DR Ensembl; ENSRNOG0000009160; Rattus norvegicus.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR18893.SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
DR KW Intermediate filament; Keratin.
SQ SEQUENCE 573 AA; 62168 MW; EBD075950B847551 CRC64;

Query Match 75.8%; Score 50; DB 2; Length 573;
Best Local Similarity 83.3%; Pred. No. 6.5;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 4 SELNRVIQRLRS 15
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Db 359 SEMNRMIQRLRS 370

RESULT 14
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ID K2C5 RAT STANDARD; PRT; 576 AA.
AC Q6P6Q2; Q7TN97;
DT 08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
DT 05-JUL-2004, sequence version 1.
DT 07-MAR-2006, entry version 18.
DE Keratin, type II cytoskeletal 5 (Cytokeratin-5) (CK-5) (Keratin-5)
(K5).
GN Name=Krt5; Synonyms=Krt2-5;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Murioidea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN
RP NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22954579; PubMed=14551252; DOI=10.1091/mbc.E03-04-0226;
RA Kierzenbaum A.L., Rivkin E., Tres L.L.;
RT "Acropaxome, an F-actin-keratin-containing plate, anchors the
acrosome to the nucleus during shaping of the spermatid head";
RL Mol. Biol. Cell 14:4628-4640(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Prostate;
RG NIH - Mammalian Gene Collection (MGC) project;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SUBUNIT: Heterotetramer of two type I and two type II keratins.
CC Keratin-5 associates with keratin-14.
CC -!- TISSUE SPECIFICITY: Expressed in the epidermis (at protein level)

CC and testis (within pachytene spermatocytes).

CC -1- MISCELLANEOUS: There are two types of cytoskeletal and

CC microfibrillar keratin: I (acidic; 40-55 kDa) [K9 to K20] and II

CC (neutral to basic; 56-70 kDa) [K1 to K8].

CC -1- SIMILARITY: Belongs to the intermediate filament family.

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

CC Distributed under the Creative Commons Attribution-NoDerivs License

ENBL; AY342389; AAQ20893.1; -; mRNA.

DR ENBL; BC062086; AAH62086.1; -; mRNA.

DR HSP; P08670; 1GK7.

DR RGD; 727894; Krt2-5.

DR InterPro; IPR001664; IF.

DR InterPro; IPR003054; Keratin II.

DR PANTHER; PTHR18893:SF5; Keratin_II; 1.

DR Pfam; PFO0038; Filament; 1.

DR PRINTS; PR01276; TYPE2KERATIN.

DR PROSITE; PS00226; IF; 1.

KW Coiled coil; Intermediate filament; Keratin; Phosphorylation.

FT CHAIN 1 576 Keratin, type II cytoskeletal 5.

FT /FtrId=PRO_0000063729.

FT REGION 1 163 Head.

FT REGION 164 473 Rod.

FT REGION 164 199 Coil 1A.

FT REGION 200 218 Linker 1.

FT REGION 219 311 Coil 1B.

FT REGION 312 334 Linker 12.

FT REGION 335 473 Coil 2.

FT REGION 474 576 Tail.

FT COMPTAS 39 135 Gly-rich.

FT COMPTAS 532 576 Ser-rich.

FT SITE 413 413 Stutter.

FT MOD_RES 60 60 Phosphoserine (By similarity).

FT CONFLICT 114 114 E -> R (in Ref. 1).

FT CONFLICT 473 473 G -> Q (in Ref. 1).

FT CONFLICT 508 508 S -> F (in Ref. 1).

FT CONFLICT 528 528 R -> L (in Ref. 1).

FT CONFLICT 562 562 K -> Q (in Ref. 1).

FT CONFLICT 575 575 K -> N (in Ref. 1).

SQ SEQUENCE 576 AA; 61826 MW; 23A1C2C47405EE3B CRC64;

Query Match 75.8%; Score 50; DB 1; Length 576;

Best Local Similarity 83.3%; Pred.No. 6.6;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps

QY 4 SELNRVITQLRLS 15

DB 383 SEMNRMIQLRLS 394

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RESULT 15

K2C5 MOUSE

ID_K2C5_MOUSE STANDARD; PRT; 580 AA.

AC Q922U2; Q920F2;

DT 08-NOV-2005, integrated into UniProtKB/Swiss-Prot.

DT 01-DEC-2001, sequence version 1.

DT 07-MAR-2006, entry version 26.

DE Keratin, type II cytoskeletal 5 (Cytokeratin-5) (CK-5) (Keratin-5) (K5).

DE Name=Krt5; Synonyms=Krt2-5;

GN Name=musculus (Mouse).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidae; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RP [1]

RN NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND TISSUE SPECIFICITY.

RP STRAIN=129/Ola;

RC MEDLINE=21301816; PubMed=11408584;

RA Peters B., Kirtel J., Bussow H., Vidal M., Magin T.M.;

RT "Complete cytokeratin and neonatal lethality in keratin 5 knockout mice reveal its fundamental role in skin integrity and in epidermolysis

Qy 4 SELNRVIQRLRS 15

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 18:28:26 ; Search time 139.029 Seconds

(without alignments)
52.618 Million cell updates/sec

Title: US-10-774-928A-9

Perfect score: 66

Sequence: 1 XXYSLENRVQLRLRSI 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_8:*

- 1: geneseqp1980s:*
- 2: geneseqp1980s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	66	100.0	16	6	AAO26395
2	66	100.0	16	9	ADV04414
3	59	89.4	16	6	AAO26389
4	55	83.3	643	6	ABG74869
5	55	83.3	644	8	ADQ17549
6	55	83.3	644	9	AEA15501
7	52	78.8	628	8	ADS85115
8	50	75.8	398	7	ADB65234
9	50	75.8	511	5	ABG94648
10	50	75.8	511	7	ADL36000
11	50	75.8	511	9	AEA15498
12	50	75.8	601	8	ADW07163
13	50	75.8	679	9	AEA20243
14	47	71.2	20	9	AED42282
15	47	71.2	92	8	ADR98933
16	47	71.2	268	8	ADR98973
17	47	71.2	295	8	ADR98974
18	47	71.2	342	7	ADE15641
19	47	71.2	551	3	AA52398
20	47	71.2	551	5	AAE20423
21	47	71.2	564	5	ABP65226
22	47	71.2	564	8	ADJ75686
23	47	71.2	564	8	ADN04684

24	47	71.2	564	8	ADN04384
25	47	71.2	564	8	ADO55108
26	47	71.2	564	8	ADQ18800
27	47	71.2	564	9	AEA15493
28	47	71.2	564	9	AEA15491
29	47	71.2	564	9	AEA15492
30	47	71.2	564	9	AEA15494
31	47	71.2	564	9	AEA17592
32	47	71.2	564	9	AEA17594
33	47	71.2	564	9	AEA87757
34	47	71.2	567	7	ADB65618
35	47	71.2	585	9	AED74047
36	47	71.2	602	6	ABR41632
37	47	71.2	625	6	ABP98825
38	47	71.2	645	5	ABG77177
39	47	71.2	645	8	ADN04309
40	47	71.2	645	9	ADV85790
41	47	71.2	645	9	AEA15500
42	46	69.7	327	7	ADJ69669
43	46	69.7	508	8	ADS10914
44	46	69.7	521	5	ABG94649
45	46	69.7	521	5	ABB78802

ALIGNMENTS

RESULT 1
AAO26395
ID AAO26395 standard; peptide; 16 AA.
AC AAO26395;
XX
DT 30-JAN-2003 (first entry)
XX
DE Psoriasis treating immunotherapeutic peptide.
XX
KW Antipsoriatic; immunostimulant; gene therapy; pharmaceutical composition;
KW vaccine; immunogenic variant; immunotherapeutic agent; psoriasis;
KW gene therapy.
XX
OS Leishmania sp.
XX
PN WO200274239-A2.
XX
PD 26-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006496.
XX
PR 16-MAR-2001; 2001US-00809003.
XX
PA (AKIV-) AKIVA LLC.
XX
PI O'daly JA;
XX
DR WPI; 2003-018763/01.
XX
PT New polypeptide and immunogenic variants comprising amino acid sequences of particulate antigens, useful for the treatment and clinical remission of psoriasis.
XX
PS Example 17; Page 43; 56pp; English.
XX
CC The invention relates to a polypeptide comprising an isolated amino acid sequence or immunogenic variants selected from any of 14 fully defined sequences of 7-16 amino acids, given in the specification. The immunotherapeutic agents and a pharmaceutical compositions comprising polynucleotides and vectors of the invention are useful for the treatment and clinical remission of psoriasis. The isolated nucleic acids are useful as probes. The sequences of the invention can be used in the treatment of disorders by gene therapy. This sequence represents an immunotherapeutic peptide related to the invention

SQ Sequence 16 AA;

Query Match 100.0%; Score 66; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YSELNRVQLRLSI 16
|||||
Db 3 YSELNRVQLRLSI 16

RESULT 2
ADV04414
ID ADV04414 standard; peptide; 16 AA.
XX
AC ADV04414;
XX
DT 24-FEB-2005 (first entry)
XX
DE Leishmania immunotherapeutic peptide SEQ ID NO:9.
XX
KW T-lymphocyte; immunogenicity; antigen; antiprosoritic; immunostimulant;
KW psoriasis.
XX
OS Leishmania sp.
XX
PN US2004241168-A1.
XX
PD 02-DEC-2004.
XX
PF 09-FEB-2004; 2004US-00774928.
XX
PR 16-MAR-2001; 2001US-00809003.
PR 17-OCT-2003; 2003US-00687892.
XX
PA (ODAL/) ODALY J A.
XX
PI Odaly JA;
XX
WPI; 2005-011563/01.
XX
XX Inhibiting selectively T-cell rolling in human, by administering compound
PT interfering with cutaneous lymphocyte antigen-E selectin interaction and
PT leukocyte function associated antigen-1 interaction.
XX
PS Claim 18; SEQ ID NO 9; 21pp; English.
XX
CC The invention relates to a novel method for selectively inhibiting T-cell
CC rolling in a human host, comprising administering a compound that
CC selectively interferes with the cutaneous lymphocyte antigen (CLA)-E
CC selectin interaction and leukocyte function associated antigen (LFA)-
CC 1/intercellular adhesion molecule (ICAM) and very late antigen
CC (VLA)/vascular cell adhesion molecule (VCAM) interactions. The compound
CC includes an immunotherapeutic agent, which comprises a purified protein
CC extract that is isolated by diethylaminoethyl Sephadex chromatography of
CC a Nonidet P-40 insoluble particulate antigen fraction derived from
CC isolated killed cells of amastigotes from one or more species of the
CC Leishmania genus, where the particulate antigen fraction is solubilized
CC with 8M urea and 0.025 M Tris(hydroxymethyl)aminomethane pH 8.3 applied
CC to diethylaminoethyl Sephadex and is eluted with a solution comprising
CC 0.1 M sodium chloride, 8 M urea and 0.025 M
CC Tris(hydroxymethyl)aminomethane pH 8.3, and the purified protein extract
CC includes polypeptides having apparent molecular weights of 73, 80 and 82
CC kDa, after total reduction and alkylation. The species is L. amazonensis,
CC L. venezuelensis, L. brasiliensis and/or L. chagasi. A compound of the
CC invention has antiprosoritic and immunostimulant activity, and inhibits T-
CC cell rolling by interfering with CLA-E selectin interaction and LFA-
CC 1/ICAM and VLA/VCAM interactions. The method is useful for selectively
CC inhibiting T-cell rolling in a human host, and for treating psoriasis.
CC The present sequence represents a Leishmania peptide used in the
CC invention.
XX
XX Sequence 16 AA;

Query Match 100.0%; Score 66; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YSELNRVQLRLSI 16
|||||
Db 3 YSELNRVQLRLSI 16

RESULT 3
AAO26389
ID AAO26389 standard; peptide; 16 AA.
XX
AC AAO26389;
XX
DT 30-JAN-2003 (first entry)
XX
DE Psoriasis treating immunotherapeutic peptide, SEQ ID No 9.
XX
KW Antiprosoritic; immunostimulant; gene therapy; pharmaceutical composition;
KW vaccine; immunogenic variant; immunotherapeutic agent; psoriasis;
KW gene therapy.
XX
OS Leishmania sp.
XX
PN WO200274239-A2.
XX
PD 26-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006496.
XX
PR 16-MAR-2001; 2001US-00809003.
XX
PA (AKIV-) AKIVA LLC.
XX
PI O'daly JA;
XX
WPI; 2003-018763/01.
XX
XX New polypeptide and immunogenic variants comprising amino acid sequences
PT of particulate antigens, useful for the treatment and clinical remission
PT of psoriasis.
XX
PS Claim 1; Page 55; 56pp; English.
XX
CC The invention relates to a polypeptide comprising an isolated amino acid
CC sequence or immunogenic variants selected from any of 14 fully defined
CC sequences of 7-16 amino acids, given in the specification. The
CC immunotherapeutic agents and a pharmaceutical compositions comprising
CC polynucleotides and vectors of the invention are useful for the treatment
CC and clinical remission of psoriasis. The isolated nucleic acids are
CC useful as probes. The sequences of the invention can be used in the
CC treatment of disorders by gene therapy. This sequence represents one of
CC the 14 immunotherapeutic peptides of the invention
XX
XX Sequence 16 AA;

Query Match 89.4%; Score 59; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVQLRLSI 16
|||||
Db 4 SELNRVQLRLSI 16

RESULT 4
ABG74869
ID ABG74869 standard; protein; 643 AA.
XX
AC ABG74869;
XX

DT 19-JUN-2003 (first entry)
XX Human cytokерatin-1 protein.
DE Cytokeratin-1; inflammation; infection; soluble; sepsis; veterinary;
XX sepsis-like systemic infection; human.
KW Homo sapiens.
XX WO2003002600-A1.
PN 09-JAN-2003.
XX 12-JUN-2002; 2002WO-EP006473.
PF 27-JUN-2001; 2001DE-01030985.
XX (BRAH-) BRAHMS AG.
PA Bergmann A, Struck J, Uehlein M;
PI WPI; 2003-201491/19.
XX New use of soluble cytokерatin-1 fragments from body fluid are tissue as
PT marker peptides or to provide therapeutics for the diagnosis, prognosis
PT and treatment of inflammatory disease and infection, including systemic
PT inflammation.
XX Claim 3; Page 38-40; 51pp; German.
XX This invention describes a novel use of soluble cytokерatin-1 fragments
CC from body fluid or tissue as marker peptides for the detection, prognosis
CC and control of inflammation and infection or as a therapeutic target for
CC inflammation and infection. The invention also describes a method of
CC producing a soluble cytokерatin-1 fragment in rich or pure form from a
CC human material rich in cytokерatin-1 by enzymatically splitting the
CC cytokерatin-1 with endoprotease to obtain the hydrolysis products and
CC purifying the resulting fragments. The novel cytokерatin fragments are
CC useful for the differential diagnosis, early recognition and prognosis,
CC evaluation of severity of sepsis and heavy infection, particularly sepsis
CC -like systemic infection. The fragments are used in human and veterinary
CC therapy, particularly the fragment or it's specific antibody is used to
CC treat inflammatory disease or infection. This sequence represents the
CC human cytokерatin-1 protein described in the disclosure of the invention
XX
SQ Sequence 643 AA;
Query Match 83.3%; Score 55; DB 6; Length 643;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 SELNRVIOQLRS 15
Db 398 SELNRVIOQLRS 409
RESULT 5
ADQ17549
ID ADQ17549 standard; protein; 644 AA.
XX AC ADQ17549;
XX 26-AUG-2004 (first entry)
XX Human soft tissue sarcoma-upregulated protein - SEQ ID 366.
DE soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX Homo sapiens.
OS WO2004048938-A2.
PN 10-JUN-2004.
PD

XX 26-NOV-2003; 2003WO-US038193.
XX 26-NOV-2002; 2002US-0429739P.
XX (PROT-) PROTEIN DESIGN LABS INC.
PA Aziz N, Ginsburg WM, Zlotnik A;
PI WPI; 2004-441208/41.
XX Early detection of soft tissue sarcoma comprises determining expression
XX of a gene in a first soft tissue sample and a normal soft tissue sample
XX and comparing the gene expression, also useful in treating soft tissue
XX sarcoma.
XX Example 2; SEQ ID NO 366; 210pp; English.
XX The invention relates to a novel method for detecting soft tissue sarcoma
XX which comprises obtaining a first soft tissue sample from an individual
XX and a normal soft tissue sample from the same or different individual,
XX determining the expression of a gene in both samples and comparing the
XX expression of the gene in both soft tissue samples, where a higher level
XX of protein expression in the first soft tissue sample indicates the
XX presence of soft tissue sarcoma. The method of the invention has
XX cyostatic applications and may be useful for detecting soft tissue
XX sarcoma, possibly via gene therapy or vaccine production. The nucleic
XX acid sequences may be useful in diagnostic and screening applications.
XX The current sequence is that of a human soft tissue sarcoma-upregulated
XX protein of the invention. The current sequence is not shown within the
XX specification per se but was submitted in CD format by the inventor.
XX Sequence 644 AA;
Query Match 83.3%; Score 55; DB 8; Length 644;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 SELNRVIOQLRS 15
Db 399 SELNRVIOQLRS 410
RESULT 6
AEA15501
ID AEA15501 standard; protein; 644 AA.
XX AC AEA15501;
XX 28-JUL-2005 (first entry)
XX Human polypeptide #120.
DE Diagnosis; prognosis; cancer; breast tumor; ovary tumor; stomach tumor;
XX colon tumor; esophagus tumor; bladder tumor; non-small-cell lung cancer;
XX cytostatic; neoplasm.
XX Homo sapiens.
OS WO2005047534-A2.
XX PN 26-MAY-2005.
XX 15-OCT-2004; 2004WO-EP011599.
XX 28-OCT-2003; 2003EP-00024565.
XX (FARB) BAYER HEALTHCARE AG.
XX Wirtz R, Munnes M;
XX WPI; 2005-372393/38.
XX N-PSDB; AEA15423.
XX

```

XX Predicting a response to cancer treatment by detecting at least 2
PT markers, which are genes or genomic nucleic acid sequences that are
PT located on one chromosomal region, which is altered in malignant
PT neoplasia.
XX
XX Claim 7; SEQ ID NO 463; 464pp; English.
XX
CC The invention relates to a method of predicting response to cancer
CC treatment comprising detection of at least 2 markers, where the markers
CC are genes and fragments or genomic nucleic acid sequences that are
CC located on one chromosomal region, which is altered in malignant
CC neoplasia. The invention also relates to a method for the prediction,
CC diagnosis or prognosis of malignant neoplasia, methods for detecting,
CC derregulations in malignant neoplasia and breast cancer, a method of
CC determining the phenotype of a cell or tissue, a method for identifying
CC genomic regions which are altered on the chromosomal level and encode
CC genes that are linked by function and are differentially expressed in
CC malignant neoplasia and breast cancer, methods of screening for agents
CC which regulate the activity of a polypeptide or a polynucleotide and
CC antibodies that specifically bind to a full length or partial
CC polypeptide. The method is useful for predicting response to cancer
CC treatment. The methods and compositions are useful for predicting,
CC diagnosing, prognosing, preventing or treating malignant neoplasia
CC including breast cancer, ovarian cancer, gastric cancer, colon cancer,
CC esophageal cancer, mesenchymal cancer, bladder cancer or non-small-cell
CC lung cancer. This sequence represents a human polypeptide used in the
XX scope of the invention.
XX
SQ Sequence 644 AA;
  Query Match      83.3%; Score 55; DB 9; Length 644;
  Best Local Similarity 100.0%; Pred. No. 0.83;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVIOQLRLS 15
   |||||
DB 399 SELNRVIOQLRLS 410
   |||||

RESULT 7
AD85115
ID ADS85115 standard; protein; 628 AA.
XX
AC ADS85115;
XX
XX 19-NOV-2004 (first entry)
XX
DE Mouse atopic dermatitis-related protein sequence SeqID117.
XX
XX atopic dermatitis; gene expression level; skin; inflammation; rash;
KW dermatological; antiinflammatory; antipsoriatic; psoriasis; mouse;
KW murine.
XX
XX Mus musculus.
XX
XX WO2004031386-A1.
XX
XX 15-APR-2004.
XX
XX 01-AUG-2003; 2003WO-JP009808.
XX
XX 06-AUG-2002; 2002JP-00229318.
PR 14-MAY-2003; 2003JP-00136543.
XX
XX (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
XX
XX Itoh M, Ogawa K, Shinagawa A, Sudo H, Ogawa H, Ra C;
PI Mitsuishi K,
XX
XX WPI; 2004-330185/30.
DR N-PSDB; ADS85114.

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XX Determination of difference in expression level of specified genes in
PT inflamed and non-inflamed skin sites for diagnosis and examination of
PT atopic dermatitis and psoriasis.
XX
XX Example 1; SEQ ID NO 117; 611pp; Japanese.
XX
XX This invention relates to a novel method for the examination of atopic
XX dermatitis in which the expression level of specified genes in specimens
XX of skin taken from inflamed (rash) areas and non-inflamed areas is
XX compared and the presence of increased or reduced expression in the
XX inflamed areas determined. The invention may be useful for the
XX development of compounds with a dermatological, antiinflammatory or
XX antipsoriatic activity acting as inhibitors and stimulators of genes
XX involved in atopic dermatitis and psoriasis. The invention may be useful
XX for treatment, prevention, diagnosis and assessment of atopic dermatitis
XX and psoriasis. The present sequence is that of an atopic dermatitis-
XX related protein which was used in the exemplification of the invention.
XX
SQ Sequence 628 AA;
  Query Match      78.8%; Score 52; DB 8; Length 628;
  Best Local Similarity 91.7%; Pred. No. 2.7;
  Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVIOQLRLS 15
   |||||
DB 407 SELNRVIOQLRLS 418
   |||||

RESULT 8
ADB65234
ID ADB65234 standard; protein; 398 AA.
XX
AC ADB65234;
XX
XX 04-DEC-2003 (first entry)
XX
DE Human protein encoded by clone TESTI20041630.
XX
XX Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
KW cell regeneration; membrane protein; signal transduction-related protein;
KW transcription-related protein; osteoporosis; neurological disease;
KW cancer; tumour.
XX
XX Homo sapiens.
XX
XX EP1308459-A2.
XX
XX 07-MAY-2003.
XX
XX 28-MAR-2002; 2002EP-00007401.
XX
XX 05-NOV-2001; 2001JP-00379298.
PR 25-JAN-2002; 2002US-00350978.
XX
XX (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
XX WPI; 2003-450961/43.
DR N-PSDB; ADB63264.
XX
XX New polynucleotides and polypeptides, useful for developing a diagnostic
PT marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.
XX
XX Claim 1; Page; 222pp; English.
XX
XX The invention discloses a polynucleotide comprising a sequence selected

```

CC from 1970 fully defined nucleotide sequences which encode novel
 CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
 CC or its partial peptide, an antibody binding to the polypeptide or peptide
 CC of the polynucleotide, immunologically assaying the polypeptide or
 CC peptide of the polynucleotide by contacting the polypeptide or peptide
 CC with the antibody of the encoded protein, and observing the binding
 CC between the two, a transformant carrying the polynucleotide in an
 CC expressible manner and an antisense polynucleotide. The oligonucleotide
 CC is useful as a primer for synthesizing the polynucleotide, or as a probe
 CC for detecting the polynucleotide. The polynucleotides and encoded
 CC proteins are useful as pharmaceutical agents and many disease-related
 CC genes may be included in them, for developing a diagnostic marker or
 CC medicines for regulation of their expression and activity, or as targets
 CC of gene therapy. The genes are involved in tissue and/or cell
 CC regeneration. Membrane proteins, signal transduction-related proteins,
 CC transcription-related proteins, disease-related proteins and genes
 CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
 CC neurological diseases, cancer, tumours). The cDNA may be used to regulate
 CC the activity or expression of the encoded protein to treat diseases. The
 CC sequence presented is a protein of the invention. Note: Some of the
 CC sequence data for this patent is not represented in the printed
 CC specification, but is based on sequence information supplied by the
 CC European Patent Office.

XX SQ Sequence 398 AA;

Query Match 75.8%; Score 50; DB 7; Length 398;
 Best Local Similarity 83.3%; Pred. No. 3.7;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVQLRLS 15
 |||||:||||:
 Db 231 SELNRLIQRLS 242

RESULT 9
 ABG94648
 ID ABG94648 standard; protein; 511 AA.

XX AC ABG94648;

DT 02-DEC-2002 (first entry)

XX DE Human NOV10b protein.

XX KW Human; NOVX; pathological condition; NOVX-associated disorder; diabetes;
 KW Von Hippel-Lindau syndrome; cirrhosis; transplantation disorder; obesity;
 KW pancreatitis; autoimmune disease; renal artery stenosis; infertility;
 KW interstitial nephritis; glomerulonephritis; polycystic kidney disease;
 KW systemic lupus erythematosus; SLE; cataract; Alzheimer's disease;
 KW acoustic trauma; cancer; cardiomyopathy; atherosclerosis; hypertension;
 KW congenital heart defect; scleroderma; endometriosis; haemophilia;
 KW dementia; stroke; Parkinson's disease; Huntington's disease; epilepsy;
 KW multiple sclerosis; anxiety; pain; leukaemia; hypothyroidism; psoriasis;
 KW acne; wound; asthma.

XX OS Homo sapiens.

XX PN WO200266643-A2.

XX PD 29-AUG-2002.

XX PF 13-NOV-2001; 2001WO-US048732.

XX PR 13-NOV-2000; 2000US-0248153P.

XX PR 17-NOV-2000; 2000US-0249598P.

XX PR 26-JAN-2001; 2001US-0264240P.

XX PR 02-FEB-2001; 2001US-0266127P.

XX PR 16-FEB-2001; 2001US-0269562P.

XX PR 10-JUL-2001; 2001US-0304348P.

XX PR 31-JUL-2001; 2001US-0309261P.

XX PR 17-AUG-2001; 2001US-0313283P.

PA (CURA-) CURAGEN CORP.

XX PI Malyankar UM, Shenoy SG, Spytek KA, Zerhusen BD, Patturajan M;
 PI Guo X, Kekuda R, Gangolli BA, Shimkets RA, Taupier RJ, Li L;
 PI Padigaru M;

XX DR WPI; 2002-706943/76.

XX DR N-PSDB; ABS71710.

XX PT New isolated NOVX polypeptides and nucleic acid molecules useful for
 PT treating, preventing, diagnosing and researching of pathological
 PT conditions in humans with a NOVX-associated disorders.

XX PS Claim 1; Page 112; 295pp; English.

XX CC The present invention relates to new NOVX polypeptides. The NOVX
 CC polypeptide, nucleic acid and antibody are useful for treating or
 CC preventing a pathological condition in humans with a NOVX-associated
 CC disorder, e.g. Von Hippel-Lindau syndrome, cirrhosis, transplantation
 CC disorders, pancreatitis, obesity, diabetes, autoimmune disease, renal
 CC artery stenosis, interstitial nephritis, glomerulonephritis, polycystic
 CC kidney disease, systemic lupus erythematosus (SLE), cataract, Alzheimer's
 CC disease, acoustic trauma, cancer, infertility, cardiomyopathies,
 CC atherosclerosis, haemophilia, dementia, stroke, Parkinson's disease,
 CC endometriosis, epilepsy, multiple sclerosis, anxiety, pain,
 CC Huntington's disease, hypothyroidism, psoriasis, acne, wounds and asthma. They are
 CC also useful for the manufacture of a medicament for treating a syndrome
 CC associated with a human disease, specifically a NOVX-associated disorder.
 CC They may also be useful in therapeutic applications including protein
 CC therapeutic, small molecule drug target, antibody target, diagnostic
 CC and/or prognostic marker, gene therapy, research tools and tissue
 CC regeneration. The present amino acid sequence represents a NOVX protein
 CC of the invention

XX SQ Sequence 511 AA;

Query Match 75.8%; Score 50; DB 5; Length 511;
 Best Local Similarity 83.3%; Pred. No. 4.8;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVQLRLS 15
 |||||:||||:
 Db 344 SELNRLIQRLS 355

RESULT 10
 ADL36000

ID ADL36000 standard; protein; 511 AA.

XX AC ADL36000;

XX DT 20-MAY-2004 (first entry)

XX DE Human NOVX polypeptide #23.

XX KW Human; NOVX; Alzheimer's disease; Parkinson's disease; stroke; epilepsy;
 KW multiple sclerosis; addiction; anxiety; pain; acne; alopecia;
 KW inflammation; rheumatoid arthritis; AIDS; cancer; psoriasis;
 KW hypertension; renal disorder; bone disease; haematopoietic disorder;
 KW wound; bacterial infection; viral infection; fungal infection;
 KW protozoal infection; urinary retention; osteoporosis;
 KW myocardial infarction; diabetes; ulcer; cirrhosis; depression.

XX OS Homo sapiens.

XX PN US2003207800-A1.

XX PD 06-NOV-2003.

XX PF 13-NOV-2001; 2001US-00015115.

XX PR 08-NOV-1999; 99US-0164240P.

```

PR 13-NOV-2000; 2000US-0248153P.
PR 17-NOV-2000; 2000US-0249598P.
PR 02-FEB-2001; 2001US-0266127P.
PR 16-FEB-2001; 2001US-0269562P.
PR 10-JUL-2001; 2001US-0304348P.
PR 31-JUL-2001; 2001US-0309261P.
PR 17-AUG-2001; 2001US-0313283P.
XX (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (LILL/) LI L.
PA (PADI/) PADIGARU M.
XX Malyankar UM, Shenoy SG, Spytek KA, Zerhusen BD, Patturajan M;
PI Guo X, Kekuda R, Gangolli EA, Shimkets RA, Taupier RJ, Li L;
PI Padigaru M;
XX WPI: 2003-875894/81.
DR N-PSDB; ADJ35999.
XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders (e.g. stroke, epilepsy,
PT AIDS, pain, diabetes or cancer) and in chromosome mapping, tissue typing
PT or pharmacogenomics.
XX Claim 1; SEQ ID NO 46; 233pp; English.
XX The invention relates to human NOVX polypeptides and the polynucleotides
CC encoding them. The invention also relates to antibodies that bind
CC immunospecifically to the polypeptides. The NOVX polypeptides,
CC polynucleotides and antibodies are useful in diagnosing, treating or
CC preventing NOVX-associated disorders such as Alzheimer's disease,
CC Parkinson's disease, stroke, epilepsy, multiple sclerosis, addiction,
CC anxiety, pain, acne, alopecia, inflammation, rheumatoid arthritis, AIDS,
CC cancer, psoriasis, hypertension, renal disorders, bone diseases,
CC haematopoietic disorders, wounds, infection (e.g. bacterial, viral,
CC fungal or protozoal), urinary retention, osteoporosis, myocardial
CC infarction, diabetes, ulcer, cirrhosis or depression. The polypeptides
CC are also useful as vaccines. This sequence represents a human NOVX
CC polypeptide of the invention.
XX SQ Sequence 511 AA;
Query Match 75.8%; Score 50; DB 7; Length 511;
Best Local Similarity 83.3%; Pred. No. 4.8;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 4 SELNRVLIQRLRS 15
DB 344 SELNRLIQRLRS 355
RESULT 11
AEA15498
ID AEA15498 standard; protein; 511 AA.
XX AEA15498;
AC AEA15498;
XX 28-JUL-2005 (first entry)
DT Human polypeptide #117.
XX Diagnosis; prognosis; cancer; breast tumor; ovary tumor; stomach tumor;
KW colon tumor; esophagus tumor; bladder tumor; non-small-cell lung cancer;
KW cytostatic; neoplasm.

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XX OS Homo sapiens.
XX WO2005047534-A2.
XX 26-MAY-2005.
XX 15-OCT-2004; 2004WO-EP011599.
XX 28-OCT-2003; 2003EP-00024565.
XX (FARB ) BAYER HEALTHCARE AG.
XX Wirtz R, Munnes M;
XX WPI: 2005-372393/38.
DR N-PSDB; AEA15420.
XX Predicting a response to cancer treatment by detecting at least 2
PT markers, which are genes or genomic nucleic acid sequences that are
PT located on one chromosomal region, which is altered in malignant
PT neoplasia.
XX Claim 7; SEQ ID NO 460; 464pp; English.
XX The invention relates to a method of predicting response to cancer
CC treatment comprising detection of at least 2 markers, where the markers
CC are genes and fragments or genomic nucleic acid sequences that are
CC located on one chromosomal region, which is altered in malignant
CC neoplasia. The invention also relates to a method for the prediction,
CC diagnosis or prognosis of malignant neoplasia, methods for detecting
CC deregulations in malignant neoplasia and breast cancer, a method of
CC determining the phenotype of a cell or tissue, a method for identifying
CC genomic regions which are altered on the chromosomal level and encode
CC genes that are linked by function and are differentially expressed in
CC malignant neoplasia and breast cancer, methods of screening for agents
CC which regulate the activity of a polypeptide or a polynucleotide and
CC antibodies that specifically bind to a full length or partial
CC polypeptide. The method is useful for predicting response to cancer
CC treatment. The methods and compositions are useful for predicting,
CC diagnosing, prognosing, preventing or treating malignant neoplasia
CC including breast cancer, ovarian cancer, gastric cancer, colon cancer,
CC esophageal cancer, mesenchymal cancer, bladder cancer or non-small-cell
CC lung cancer. This sequence represents a human polypeptide used in the
CC scope of the invention.
XX SQ Sequence 511 AA;
Query Match 75.8%; Score 50; DB 9; Length 511;
Best Local Similarity 83.3%; Pred. No. 4.8;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 4 SELNRVLIQRLRS 15
DB 344 SELNRLIQRLRS 355
RESULT 12
ADW07163
ID ADW07163 standard; protein; 601 AA.
XX ADW07163;
AC ADW07163;
XX 10-MAR-2005 (first entry)
DT Bos taurus keratin 5 protein sequence SeqID3.
XX animal breeding; DNA type; epidermolysis bullosa simplex; keratin.
KW Bos taurus.
XX Key Location/Qualifiers
FH Misc-difference 478
FT

```

FT /note= "wild-type glutamic acid may be substituted by
 TT lysine as the result of a single nucleotide polymorphism"

XX NZ525023-A.

XX 27-AUG-2004.

XX 28-MAR-2003; 2003NZ-00525023.

XX 28-MAR-2003; 2003NZ-00525023.

XX (SNEL/) SNELL R G.

PA (FORD/) FORD C A.

PA (SUTH/) SUTHERLAND G T.

PA (STAN/) STANFIELD A M.

PA (SPEL/) SPELTMAN R J.

PA (ANKE/) ANKERSMIT-UDY A E L.

XX Snell RG, Ford CA, Sutherland GT, Stanfield AM, Spelman RJ;

PI Ankersmit-Udy AEL;

XX WPI; 2004-811782/80.

DR N-PSDB; ADW07161, ADW07162.

XX Assessing genetic merit of bovine with respect to epidermolysis bullosa
 PT simplex involves determining keratin 5 genotypic state of bovine.
 PT

XX Claim 4; SEQ ID NO 3; 40pp; English.

XX This invention relates to a novel method for assessing the genetic merit
 CC of a bovine with respect to epidermolysis bullosa (EB) simplex which
 CC involves determining the keratin 5 genotypic state of the bovine. The
 CC method of the invention enables a farmer or animal breeder to eliminate
 CC or select against the disease (EB) in their animal population. The
 CC present sequence is that of the bovine keratin 5 protein and which was
 CC used in the method of the invention.

XX Sequence 601 AA;

Query Match 75.8%; Score 50; DB 8; Length 601;

Best Local Similarity 83.3%; Pred. No. 5.8;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVQLRLS 15

DB 388 SEMNMIQLRLS 399

RESULT 13

AEA20243

ID AEA20243 standard; protein; 679 AA.

XX AEA20243;

XX 11-AUG-2005 (first entry)

XX Novel human polypeptide SEQ ID NO 937.

DE vulnery; CNS-gen.; gene therapy; diagnostic; forensic; mapping;

XX DNA purification; protein purification; osteoarthritis; antiarthritic;
 KW osteopathic; musculoskeletal disease; osteoporosis; endocrine disease;
 KW periodontal disease; antiinflammatory; mouth disease; burns; injury;
 KW peripheral neuropathy; Alzheimer's disease; neuroprotective; neurologic;
 KW degeneration; parkinson's disease; antiparkinsonian; neurological disease;
 KW cerebrovascular ischemia; cerebroprotective; vasotropic;
 KW cardiovascular disease; autoimmune disease; immunosuppressive;
 KW immune disorder; viral infection; virucide; infection; cancer;
 KW cytostatic; neoplasm.

XX Homo sapiens.

OS WO2005049806-A2.

XX 15-DEC-2005 (first entry)

XX

PD 02-JUN-2005.

XX 11-MAR-2004; 2004WO-US007412.

XX 14-MAR-2003; 2003US-00389559.

XX (NUVE-) NUVELO INC.

XX Tang TY, Wang J, Wang ZW, Zhang J, Ren F, Zhou P, Ma Y;

PI Ghosh M, Xue A, Asundi V, Zhao Q, Wang D, Goodrich R, Chen R;

PI Wehrman T, Weng G, Boyle B;

XX WPI; 2005-417730/42.

DR N-PSDB; AEA19676.

XX New polynucleotide encoding a polypeptide with biological activity.

PT useful for treating a disease or disorder, e.g. osteoarthritis, burns,

PT CNS and peripheral disease, stroke, autoimmune disorders, viral

PT infection, or cancer.

XX Claim 20; SEQ ID NO 937; 500pp; English.

PS The invention describes a new isolated polynucleotide (I) encoding a

XX polypeptide with biological activity comprising: a nucleotide sequence of

CC SEQ ID NOS: 1-567 (fully defined); a nucleotide sequence that hybridizes

CC to the sequence of (i) under stringent hybridization conditions; or a

CC nucleotide sequence having greater than 99% sequence identity with the

CC sequence of (i). Also described are: a(n) (expression) vector comprising

CC (1); a host cell genetically engineered to comprise (i) operatively,

CC associated with a regulatory sequence that modulates expression of the

CC polynucleotide in the host cell; an isolated polypeptide comprising a

CC sequence of SEQ ID NOS: 568-1134 (fully defined), where the polypeptide

CC is: a polypeptide encoded by (1); or a polypeptide encoded by a

CC polynucleotide hybridizing under stringent conditions with any one of SEQ

CC ID NOS: 1-567; a composition comprising the polypeptide of (3) and a

CC carrier; an antibody directed against the polypeptide of (3); a method

CC for detecting (1) in a sample; a method for identifying a compound that binds to the

CC (3) in a sample; a method for producing the polypeptide of (3); and a

CC collection of polynucleotides, where the collection comprising of at

CC least one of SEQ ID NOS: 1-567. (I) is a polynucleotide comprising any of

CC the sequences of SEQ ID NOS: 1-567 encoding a polypeptide with biological

CC activity, which comprises any of the amino acid sequence of SEQ ID NOS:

CC 568-1134. All sequences are fully defined in the specification. The

CC sequences and methods are useful in diagnostics, forensic, and gene

CC mapping, in identifying of mutations responsible for genetic disorders or

CC other traits, in assessing biodiversity, and for producing many other

CC types of data and products dependent on DNA and amino acid sequences. The

CC composition and method are useful for treating a disease or disorder,

CC e.g. osteoporosis, osteoarthritis, periodontal disease, burns, CNS and

CC peripheral disease, Alzheimer's disease, Parkinson's disease, stroke,

CC autoimmune disorders, viral infection, or cancer. This is the amino acid

CC sequence of a novel polypeptide of the invention.

XX Sequence 679 AA;

QY Query Match 75.8%; Score 50; DB 9; Length 679;

DB Best Local Similarity 83.3%; Pred. No. 6.6;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVQLRLS 15

DB 512 SELNRLIQLRLS 523

XX RESULT:14

XX AEA20243

XX ID AEA20243 standard; peptide; 20 AA.

XX AEA20243;

XX 15-DEC-2005 (first entry)

DE Human protein-protein complex forming polypeptide fragment, SEQ ID 348.
XX
KW Cytostatic; Vasotropic; Cerebroprotective; Immunosuppressive;
KW Antidiabetic; Cardiant; Neuroprotective; Antiasthmatic; Antiinflammatory;
KW Antibacterial; Osteopathic; Anorectic; Virucide; Anti-HIV; Nephrotropic;
KW Antiartherosclerotic; Muscular-Gen.; protein interaction;
KW protein microarray; cancer; familial adenomatous polyposis;
KW gastrointestinal-gen.; ischemia; cerebrovascular ischemia;
KW autoimmune disease; diabetes; heart disease; neurodegenerative disease;
KW asthma; inflammation; sepsis; osteoporosis; obesity; viral infection;
KW acquired immune deficiency syndrome; glomerulonephritis; atherosclerosis;
KW muscular dystrophy.
XX
OS Homo sapiens.
XX
XX
XX US2005222029-A1.
XX
XX
XX 06-OCT-2005.
XX
XX 07-MAR-2005; 2005US-00075234.
XX
XX 04-JAN-2001; 2001US-0259571P.
XX
XX 14-JAN-2001; 2001US-0259573P.
XX
XX 14-MAR-2001; 2001US-0276259P.
XX
XX 15-MAR-2001; 2001US-0276179P.
XX
XX 19-MAR-2001; 2001US-0277013P.
XX
XX 16-APR-2001; 2001US-0284095P.
XX
XX 17-APR-2001; 2001US-0284220P.
XX
XX 17-APR-2001; 2001US-0284404P.
XX
XX 19-APR-2001; 2001US-0285324P.
XX
XX 30-APR-2001; 2001US-0287513P.
XX
XX 10-JUL-2001; 2001US-0304101P.
XX
XX 23-JUL-2001; 2001US-0307233P.
XX
XX 22-OCT-2001; 2001US-0347829P.
XX
XX 25-OCT-2001; 2001US-034818P.
XX
XX 04-JAN-2002; 2002US-00035344.
XX
XX 07-JAN-2002; 2002US-0346384P.
XX
XX 17-JAN-2002; 2002US-034943P.
XX
XX 06-FEB-2002; 2002US-0354899P.
XX
XX 14-MAR-2002; 2002US-00098979.
XX
XX 14-MAR-2002; 2002US-00099924.
XX
XX 15-MAR-2002; 2002US-00100503.
XX
XX 15-APR-2002; 2002US-00122573.
XX
XX 17-APR-2002; 2002US-00124550.
XX
XX 17-APR-2002; 2002US-00124767.
XX
XX 18-APR-2002; 2002US-00125639.
XX
XX 29-APR-2002; 2002US-00135802.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Bartel P, Cimbora D, Sugiyama J, Wettstein DA, Heichman K;
XX
XX WPI; 2005-664172/68.
XX
XX
XX New isolated protein complex having a first protein interacting with a
XX second protein, useful for treating or preventing, e.g. cancer, ischemia,
XX stroke, autoimmune diseases, diabetes, coronary heart disease, or asthma.
XX
XX
XX Disclosure; SEQ ID NO 348; 198pp; English.
XX
XX
XX The invention relates to a novel isolated protein complex having a first
XX protein interacting with a second protein. The invention further
XX comprises a protein microarray comprising the protein complex; a method
XX for selecting modulators of the protein complex; a method of selecting
XX modulators of an interaction between a first protein and a second protein
XX ; and the treating and/or preventing of diseases and disorders associated
XX with the protein complexes. The protein complexes are useful in screening
XX assays for identifying compounds effective in modulating the protein
XX complexes, and in treating and/or preventing diseases and disorders
XX associated with the protein complexes. The diseases and disorders include
XX cancer, adenomatous polyposis, ischemia, stroke, autoimmune diseases,
XX diabetes, coronary heart disease, neurodegenerative diseases, asthma,
XX inflammatory disorders, sepsis, osteoporosis, obesity, viral infection,

CC AIDS, glomerulonephritis, atherosclerosis, and muscular dystrophy. This
CC sequence represents polypeptide fragment of a human protein which forms
CC part of a protein-protein complex of the invention.
XX
XX Sequence 20 AA;
XX
XX Query Match 71.2%; Score 47; DB 9; Length 20;
XX Best Local Similarity 75.0%; Pred No. 0.47;
XX Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 SELNRVIQLRS 15
XX : : : : :
XX Db 2 ABINRMQLRS 13
XX
XX
XX RESULT 15
XX ADR98933
XX ID ADR98933 standard; protein; 92 AA.
XX
XX AC ADR98933;
XX
XX DT 18-NOV-2004 (first entry)
XX
XX DE Lung specific gene splice variant encoded protein #105.
XX
XX KW cytostatic; gene therapy; vaccine; lung; diagnosis; cancer;
XX non-cancerous lung disease; lung tissue; antagonist; gene therapy;
XX transgenic animal; splice variant.
XX
XX OS Homo sapiens.
XX
XX PN WO2004074430-A2.
XX
XX PD 02-SEP-2004.
XX
XX PF 08-DEC-2003; 2003WO-US038896.
XX
XX PR 06-DEC-2002; 2002US-0431307P.
XX
XX PR 06-DEC-2002; 2002US-0431510P.
XX
XX PR 06-DEC-2002; 2002US-0431516P.
XX
XX (DIAD-) DIADEXUS INC.
XX
XX Macina RA, Turner LR, Sun Y, Liu S;
XX
XX WPI; 2004-635553/61.
XX
XX N-PSDB; ADR98793.
XX
XX New isolated human lung specific nucleic acid molecule, useful for
XX identifying, diagnosing, monitoring, staging, imaging and treating lung
XX cancer and non-cancerous diseases of the lung.
XX
XX PS Claim 1; SEQ ID NO 218; 542pp; English.
XX
XX
XX The invention relates to a new isolated lung specific nucleic acid
XX molecule (I) comprising any of 113 fully defined nucleotide sequences
XX given in the specification, their encoded protein sequences, sequences
XX selectively hybridizing to the nucleotide sequences or a sequence having
XX at least 60% identity to the nucleotide sequences. The methods and
XX compositions of the present invention are useful for identifying,
XX diagnosing, monitoring, staging, imaging and treating lung cancer and non
XX -cancerous diseases of the lung. They are also used for identifying lung
XX tissue, monitoring and identifying and/or designing antagonists of the
XX polypeptide of the invention, gene therapy, production of transgenic
XX animals and production of engineered lung tissue for treatment and
XX research. Lung specific genes (LUGs) were identified by a systematic
XX analysis of gene expression data in the LIFESEQ Gold database using the
XX data mining software package candidate lead automatic search program
XX (CLASP). Genes were grouped into gene bins where each bin is a cluster of
XX sequences grouped together where they share a common contig.
XX Differentially expressed tissue-specific genes were selected based on the
XX percentage level in the targeted tissue versus all the other tissues. The
XX expression levels for each gene in libraries of normal tissues or non-

CC tumour tissues from cancer patients were compared with the expression
CC levels in tissue libraries associated with tumour or disease. This
CC sequence represents a protein of the invention.

XX

SQ Sequence 92 AA;

Query Match 71.2%; Score 47; DB 8; Length 92;
Best Local Similarity 75.0%; Pred. No. 2.5;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVQLRLRS 15

||:|:|:|:|:|:

Db 21 SEWNRMIQLRLRA 32

Search completed: July 5, 2006, 18:43:56
Job time : 140.029 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 20:38:52 ; Search time 117.126 Seconds
(without alignments)
63.277 Million cell updates/sec

Title: US-10-774-928A-9

Perfect score: 66

Sequence: 1 XXSELNRIQLRSI 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /EMC_Celerra_SID33/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SID33/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SID33/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SID33/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	59	89.4	16	5	US-10-774-928-9
2	55	83.3	643	5	US-10-480-848A-3
3	55	83.3	644	5	US-10-723-860-366
4	50	75.8	398	4	US-10-104-047-3388
5	50	75.8	398	6	US-11-072-512-3388
6	50	75.8	511	4	US-10-015-115-46
7	49	74.2	524	3	US-09-976-782-88
8	47	71.2	20	6	US-11-075-234-348
9	47	71.2	551	3	US-09-976-782-89
10	47	71.2	551	3	US-09-976-782-90
11	47	71.2	551	4	US-10-015-115-127
12	47	71.2	551	4	US-10-231-913-116
13	47	71.2	551	4	US-10-231-913-117
14	47	71.2	551	5	US-10-719-993-865
15	47	71.2	557	5	US-10-719-993-864
16	47	71.2	564	4	US-10-170-385-421
17	47	71.2	564	5	US-10-723-860-1619
18	47	71.2	564	5	US-10-756-149-5130
19	47	71.2	564	5	US-10-631-467-938
20	47	71.2	564	6	US-11-037-713-27
21	47	71.2	567	4	US-10-104-047-3772
22	47	71.2	567	6	US-11-072-512-3772
23	47	71.2	585	5	US-10-821-234-875
24	47	71.2	645	3	US-09-919-172-41
25	47	71.2	645	5	US-10-752-986-41
26	46	69.7	222	4	US-10-231-913-263
27	46	69.7	315	4	US-10-231-913-259

Sequence 261, App
Sequence 1475, App
Sequence 10, Appl
Sequence 48, Appl
Sequence 32, Appl
Sequence 11, Appl
Sequence 85, Appl
Sequence 87, Appl
Sequence 87, Appl
Sequence 87, Appl
Sequence 38, Appl
Sequence 2446, App
Sequence 264194,
Sequence 124, App
Sequence 85, Appl
Sequence 115, App
Sequence 123, App
Sequence 83, Appl

46 69.7 318 4 US-10-231-913-261
46 69.7 327 4 US-10-408-765A-1475
46 69.7 521 3 US-09-976-782-10
46 69.7 521 4 US-10-015-115-48
46 69.7 526 4 US-10-231-913-32
46 69.7 529 4 US-10-250-613-11
46 69.7 534 3 US-09-976-782-86
46 69.7 534 3 US-09-976-782-87
46 69.7 534 4 US-10-231-913-86
46 69.7 534 4 US-10-231-913-87
46 69.7 534 5 US-10-367-057-38
46 69.7 608 4 US-10-094-749-2446
45 68.2 95 4 US-10-425-115-264194
44 66.7 441 4 US-10-015-115-124
44 66.7 441 4 US-10-231-913-85
44 66.7 441 4 US-10-231-913-115
44 66.7 523 4 US-10-015-115-123
44 66.7 523 4 US-10-231-913-83

ALIGNMENTS

RESULT 1
US-10-774-928-9
; Sequence 9, Application US/10774928
; Publication No. US20040241168A1
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; FILE REFERENCE: 302178
; CURRENT APPLICATION NUMBER: US/10/774,928
; CURRENT FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 9
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Leishmania
; FEATURE:
; NAME/KEY: Xaa
; LOCATION: (1)..(3)
; OTHER INFORMATION: Xaa is an unknown amino acid.
US-10-774-928-9

Query Match 89.4%; Score 59; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVIQLRSI 16
| | | | | | | | | | | | | | | |
Db 4 SELNRVIQLRSI 16

RESULT 2
US-10-480-848A-3
; Sequence 3, Application US/10480848A
; Publication No. US20040219597A1
; GENERAL INFORMATION:
; APPLICANT: B.R.A.H.M.S Aktiengesellschaft
; TITLE OF INVENTION: Use of soluble cytochrome c fragments in diagnosis and
; FILE REFERENCE: 3537PCTNAT
; CURRENT APPLICATION NUMBER: US/10/480,848A
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: DE 101 30 985.6
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 643
; TYPE: PRT

```

; ORGANISM: Homo sapiens
; PUBLIC INFORMATION:
; TITLE: L.Johnson et al., Structure of a gene for the human
; TITLE: epidermal 67-kDa keratin
; JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
; VOLUME: 1985
; ISSUE: 82
; PAGES: 1896-1900
US-10-480-848A-3

Query Match      83.3%; Score 55; DB 5; Length 643;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 SELNRVIOQLRS 15
Db      398 SELNRVIOQLRS 409
|||||:|||||

RESULT 3
US-10-723-860-366
; Sequence 366, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 366
; LENGTH: 644
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-366

Query Match      83.3%; Score 55; DB 5; Length 644;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 SELNRVIOQLRS 15
Db      399 SELNRVIOQLRS 410
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RESULT 4
US-10-104-047-3388
; Sequence 3388, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3388
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3388

Query Match      75.8%; Score 50; DB 4; Length 398;
Best Local Similarity 83.3%; Pred. No. 4.6;
Matches 10; Indels 0; Gaps 0;

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```

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      4 SELNRVIOQLRS 15
Db      231 SELNRVIOQLRS 242
|||||:|||||

RESULT 5
US-11-072-512-3388
; Sequence 3388, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3388
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3388

Query Match      75.8%; Score 50; DB 6; Length 398;
Best Local Similarity 83.3%; Pred. No. 4.6;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      4 SELNRVIOQLRS 15
Db      231 SELNRVIOQLRS 242
|||||:|||||

RESULT 6
US-10-015-115-46
; Sequence 46, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangolli, Esha A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of

```

US-10-015-115-46

TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-211
CURRENT APPLICATION NUMBER: US/10/015,115
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/248,153
PRIOR FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: 60/249,598
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/264,240
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/266,127
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/269,562
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/304,348
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/309,261
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/313,283
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 205
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 46
LENGTH: 511
TYPE: PRT
ORGANISM: Homo sapiens

Query Match 75.8%; Score 50; DB 4; Length 511;
Best Local Similarity 83.3%; Pred. No. 6;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SELNRVIOQLRS 15
Db 344 SELNRIOQLRS 355

RESULT 7

US-09-976-782-88

Sequence 88, Application US/09976782
Publication No. US20030190715A1

GENERAL INFORMATION:
APPLICANT: Grosse et al
TITLE OF INVENTION: No. US20030190715A1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-157
CURRENT APPLICATION NUMBER: US/09/976,782
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,113
PRIOR FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: 60/240,662
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 60/240,732
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 60/240,625
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 60/240,703
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 60/241,190
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 60/240,637
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 60/240,669
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 60/262,455
PRIOR FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: 60/240,648
PRIOR FILING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 127
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 88
LENGTH: 524
TYPE: PRT
ORGANISM: Homo sapiens

US-09-976-782-88

Query Match 74.2%; Score 49; DB 3; Length 524;
Best Local Similarity 83.3%; Pred. No. 9.1;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SELNRVIOQLRS 15
Db 365 SELNRVIOQLRS 376

RESULT 8

US-11-075-234-348

Sequence 348, Application US/11075234
Publication No. US20050222029A1

GENERAL INFORMATION:
APPLICANT: Myriad Genetics
APPLICANT: Bartel, Paul
APPLICANT: Cimborra, Daniel
APPLICANT: Sugiyama, Janice
APPLICANT: Wettstein, Daniel A
APPLICANT: Heichman, Karen
TITLE OF INVENTION: Compositions and Methods for Treating Diseases
FILE REFERENCE: 1835.01
CURRENT APPLICATION NUMBER: US/11/075,234
CURRENT FILING DATE: 2005-03-08
PRIOR APPLICATION NUMBER: US 10/135802
PRIOR FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 10/035344
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: US 10/098979
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 10/099924
PRIOR FILING DATE: 2002-04-14
PRIOR APPLICATION NUMBER: US 10/122573
PRIOR FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 10/124550
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 10/124767
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 10/125639
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: US 10/100503
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 469
SOFTWARE: PatentIn version 3.3
SEQ ID NO 348
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens

Query Match 71.2%; Score 47; DB 6; Length 20;
Best Local Similarity 75.0%; Pred. No. 0.58;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SELNRVIOQLRS 15
Db 2 AEINRMIQLRS 13

RESULT 9

US-09-976-782-89

Sequence 89, Application US/09976782
Publication No. US20030190715A1

GENERAL INFORMATION:
APPLICANT: Grosse et al
TITLE OF INVENTION: No. US20030190715A1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-157
CURRENT APPLICATION NUMBER: US/09/976,782
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,113
PRIOR FILING DATE: 2000-10-12

; PRIOR APPLICATION NUMBER: 60/240,662
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,732
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,625
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,703
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/241,190
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,637
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,669
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/262,455
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/240,648
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-782-89

Query Match 71.2%; Score 47; DB 3; Length 551;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVQLRLS 15
||:|||||:
Db 368 SEMNRMIQLRA 379

RESULT 10
US-09-976-782-90
; Sequence 90, Application US/09976782
; Publication No. US20030190715A1
; GENERAL INFORMATION:
; APPLICANT: Grosse et al
; TITLE OF INVENTION: No. US20030190715A1e1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-157
; CURRENT APPLICATION NUMBER: US/09/976,782
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,113
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,662
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,732
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,625
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,703
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/241,190
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,637
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,669
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/262,455
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/240,648
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-976-782-90

Query Match 71.2%; Score 47; DB 3; Length 551;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVQLRLS 15
||:|||||:
Db 368 SEMNRMIQLRA 379

RESULT 11
US-10-015-115-127
; Sequence 127, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangolli, Esha A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015,115
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/248,153
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/249,598
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/264,240
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/266,127
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/269,562
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/304,348
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/309,261
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,283
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 127
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-115-127

Query Match 71.2%; Score 47; DB 4; Length 551;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVQLRLS 15
||:|||||:
Db 368 SEMNRMIQLRA 379

RESULT 12
US-10-231-913-116
; Sequence 116, Application US/10231913
; Publication No. US2004000576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.

; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231.913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 116
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-913-116

Query Match 71.2%; Score 47; DB 4; Length 551;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SELNRVIOQLRS 15
Db 368 SEMNRMIQLRA 379

RESULT 13
US-10-231-913-117
; Sequence 117, Application US/10231913
; Publication No. US2004000576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit

; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231.913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 117
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-913-117

Query Match 71.2%; Score 47; DB 4; Length 551;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SELNRVIOQLRS 15
Db 368 SEMNRMIQLRA 379

RESULT 14
US-10-719-993-865
; Sequence 865, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 865
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-719-993-865

Query Match 71.2%; Score 47; DB 5; Length 551;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SELNRVIOQLRS 15
Db 368 SEMNRMIQLRA 379

Db 368 SEMNRMIQRLRA 379

RESULT 15
 US-10-719-993-864
 ; Sequence 864, Application US/10719993
 ; Publication No. US20040265849A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; FILE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001496
 ; CURRENT APPLICATION NUMBER: US/10/719,993
 ; CURRENT FILING DATE: 2003-11-24
 ; NUMBER OF SEQ ID NOS: 55342
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 864
 ; LENGTH: 557
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-719-993-864

Query Match 71.2%; Score 47; DB 5; Length 557;
 Best Local Similarity 75.0%; Pred. No. 21;
 Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SELNRVIOQLRS 15

Db 374 SEMNRMIQRLRA 385

Search completed: July 5, 2006, 20:52:01
 Job time : 118.126 secs

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-178-538-55

Query Match 56.1%; Score 37; DB 7; Length 309;
Best Local Similarity 58.3%; Pred. No. 30;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YSELNRVQRLR 14
| | | | | | | | | |
Db 68 YEELRVVLRK 79

RESULT 3

US-11-178-538-62
; Sequence 62, Application US/11178538
; Publication No. US20060110792A1
; GENERAL INFORMATION:
; APPLICANT: Pausch, Mark H
; APPLICANT: Price, Laura A
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
; TITLE OF INVENTION: AND METHODS OF USING SAME
; FILE REFERENCE: 01142.0122 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/11/178,538
; CURRENT FILING DATE: 2005-07-12
; PRIOR APPLICATION NUMBER: US/08/816,011
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: 07/332,312
; PRIOR FILING DATE: 1994-10-31
; PRIOR APPLICATION NUMBER: PCT/US95/14364
; PRIOR FILING DATE: 1995-10-25
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-178-538-62

Query Match 56.1%; Score 37; DB 7; Length 309;
Best Local Similarity 58.3%; Pred. No. 30;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YSELNRVQRLR 14
| | | | | | | | | |
Db 68 YEELRVVLRK 79

RESULT 4

US-10-449-902-40943
; Sequence 40943, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40943
; LENGTH: 533
; TYPE: PRT

; ORGANISM: Oryza sativa
US-10-449-902-40943

Query Match 56.1%; Score 37; DB 6; Length 533;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ELNRVQRLRS 15
| | | | | | | | | |
Db 308 ELLRVQLRNS 318

RESULT 5

US-10-953-349-24947
; Sequence 24947, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24947
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-24947

Query Match 54.5%; Score 36; DB 6; Length 141;
Best Local Similarity 50.0%; Pred. No. 19;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 YSELNRVQRLRSI 16
| | | | | | | | | |
Db 103 YGEMNRLSILQOI 116

RESULT 6

US-10-953-349-24946
; Sequence 24946, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24946
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-24946

Query Match 54.5%; Score 36; DB 6; Length 147;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 YSELNRVQRLRSI 16
| | | | | | | | | |
Db 109 YGEMNRLSILQOI 122

RESULT 7

US-10-953-349-24945
; Sequence 24945, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

```
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24945
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Glycine max
; US-10-953-349-24945

Query Match      54.5%; Score 36; DB 6; Length 149;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      3 YSELNRVQIQLRSI 16
Db      111 YGENRLISILQQI 124

RESULT 8
US-10-953-349-37808
; Sequence 37808, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37808
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; US-10-953-349-37808

Query Match      54.5%; Score 36; DB 6; Length 163;
Best Local Similarity 46.2%; Pred. No. 23;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy      3 YSELNRVQIQLRS 15
Db      129 FYEYNRVVKVRT 141

RESULT 9
US-10-449-902-44210
; Sequence 44210, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 44210
; LENGTH: 663
; TYPE: PRT
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```
; ORGANISM: Oryza sativa
; US-10-449-902-44210

Query Match      54.5%; Score 36; DB 6; Length 663;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy      3 YSELNRVQIQLRSI 16
Db      186 YSEDHRVVOQMTDI 199

RESULT 10
US-10-953-349-26148
; Sequence 26148, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26148
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Triticum aestivum
; US-10-953-349-26148

Query Match      53.0%; Score 35; DB 6; Length 398;
Best Local Similarity 70.0%; Pred. No. 88;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      5 ELNRVQIQLR 14
Db      367 ELKRVQIQRVK 376

RESULT 11
US-10-953-349-26147
; Sequence 26147, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26147
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Triticum aestivum
; US-10-953-349-26147

Query Match      53.0%; Score 35; DB 6; Length 402;
Best Local Similarity 70.0%; Pred. No. 88;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      5 ELNRVQIQLR 14
Db      371 ELKRVQIQRVK 380

RESULT 12
US-10-953-349-26146
; Sequence 26146, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
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; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31041
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-31041

Query Match          51.5%; Score 34; DB 6; Length 216;
Best Local Similarity 70.0%; Pred. No. 68;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 YSELNRVRIQR 12
      ||| |||:
Db      179 YSLSERVIIQ 188

RESULT 15
US-10-449-902-32497
; Sequence 32497, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32497
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-32497

Query Match          51.5%; Score 34; DB 6; Length 235;
Best Local Similarity 41.7%; Pred. No. 74;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY      3 YSELNRVRIQRLR 14
      |||: |||:
Db      17 YAKIDRVLTIR 28

Search completed: July 5, 2006, 20:53:04
Job time : 9.16505 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 5, 2006, 19:18:42 ; Search time 36.0388 Seconds
(without alignments)
38.861 Million cell updates/sec

Title: US-10-774-928A-9

Perfect score: 66

Sequence: 1 XXYSLNRVQLRLSI 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SID33/ptodata/2/iaa/5 COMB.pcp.*
- 2: /EMC_Celerra_SID33/ptodata/2/iaa/6 COMB.pcp.*
- 3: /EMC_Celerra_SID33/ptodata/2/iaa/7 COMB.pcp.*
- 4: /EMC_Celerra_SID33/ptodata/2/iaa/H COMB.pcp.*
- 5: /EMC_Celerra_SID33/ptodata/2/iaa/PCTUS COMB.pcp.*
- 6: /EMC_Celerra_SID33/ptodata/2/iaa/RE COMB.pcp.*
- 7: /EMC_Celerra_SID33/ptodata/2/iaa/backfilesl.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	89.4	16	2	US-09-809-003A-9
2	55	83.3	637	2	US-09-949-016-8152
3	55	83.3	643	2	US-09-538-092-844
4	50	75.8	398	2	US-10-104-047-3388
5	47	71.2	551	1	US-09-067-351-2
6	47	71.2	551	2	US-09-360-490-2
7	47	71.2	564	2	US-09-949-016-6628
8	47	71.2	567	2	US-10-104-047-3772
9	47	71.2	569	2	US-09-949-016-11035
10	47	71.2	569	2	US-09-949-016-11036
11	47	71.2	645	2	US-09-919-172-41
12	46	69.7	608	2	US-10-094-749-2446
13	42	63.6	469	2	US-09-077-606-3
14	42	63.6	476	2	US-09-949-016-9096
15	42	63.6	546	1	US-09-067-351-1
16	42	63.6	546	2	US-09-360-490-1
17	41	62.1	149	2	US-09-270-767-58244
18	41	62.1	313	2	US-09-270-767-42921
19	40	60.6	235	2	US-09-620-405B-487
20	40	60.6	235	2	US-09-604-287A-487
21	40	60.6	235	2	US-09-834-759-487
22	40	60.6	235	2	US-10-076-622-487
23	40	60.6	235	2	US-10-124-805-487
24	40	60.6	274	2	US-09-949-016-9095
25	40	60.6	366	2	US-09-252-991A-16760
26	40	60.6	384	2	US-09-134-000C-5839

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27 40 60.6 493 2 US-09-949-016-6203 Sequence 6203, Ap
28 40 60.6 505 2 US-09-620-405B-478 Sequence 478, App
29 40 60.6 505 2 US-09-620-405B-485 Sequence 485, App
30 40 60.6 505 2 US-09-604-287A-478 Sequence 478, App
31 40 60.6 505 2 US-09-604-287A-485 Sequence 485, App
32 40 60.6 505 2 US-09-834-759-478 Sequence 478, App
33 40 60.6 505 2 US-09-834-759-485 Sequence 485, App
34 40 60.6 505 2 US-09-590-751A-478 Sequence 478, App
35 40 60.6 505 2 US-09-551-621-478 Sequence 478, App
36 40 60.6 505 2 US-09-551-621A-478 Sequence 478, App
37 40 60.6 505 2 US-10-076-622-478 Sequence 485, App
38 40 60.6 505 2 US-10-076-622-485 Sequence 485, App
39 40 60.6 505 2 US-10-124-805-478 Sequence 478, App
40 40 60.6 505 2 US-10-124-805-485 Sequence 485, App
41 40 60.6 528 2 US-09-949-016-9678 Sequence 9678, A
42 39 59.1 368 2 US-09-252-991A-32075 Sequence 32075, A
43 39 59.1 952 2 US-09-248-796A-20878 Sequence 20878, A
44 37 56.1 54 2 US-09-513-999C-5139 Sequence 5139, Ap
45 37 56.1 318 2 US-09-107-532A-5738 Sequence 5738, Ap

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ALIGNMENTS

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RESULT 1
US-09-809-003A-9
; Sequence 9, Application US/09809003A
; Patent No. 6673351
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 302178
; CURRENT APPLICATION NUMBER: US/09/809,003A
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 9
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Leishmania
; FEATURE:
; NAME/KEY: Xaa
; LOCATION: (1)..(3)
; OTHER INFORMATION: Xaa is an unknown amino acid.
US-09-809-003A-9

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Query Match 89.4%; Score 59; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 SELNRVQLRLSI 16
|||||
Db 4 SELNRVQLRLSI 16

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```

RESULT 2
US-09-949-016-8152
; Sequence 8152, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08

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```
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8152
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8152

Query Match      83.3%; Score 55; DB 2; Length 637;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 SELNRVQLRLS 15
Db      399 SELNRVQLRLS 410
|||||:|||||

RESULT 3
US-09-538-092-844
; Sequence 844, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatter Version 0.9
; SEQ ID NO 844
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P04264
US-09-538-092-844

Query Match      83.3%; Score 55; DB 2; Length 643;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 SELNRVQLRLS 15
Db      398 SELNRVQLRLS 409
|||||:|||||

RESULT 4
US-10-104-047-3388
; Sequence 3388, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3388
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3388

Query Match      75.8%; Score 50; DB 2; Length 398;
Best Local Similarity 83.3%; Pred. No. 0.95;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      4 SELNRVQLRLS 15
Db      231 SELNRVQLRLS 242
|||||:|||||

RESULT 5
US-09-067-351-2
; Sequence 2, Application US/09067351
; Patent No. 5994081
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN KERATINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,351
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0511 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 551 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KERANOT02
; CLONE: 2029060
US-09-067-351-2

Query Match      71.2%; Score 47; DB 1; Length 551;
Best Local Similarity 75.0%; Pred. No. 4.4;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      4 SELNRVQLRLS 15
Db      368 SEMNRMIQLRLA 379
|||||:|||||

RESULT 6
US-09-360-490-2
; Sequence 2, Application US/09360490
; Patent No. 6221843
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN KERATINS
```

; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/360,490
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/067,351
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0511 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 551 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KERANOT02
; CLONE: 2029060
; US-09-360-490-2

Query Match 71.2%; Score 47; DB 2; Length 551;
Best Local Similarity 75.0%; Pred. No. 4.4;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVIOQLRS 15
DB 368 SEMNRMIQLRLA 379

RESULT 7
US-09-949-016-6628
; Sequence 6628, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6628
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6628

Query Match 71.2%; Score 47; DB 2; Length 564;

Best Local Similarity 75.0%; Pred. No. 4.5;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVIOQLRS 15
DB 382 AEINRMIOQLRS 393

RESULT 8
US-10-104-047-3772
; Sequence 3772, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3772
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-104-047-3772

Query Match 71.2%; Score 47; DB 2; Length 567;
Best Local Similarity 75.0%; Pred. No. 4.6;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVIOQLRS 15
DB 364 SEMNRMIQLRLA 375

RESULT 9
US-09-949-016-11035
; Sequence 11035, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11035
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11035

Query Match 71.2%; Score 47; DB 2; Length 569;
Best Local Similarity 75.0%; Pred. No. 4.6;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVIOQLRS 15
DB 387 AEINRMIOQLRS 398

RESULT 10
US-09-949-016-11036

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; Sequence 11036, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11036
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Human
;
US-09-949-016-11036

Query Match 71.2%; Score 47; DB 2; Length 569;
Best Local Similarity 75.0%; Pred. No. 4.6;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVQRLRS 15
Db 387 AEINRMQRLRS 398
:|:|:|:|:|:|

RESULT 11
US-09-919-172-41
; Sequence 41, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 41
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 1798379CD1
;
US-09-919-172-41

Query Match 71.2%; Score 47; DB 2; Length 645;
Best Local Similarity 90.3%; Pred. No. 5.2;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVQRLR 14
Db 403 SELNRVQRLQ 413
|:|:|:|:|:|:|

RESULT 12
US-10-094-749-2446
; Sequence 2446, Application US/10094749
; Patent No. 6979557
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
```

```
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOMYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2446
; LENGTH: 608
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-094-749-2446

Query Match 69.7%; Score 46; DB 2; Length 608;
Best Local Similarity 75.0%; Pred. No. 7.4;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 SELNRVQRLRS 15
Db 444 AELNRMIQRLRA 455
:|:|:|:|:|:|

RESULT 13
US-09-077-606-3
; Sequence 3, Application US/09077606
; Patent No. 6774220
; GENERAL INFORMATION:
; APPLICANT: JIANG, Pan Hong
; APPLICANT: KABA, Aboubacar
; APPLICANT: CHANY-FOURNIER, Françoise
; APPLICANT: CERUTTI, Italina
; APPLICANT: CHANY, Charles
; TITLE OF INVENTION: COMPOUNDS HAVING LECTINIC PROPERTIES AND THEIR
; BIOLOGICAL APPLICATIONS
; FILE REFERENCE: 040388/0113
; CURRENT APPLICATION NUMBER: US/09/077,606
; CURRENT FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: WO PCT/FR96/01937
; EARLIER FILING DATE: 1996-12-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-077-606-3

Query Match 63.6%; Score 42; DB 2; Length 469;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 SELNRVQRLRS 15
Db 309 SENNRVQRLQA 320
|:|:|:|:|:|:|
```


RESULT 14
US-09-949-016-9096
; Sequence 9096, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9096
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9096

Query Match 63.6%; Score 42; DB 2; Length 476;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 SELNRVIOQLRS 15
DB 316 SEMNRAIQRLQA 327

RESULT 15
US-09-067-351-1
; Sequence 1, Application US/09067351
; Patent No. 5994081
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN KERATINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,351
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0511 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 546 amino acids
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PANTUT02
; CLONE: 1467090
US-09-067-351-1

Query Match 63.6%; Score 42; DB 1; Length 546;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 SELNRVIOQLRS 15
DB 386 SEMNRAIQRLQA 397

Search completed: July 5, 2006, 19:24:27
Job time : 36.0388 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 19:09:18 ; Search time 9.70874 Seconds
(without alignments)
79.283 Million cell updates/sec

Title: US-10-774-928a-10

Perfect score: 43

Sequence: 1 AQYEDYQAQ 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	35	81.4	629	2	A29666	keratin, 65K type
2	35	81.4	629	2	S42629	keratin K3 - rabbi
3	35	81.4	636	2	S09246	coagulase precurs
4	35	81.4	729	2	S76065	hypothetical prote
5	35	81.4	1979	2	JW0059	mtprp protein - mo
6	34	79.1	730	2	T49736	hypothetical prote
7	32	74.4	163	2	G87551	hypothetical prote
8	32	74.4	305	2	E69946	hypothetical prote
9	32	74.4	522	2	S52216	vital proteinase -
10	32	74.4	603	2	H90061	hypothetical prote
11	32	74.4	1084	2	G71329	hypothetical prote
12	32	74.4	5255	2	T31677	bacitracin synthet
13	31	72.1	122	2	S24287	ig heavy chain V r
14	31	72.1	140	2	T30210	hypothetical prote
15	31	72.1	156	2	T32236	hypothetical prote
16	31	72.1	205	1	F71193	hypothetical prote
17	31	72.1	296	2	A70973	hypothetical prote
18	31	72.1	307	2	D69521	hypothetical prote
19	31	72.1	380	2	A82589	hypothetical prote
20	31	72.1	384	2	I61769	keratin 6d, type I
21	31	72.1	446	2	AH1957	hypothetical prote
22	31	72.1	503	2	T24985	hypothetical prote
23	31	72.1	506	2	AF2192	bifunctional purin
24	31	72.1	522	2	S67704	hypothetical prote
25	31	72.1	524	2	A23518	keratin, 57K type
26	31	72.1	534	2	I37942	keratin 4, type II
27	31	72.1	544	2	F81059	YhBX/YhJW/VjP/Vjd
28	31	72.1	564	1	KRHUEA	keratin 6a, type I
29	31	72.1	564	1	KRHUEB	keratin 6b, type I

30	31	72.1	564	2	D83211	probable malic enz
31	31	72.1	564	2	I61770	keratin 6e, type I
32	31	72.1	564	2	I61768	keratin 6c, type I
33	31	72.1	564	2	I61771	keratin 6f, type I
34	31	72.1	565	2	AC0184	malate dehydrogena
35	31	72.1	574	2	B64901	malate dehydrogena
36	31	72.1	574	2	F85728	NAD-linked malate
37	31	72.1	574	2	C90889	NAD-linked malate
38	31	72.1	577	2	A10672	NAD-linked malic e
39	31	72.1	588	2	A82232	malate oxidoreduct
40	31	72.1	645	2	A44861	keratin, 67K type
41	31	72.1	755	2	B41836	amine oxidase (fla
42	31	72.1	757	2	E84889	amine oxidase (cop
43	31	72.1	1027	2	T27970	hypothetical prote
44	31	72.1	1286	2	T18734	hypothetical prote
45	31	72.1	1307	2	T25563	hypothetical prote

ALIGNMENTS

RESULT 1

A29666

keratin, 65K type II cytoskeletal - human

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 20-Apr-2001

C:Accession: A29666

R:Klinge, E.M.; Sylvestre, Y.R.; Freedberg, I.M.; Blumenberg, M.

J. Mol. Evol. 24, 319-329, 1987

A:Title: Evolution of keratin genes: different protein domains evolve by different pathwa

A:Reference number: A29666; MUID:87254239; PMID:2439698

A:Accession: A29666

A:Molecule type: DNA

A:Residues: 1-629 <KLI>

A:Cross-references: UNIPARC:UPI0000161C35; GB:X05418; NID:G34040; PIDN:CAA28991.1; PID:G

92; PIDN:CAA28994.1; PID:G1335193; PIDN:CAA28995.1; PID:G1335194; GB:X05421; NID:G34047;

A>Note: the authors translated the codon AAC for residue 63 as Asp and ACA for residue 2;

A>Note: the complete translation is not annotated in GenBank entries HSKER65A, HSKER65B,

s mistranslated as a Met initiator codon

C:Genetics:

A:Introns: 215/3; 289/2; 309/3; 341/3; 396/3; 438/3; 512/2; 525/1

C:Superfamily: cytoskeletal keratin

C:Keywords: coiled coil

Query Match 81.4%; Score 35; DB 2; Length 629;
Best Local Similarity 87.5%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	AQYEDYQAQ	8
DB	376	AQYEDYQAQ	383

RESULT 2

S42629

keratin K3 - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S42629

R:Wu, R.L.; Galvin, S.; Wu, S.K.; Xu, C.; Blumenberg, M.; Sun, T.T.

J. Cell Sci. 105, 303-316, 1993

A:Title: A 300 bp 5'-upstream sequence of a differentiation-dependent rabbit K3 keratin s

A:Reference number: S42629; MUID:94013038; PMID:7691837

A:Accession: S42629

A:Molecule type: DNA

A:Residues: 1-629 <WUB>

A:Cross-references: UNIPROT:Q29426; UNIPARC:UPI0000087A39; EMBL:X74371; NID:G433957; PID

C:Genetics:

A:Introns: 200/3; 274/2; 294/3; 326/3; 381/3; 423/3; 497/2; 509/1

C:Superfamily: cytoskeletal keratin

Query Match 81.4%; Score 35; DB 2; Length 629;

Best Local Similarity 87.5%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AQYEDYQA 8
|||||
Db 361 AQYEDYQA 368

RESULT 3
S09246
coagulase precursor - Staphylococcus aureus (strain 8325-4)
C:Species: Staphylococcus aureus
A:Variety: strain 8325-4
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
C:Accession: S09246
R:Phonindaeng, P.; O'Reilly, M.; Nowlan, P.; Bramley, A.J.; Foster, T.J.
Mol. Microbiol. 4, 393-404, 1990
A:Title: The coagulase of Staphylococcus aureus 8325-4. Sequence analysis and virulence
A:Reference number: S09246; MUID:90286916; PMID:2355852
A:Accession: S09246
A:Molecule type: DNA
A:Residues: 1-636 <PHO>
A:Cross-references: UNIPROT:Q53655; UNIPARC:UPI00000BC8C5; EMBL:X17679; NID:g46539; PIDN
C:Genetics:
A:Gene: coa
C:Keywords: extracellular protein
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-636/Product: coagulase #status predicted <MAT>

Query Match 81.4%; Score 35; DB 2; Length 636;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AQYEDYQA 8
:|||||
Db 105 SQYEDYKQ 112

RESULT 4
S76065
hypothetical protein slr0337 - Synchocystis sp. (strain PCC 6803)
C:Species: Synchocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S76065
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76065
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-729 <KAN>
A:Cross-references: UNIPROT:Q55545; UNIPARC:UPI00000C105B; EMBL:D63999; GB:AB001339; NID
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 81.4%; Score 35; DB 2; Length 729;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AQYEDYQA 8
|||||
Db 69 AQLEDYQA 76

RESULT 5
JW0059
mtprd protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
C:Accession: JW0059

R;Tsukahara, F.; Urakawa, I.; Hattori, M.; Hirai, M.; Ohba, K.; Yoshioka, T.; Sakaki, Y.;
J. Biochem. 123, 1055-1063, 1998
A:Title: Molecular characterization of the mouse mtprd gene, a homologue of human TPRD: t
A:Reference number: JW0059; MUID:98269034; PMID:9603993
A:Accession: JW0059
A:Molecule type: protein
A:Residues: 1-1979 <TSU>
A:Cross-references: UNIPROT:O88196; UNIPARC:UPI00001790C6
C:Comment: This protein has three units of tetratics-peptide repeats.
C:Genetics:
A:Gene: mtprd
A:Map position: 16C3.3-4
C:Superfamily: mtprd protein; tetratics-peptide repeat homology
F:1927-1976/Domain: RING finger homology <RRN>

Query Match 81.4%; Score 35; DB 2; Length 1979;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QYEDYQA 8
|||||
Db 51 QYKDYQA 57

RESULT 6
T49736
hypothetical protein B24B19.80 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 15-Mar-2004
C:Accession: T49736
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A:Reference number: 225022
A:Accession: T49736
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-730 <SCH>
A:Cross-references: UNIPARC:UPI000017B482; EMBL:AL356192; GSPDB:GN00116; NCSP:B24B19.80
A:Experimental source: BAC clone B24B19; strain OR74A
C:Genetics:
A:Gene: NCSP:B24B19.80
A:Map position: 6
A:Introns: 86/1
F:70-108/Domain: GAL4 zinc binuclear cluster homology <GL4>

Query Match 79.1%; Score 34; DB 2; Length 730;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YEDYQA 8
|||||
Db 597 YEDYQA 602

RESULT 7
G87551
hypothetical protein CC2440 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: G87551
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: G87551
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-163 <STO>
A:Cross-references: UNIPROT:Q9A5K7; UNIPARC:UPI00000C7721; GB:AE005673; NID:g13423985; PJ
C:Genetics:
A:Gene: CC2440

Query Match 74.4%; Score 32; DB 2; Length 163;
Best Local Similarity 75.0%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

QY 1 AQVEDYQAQ 8
|||||:
66 AQVEDQAE 73

Db

RESULT 8
E69946
hypothetical protein yqBB - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: E69946
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumsstein, E.; Yoshikawa, H.; Danchin, A. Bacillus subtilis.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: E69946
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-305 <UN>
A:Cross-references: UNIPROT:P45918; UNIPARC:UPI000006079D; GB:Z99117; GB:AL009126; NID:9
A:Experimental source: strain 168
C:Genetics:
A:Gene: yqBB

Query Match 74.4%; Score 32; DB 2; Length 305;
Best Local Similarity 75.0%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQVEDYQAQ 8
|||||:
204 AQHESYQAQ 211

Db

RESULT 9
S52216
viral proteinase - rabies virus
C:Species: rabies virus
C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Aug-1998
C:Accession: S52216
R:Camacho, A.; Tabaro, E.
submitted to the EMBL Data Library, June 1994
A:Reference number: S52215
A:Accession: S52216
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-522 <CAM>
A:Cross-references: UNIPARC:UPI0000178490; EMBL:X79983
A>Note: the source is designated as pseudorabies virus
C:Superfamily: varicella-zoster virus gene 33 protein

Query Match 74.4%; Score 32; DB 2; Length 522;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QVEDYQAQ 8
:|||||

Db

RESULT 10
H90061
hypothetical protein SA2354 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90061
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogut
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; I
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayaashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90061
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-603 <KUR>
A:Cross-references: UNIPROT:Q99R71; UNIPARC:UPI00000548D5; GB:BA000018; PID:gl3702517; P3
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA2354

Query Match 74.4%; Score 32; DB 2; Length 603;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQVEDYQAQ 8
:|||||:
488 SQKYDYAK 495

Db

RESULT 11
G71329
hypothetical protein TP0408 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: G71329
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: G71329
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1084 <COL>
A:Cross-references: UNIPROT:O83423; UNIPARC:UPI00000C0A6F; GB:AE001218; GB:AE000520; NID
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0408

Query Match 74.4%; Score 32; DB 2; Length 1084;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QVEDYQAQ 8
:|||||:
671 QYEDFSQ 677

Db

RESULT 12
T31677
bacitracin synthetase 1 - Bacillus licheniformis
C:Species: Bacillus licheniformis
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31677
R:Konz, D.; Klens, A.; Schorgendorfer, K.; Marahiel, M.A.
Chem. Biol. 4, 927-937, 1997
A:Title: The bacitracin biosynthesis operon of Bacillus licheniformis ATCC 10716: molecu
A:Reference number: Z21058; MUID:98089193; PMID:9427658

A:Accession: T31677
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5255 <KON>
A:Cross-references: UNIPROT:O68006; UNIPARC:UPI000013C49A; EMBL:AF007865; NID:g4464275;
C:Genetics:
A:Gene: bacA
C:Keywords: carrier protein
F:83-524/Domain: acetate-CoA ligase homology <ACU1>
F:542-610/Domain: acyl carrier protein homology <ACP1>
F:1134-1561/Domain: acetate-CoA ligase homology <ACU2>
F:1583-1651/Domain: acyl carrier protein homology <ACP2>
F:2171-2601/Domain: acetate-CoA ligase homology <ACU3>
F:2619-2687/Domain: acyl carrier protein homology <ACP3>
F:3195-3642/Domain: acetate-CoA ligase homology <ACU4>
F:3662-3729/Domain: acyl carrier protein homology <ACP4>
F:4712-5151/Domain: acetate-CoA ligase homology <ACU5>
F:5169-5237/Domain: acyl carrier protein homology <ACP5>

Query Match 74.4%; Score 32; DB 2; Length 5255;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYEDYQA 8
|||:
Db 2860 QYKDYAE 2866
|||:
|||:

RESULT 13
S24287
Ig heavy chain V region (JS28/32) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C:Accession: S24287
R:Monchamont, B.
submitted to the EMBL Data Library, September 1991
A:Description: Cloning and sequencing of the cDNA coding for the variable regions of the
A:Reference number: S24287
A:Accession: S24287
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <MON>
A:Cross-references: UNIPARC:UPI0000116004; EMBL:X62706; NID:g51669; PIDN:CAA44588.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.1%; Score 31; DB 2; Length 122;
Best Local Similarity 71.4%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQYEDYA 7
:|||||
Db 102 SRYEDYA 108
:|||||

RESULT 14
T30210
hypotheical protein 3 - Staphylococcus epidermidis
C:Species: Staphylococcus epidermidis
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30210
R:Heilmann, C.; Hussain, M.; Peters, G.; Gotz, F.
Mol. Microbiol. 24, 1013-1024, 1997.
A>Title: Evidence for autolysin-mediated primary attachment of Staphylococcus epidermidis
A:Reference number: 220779; PMID:97363715; PMID:9220008
A:Accession: T30210
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140 <HEI>
A:Cross-references: UNIPROT:O33634; UNIPARC:UPI00000DC9D3; EMBL:U71377; NID:g2267238; PI
C:Superfamily: hypotheical protein YJCF

Query Match 72.1%; Score 31; DB 2; Length 140;
Best Local Similarity 83.3%; Pred. No. 49;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYEDYA 7
|||:
Db 36 QYEDYS 41
|||:

RESULT 15
T32236
hypotheical protein ZK488.10 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T32236
R:Wilson, R.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid ZK488.
A:Reference number: Z21138
A:Accession: T32236
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-156 <WIL>
A:Cross-references: UNIPROT:O17024; UNIPARC:UPI0000081A63; EMBL:AF022984; PIDN:AAB69957.1
A:Experimental source: strain Bristol N2; clone ZK488
C:Genetics:
A:Gene: CESP:ZK488.10
A:Map position: 5
A:Introns: 74/3

Query Match 72.1%; Score 31; DB 2; Length 156;
Best Local Similarity 62.5%; Pred. No. 55;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AQYEDYQA 8
:|||||
Db 75 SQYSDYTQ 82
:|||||

Search completed: July 5, 2006, 19:20:28
Job time : 10.7087 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 18:28:56 ; Search time 81.8641 Seconds
(without alignments)
90.395 Million cell updates/sec

Title: US-10-774-928A-10
Perfect score: 43
Sequence: 1 AQYEDYAQ 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	90.7	587	Q40275_KINRA	Q40275_kineococcus
2	38	86.4	948	Q35AN0_5BRAD	Q35AN0_bradyniob
3	37	86.0	212	Q8FRV4_COREF	Q8FRV4_corynebacte
4	36	83.7	198	Q9IB36_KATPE	Q9IB36_katsuwonus
5	35	81.4	210	Q3KDJ2_PSEPF	Q3KDJ2_pseudomonas
6	35	81.4	278	Q9CV72_MOUSE	Q9CV72_mus musculus
7	35	81.4	300	Q8C1Z6_MOUSE	Q8C1Z6_mus musculus
8	35	81.4	359	Q8C886_MOUSE	Q8C886_mus musculus
9	35	81.4	462	Q9ADR7_STAAU	Q9ADR7_staphylococ
10	35	81.4	503	Q414S5_GIBZE	Q414S5_gibberella
11	35	81.4	513	Q75BS7_ASHGO	Q75BS7_ashbya goss
12	35	81.4	552	K2C6A_MOUSE	P50446_mus musculus
13	35	81.4	554	Q3UV11_MOUSE	Q3UV11_mus musculus
14	35	81.4	561	K2C6B_MOUSE	Q92331_mus musculus
15	35	81.4	581	K2C6F25_RAT	Q61f25_rattus norv
16	35	81.4	594	K2C3UV17_MOUSE	Q3UV17_mus musculus
17	35	81.4	629	K2C3_HUMAN	P12035_homo sapien
18	35	81.4	629	K2C3_RABIT	Q29426_oryctolagus
19	35	81.4	636	Q53655_STAAU	Q53655_staphylococ
20	35	81.4	636	Q5HJ99_STAAU	Q5HJ99_staphylococ
21	35	81.4	690	Q8R9NE_STAAU	Q8R9NE_staphylococ
22	35	81.4	711	Q8BPM4_MOUSE	Q8BPM4_mus musculus
23	35	81.4	729	Q55545_SYNY3	Q55545_synecocyst
24	35	81.4	1136	Q8C2N6_MOUSE	Q8C2N6_mus musculus
25	35	81.4	1165	Q6PG61_MOUSE	Q6PG61_mus musculus
26	35	81.4	1217	Q5DTM5_MOUSE	Q5DTM5_mus musculus
27	35	81.4	1979	Q88196_MOUSE	Q88196_mus musculus
28	35	81.4	3774	Q2U2A1_ASPOR	Q2U2A1_aspergillus
29	35	81.4	4186	Q4ZVR9_PSEU2	Q4ZVR9_pseudomonas
30	35	81.4	4190	Q83Y48_PSEUX	Q83Y48_pseudomonas
31	34	79.1	93	Q6F7V2_ACIA	Q6F7V2_acinetobact

32	34	79.1	94	2	Q7VW78 BORPE	Q7VW78 bordetella
33	34	79.1	94	2	Q7WSN8 BORPA	Q7WSN8 bordetella
34	34	79.1	94	2	Q7WD74 BORBR	Q7WD74 bordetella
35	34	79.1	228	2	Q898V5_CLOTE	Q898V5 clostridium
36	34	79.1	532	2	Q75DG5_ASHGO	Q75DG5 ashbya goss
37	34	79.1	670	1	REP_BUGBP	Q89A21 buchnera ap
38	34	79.1	703	2	Q7NBD8_MYCGA	Q7NBD8 mycoplasma
39	34	79.1	730	2	Q7RUA4_NEUCR	Q7RUA4 neurospora
40	34	79.1	740	2	Q6W901_NEUCR	Q6W901 neurospora
41	34	79.1	823	2	Q2NKG6_ECOLI	Q2NKG6 escherichia
42	34	79.1	823	2	O50330_ECOLI	O50330 escherichia
43	34	79.1	950	2	Q3P2E1_NITHA	Q3P2E1 nitrobacter
44	34	79.1	1009	2	Q2RQ71_RHORU	Q2RQ71 rhodospirill
45	34	79.1	1101	2	Q50XY2_ENTHI	Q50XY2 entamoeba h

ALIGNMENTS

RESULT 1
Q40275_KINRA PRELIMINARY; PRT; 587 AA.
ID Q40275_KINRA PRELIMINARY; PRT; 587 AA.
AC Q40275;
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Similar to Coenzyme F420-dependent N5 N10-methylene
DE tetrahydromethanopterin reductase and related flavin-dependent
DE oxidoreductases.
GN ORFNames=KradRAFT 1489;
OS Kineococcus radiotolerans SRS30216.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Frankineae; Kineosporiaceae; Kineococcus.
OX NCBI_TaxID=266940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-SRS30216;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Istrani S., Pitluck S., Richardson P.,
RT "Sequencing of the draft genome and assembly of Kineococcus
radiotolerans SRS30216".
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-SRS30216;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.,
RT "Annotation of draft genome assembly of Kineococcus radiotolerans
SRS30216".
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-SRS30216;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Istrani S., Pitluck S., Richardson P.,
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC
CC EMBL; AAF02000040; EAM74395.1; -; Genomic_DNA.
DR InterPro; IPR011251; Luciferase-like
SQ SEQUENCE 587 AA; 64579 MW; 86DB19E29DCFE925 CRC64;

Query Match 90.7%; Score 39; DB 2; Length 587;
Best Local Similarity 87.5%; Pred. No. 80;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 AQYEDYQAQ 8
Db      422 AKYEDYQAQ 429

RESULT 2
Q35ANO_9BRAD      PRELIMINARY;      PRT;      948 AA.
AC Q35ANO;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DE Transaldolase subfamily.
GN ORNames=BrADRAFT_1619;
OS Bradyrhizobium sp. BTail.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=288000;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BTail;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pittluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Bradyrhizobium sp
RT BTail";
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BTail;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome of Bradyrhizobium sp. BTail.";
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AALJ01000012; EAP27068.1; -; Genomic_DNA.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0004347; F:glucose-6-phosphate isomerase activity; IEA.
DR GO; GO:0004801; F:transaldolase activity; IEA.
DR GO; GO:0005975; F:carbohydrate metabolism; IEA.
DR GO; GO:0006094; P:gluconeogenesis; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
SQ SEQUENCE 948 AA; 102058 MW; 02AB526AE5BC5378 CRC64;

Query Match      88.4%; Score 38; DB 2; Length 948;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AQYEDYQAQ 8
Db      439 ADYEDYQAQ 446

RESULT 3
Q8FRV4_COREF      PRELIMINARY;      PRT;      212 AA.
AC Q8FRV4;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DE Hypothetical protein.
GN OrderedLocusNames=CE0654;
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;

```

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RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Y8-314 / AJ 12310 / DSM 44549 / JCM 11189;
RX MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA Gojobori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RT efficiens.";
RL Genome Res. 13:1572-1579 (2003).
CC -----
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CC -----
DR EMBL; BA000035; BAC17464.1; -; Genomic_DNA.
DR Biocyc; CEFF196164; CE0654-MONOMER; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 212 AA; 22515 MW; EFDD9C365DC0E0E5 CRC64;

Query Match      86.0%; Score 37; DB 2; Length 212;
Best Local Similarity 87.5%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AQYEDYQAQ 8
Db      171 AYEDYQAQ 178

RESULT 4
Q9IB36_KATPE      PRELIMINARY;      PRT;      198 AA.
ID Q9IB36_KATPE
AC Q9IB36;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Myosin light chain 1.
GN Name=mlc1.
OS Katsuwonus pelamis (Skipjack tuna) (Bonito).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Katsuwonus.
OX NCBI_TaxID=8226;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ishizaki S., Masuda Y., Tanaka M., Hirayama Y., Watabe S.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; AB042037; BAA95126.1; -; mRNA.
DR HSSP; P14649; 1OE9.
DR SMR; Q9IB36; 1-279, 139-347, 373-427.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR011992; EF-Hand type.
DR InterPro; IPR002048; EF-hand_Ca_bd.
DR Pfam; PF00036; ehand; 2.
DR ProDom; PD000012; EF-hand; 2.
DR PROSITE; PS50222; EF_HAND_2; 2.
KW Repeat.
SQ SEQUENCE 198 AA; 21349 MW; 31D1BC98D780D46C CRC64;

Query Match      83.7%; Score 36; DB 2; Length 198;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 AQYEDYQAQ 8
Db      131 AQYEDYVE 138

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RESULT 5
Q3KDJ2_PSEPF
ID Q3KDJ2_PSEPF PRELIMINARY; PRT; 210 AA.
AC Q3KDJ2;
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 08-NOV-2005, sequence version 1.
DT 21-FEB-2006, entry version 5.
DE Glutathione S-transferase-like.
GN OrderedLocustNamesPfl12422;
OC Pseudomonas fluorescens (strain Pfo-1).
OC Bacteria; Proteobacteria; Gramnegativebacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=205922;
RN [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP US DOE Joint Genome Institute;
RG Copeland A., Lucas S., Litlick S., Saunders E.H., Schmutz J.,
RA Hammon N., Istani S., Patiluck S., Land M., Kyripides N., Anderson I., Richardson P.;
RA Larimer F., Land M., Kyripides N., Anderson I., Richardson P.;
RT "Complete sequence of Pseudomonas fluorescens Pfo-1."
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the GST superfamily.
CC
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CC
CC EMBL; CP000094; ABA74163.1; -; Genomic DNA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR004045; GST_N.
DR InterPro; IPR012336; Thioredoxin-like fold.
DR InterPro; IPR012335; Thioredoxin fold.
DR Pfam; PF02798; GST_N; 1.
KW Complete proteome; Transferase.
SQ SEQUENCE 210 AA; 24148 MW; FDE66BC52C7BC9E9 CRC64;

Query Match 81.4%; Score 35; DB 2; Length 210;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQEDYQAQ 8
Db 184 AQEDYQAQ 191

RESULT 6
Q9CV72_MOUSE
ID Q9CV72_MOUSE PRELIMINARY; PRT; 278 AA.
AC Q9CV72;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Adult male tongue cDNA, RIKEN full-length enriched library,
DE clone:231008N03 product:keratin complex 2, basic, gene 6b, full
DE insert sequence. (Fragment).
GN Name=Krt2-6b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
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RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
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RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
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RX MEDLINE=21095660; PubMed=11217851;
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RL Nature 409:685-690 (2001).
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RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
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RT prepare full-length cDNA libraries for rapid discovery of new genes.";
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RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
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RT "RIKEN integrated sequence analysis (RISA) system-384-format
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RN [8]
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RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
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RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayaishizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AK009241; BAB26162.1; -; mRNA.

DR HSP: P08670; 1GK4.
DR Ensembl: ENSMUSG00000023041; Mus musculus.
DR MGI: MGI:1333768; Krt2-6b.
DR GO: GO:0016021; C:integral to membrane; RCA.
DR GO: GO:0005739; C:mitochondrion; IDA.
DR GO: GO:0045109; P:intermediate filament organization; IGI.
DR GO: GO:0031424; P:keratinization; IGI.
DR GO: GO:0002009; P:morphogenesis of an epithelium; IGI.
DR InterPro: IPR001664; IF.
DR InterPro: IPR003054; Keratin_II.
DR PANTHER: PTHR1893;SFS; Keratin_II; 1.
DR Pfam: PF00038; Filament; 1.
DR PRINTS: PR01276; TYPE2KERATIN.
DR PROSITE: PS00226; IF; 1.
KW Intermediate filament; Keratin.
FT NON_TER 1
SQ SEQUENCE 278 AA; 30011 MW; BC641612D2959191 CRC64;

Query Match 81.4%; Score 35; DB 2; Length 278;
Best Local Similarity 87.5%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AQYEDYQA 8
Db 52 AQYEDYQA 59

RESULT 7
Q8C1Z6_MOUSE
AC Q8C1Z6;
ID Q8C1Z6_MOUSE PRELIMINARY; PRT; 300 AA.
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 21.
DE CRU-2116 JC cDNA, RIKEN full-length enriched library, clone:G430037M14
DE product:tetratrico peptide repeat domain, full insert sequence.
GN Name=Tctc3;
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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RX PubMed=16141072; DOI=10.1126/science.1112014;
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RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AK089974; BAC11023.1; -; mRNA.
DR HSSP; P53041; 1A17.
DR Ensembl; ENSMUSG00000040785; Mus musculus.
DR MGI; MGI:1276539; Ttc3.
DR InterPro; IPR013026; TPR_region.
DR PROSITE; P550005; TPR; 1.
SQ SEQUENCE 300 AA; 35253 MW; D6F6AFCD4CA19EDA CRC64;
Query Match 81.4%; Score 35; DB 2; Length 300;
Best Local Similarity 85.7%; Pred No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 QYEDYQAQ 8
DB 51 QYKDYQAQ 57
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||:||||
RESULT 8
Q8C886 MOUSE
ID Q8C886 MOUSE PRELIMINARY; PRT; 359 AA.
AC Q8C886
BT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE 16 days embryo head cDNA, RIKEN full-length enriched library,
DE clone: C130033M06 product: inferred: hypothetical protein (Homo
DE sapiens), full insert sequence.
DE Name=Plekhn1,
GN

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
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Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chaik A.M.,
Chau K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
Crome M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
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Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
Liu S., McWilliam S., Madan Babu M., Madera M., Marchionni J.,
Matsuda H., Matsuzawa S., Miki H., Mignone P., Miyake S., Morris K.,
Mortrud T., Muller N., Nakano N., Nakachi H., Ng P.,
Nilsen R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
Petkovski N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
Roos B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
Schonbach C., Sekiguchi K., Sempke C.A., Seno S., Sessa L., Sheng Y.,
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Sperling S., Stupka E., Sugitara K., Sultana R., Takenaka Y., Taki K.,
Tamajima K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
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Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
(Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Oeato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
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Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
Gaasterland T., Gariboldi M., Giasi C., Godzik A., Gough J.,
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Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
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Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
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RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Mateumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;

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RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saio R., Saichon H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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CC
DR MG1; AK048084; BAC33236.1; -; mRNA.
DR InterPro: IPR011993; PH_type.
KW Hypothetical protein.
SQ SEQUENCE 359 AA; 39358 MW; F42CF809DFDAE7DD CRC64;
Query Match 81.4%; Score 35; DB 2; Length 359;
Best Local Similarity 75.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 AQYEDYQAQ 8
Db 117 ASYEDYSQ 124
RESULT 9
Q9ADR7 STAAU PRELIMINARY; PRT; 462 AA.
AC Q9ADR7;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Coagulase (fragment).
GN Name=coa;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=mrsea;
RA Carter P.E., Begbie K., Thomson-Carter F.M.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; AJ309189; CAC36440.1; -; Genomic_DNA.
FT NON_TER 1
FT TER 462
SQ SEQUENCE 462 AA; 52952 MW; 1C9BDA535AC86238 CRC64;
Query Match 81.4%; Score 35; DB 2; Length 462;
Best Local Similarity 75.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 AQYEDYQAQ 8
Db 77 SQYEDYKQ 84
RESULT 10
Q414S5 GIBZE
ID Q414S5-GIBZE PRELIMINARY; PRT; 503 AA.
AC Q414S5;
DT 16-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
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DE Hypothetical protein.
GN ORFNames=FG07783.1;
OS Gibberella zeae (Fusarium graminearum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocrymnetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=5518;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PH-1 / NRRL 31084;
RA Birren B.W., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Archchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepl Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D.,
RA Galagan J.E., Gardyna S., Gnerre S., Graham L., Grand-Pierre N.,
RA Hafez N., Hagopian D., Hagos B., Hall J., Horton L., Hulme W.,
RA Iliev I., Jaffe D., Johnson R., Jones C., Kamal M., Kamat A.,
RA Karatas A., Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G.,
RA Lui A., Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J.,
RA Manning J., Matthews C., Mauceli E., McCarthy M., Meldrim J.,
RA Menes L., Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C.,
RA Nicol R., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P.,
RA O'Neill D., Oliver J., Peterson K., Phunkhang P., Pierre N.,
RA Purcell S., Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C.,
RA Rogov P., Roman J., Schauer S., Schupbach R., Seaman S., Severy P.,
RA Smirnov S., Smith C., Spencer B., Stange-Thomann N., Stojanovic N.,
RA Stubbs M., Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.S.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC
DR EMBL; AACM01000320; EAA7977.1; -; Genomic DNA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 503 AA; 56594 MW; 86EDA10D50C8D473 CRC64;
Query Match 81.4%; Score 35; DB 2; Length 503;
Best Local Similarity 75.0%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 AQYEDYQAQ 8
Db 118 AEYEDYIQ 125
RESULT 11
Q75BS7 ASHGO PRELIMINARY; PRT; 513 AA.
ID Q75BS7;
AC Q75BS7;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE ACR194Cp.
GN Ordered accession=ACR194C;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 10895;
RX PubMed=15001715; DOI=10.1126/science.1095781;
RA Dietrich F.S., Voegel S., Brachat S., Lerch A., Gates K., Steiner S.,
RA Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavler A.,
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RA Gaffney T.D., Philippen P.;
RT "The Ahbaya gossypii genome as a tool for mapping the ancient
RT Saccharomyces cerevisiae genome.";
RL Science 304:304-307(2004).
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CC -----
CC EMBL; AE016816; AAS51420.1; -; Genomic_DNA.
DR AGD; ACR194C; -.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 3.
DR PRINTS; PR00320; GPROTEINBRPT.
DR SMART; SM00320; WD40; 2.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
DR PROSITE; PS00082; WD_REPEATS_2; 1.
DR PROSITE; PS02094; WD_REPEATS_REGION; 1.
KW Complete proteome; Repeat; WD repeat.
SQ SEQUENCE 513 AA; 57793 MW; 6B92DD1938891760 CRC64;

Query Match 81.4%; Score 35; DB 2; Length 513;
Best Local Similarity 85.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AQYEDYA 7
Db 371 SQYEDYA 377

RESULT 12
K2C6A MOUSE
ID K2C6A MOUSE STANDARD; PRT; 552 AA.
AC P0446; O9Z332;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2005, sequence version 2.
DT 21-FEB-2006, entry version 42.
DE Keratin, type II cytoskeletal 6A (Cytokeratin-6A) (CK 6A) (K6a
DE keratin) (Keratin-6 alpha) (mk6-alpha).
GN Name=Krt6a; Synonyms=Ker2, Krt2-6, Krt2-6a, Krt6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Epidermis;
RX MEDLINE=85014838; PubMed=6207530;
RA Steinert P.M., Parry D.A.D., Racoosin E.L., Idler W.W., Steven A.C.,
RA Trus B.L., Roop D.R.;
RA "The complete cDNA and deduced amino acid sequence of a type II mouse
RT epidermal keratin of 60,000 Da: analysis of sequence differences
RT between type I and type II keratins.";
RT Proc. Natl. Acad. Sci. U.S.A. 81:5709-5713(1984).
[2]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION.
RC STRAIN=129/Sv; TISSUE=Skin;
RX MEDLINE=95009332; PubMed=9790766; DOI=10.1073/pnas.242603899;
RA Takahashi K., Yan B., Yamanishi K., Imanura S., Coulombe P.A.;
RA "The two functional keratin 6 genes of mouse are differentially
RT regulated and evolved independently from their human orthologs.";
RT Genomics 53:170-183(1998).
[3]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Jaw, and Limb;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore H., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci F., Prange C.,

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
RN NUCLEOTIDE SEQUENCE OF 527-552.
RP PubMed=1713533;
RX Finch J., Andrews K., Krieg P., Furstenberger G., Slaga T.,
RA Otsuyama A., Tanooka H., Bowden G.T.;
RT "Identification of a cloned sequence activated during multi-stage
RT carcinogenesis in mouse skin.";
RT Carcinogenesis 12:1519-1522(1991).
RL CC -!- FUNCTION: There are two types of cytoskeletal and microfibrillar
CC keratin: I (acidic; 40-55 kDa) [K9 to K20] and II (neutral to
CC basic; 56-70 kDa) [K1 to K8]. Both a basic and an acidic keratin
CC are required for filament assembly.
CC -!- SUBUNIT: Heterodimer of a type I and a type II keratin. KRT6
CC isomers associate with KRT16 and/or KRT17.
CC -!- TISSUE SPECIFICITY: Predominates in the adult trunk skin, tongue,
CC trachea/esophagus and eye. In adult skin, localization is
CC restricted to hair follicles, where it is localized predominantly
CC in the outer root sheath.
CC -!- INDUCTION: With the exception of specific body sites, keratin 6
CC expression is induced under conditions of epithelial
CC hyperproliferation such as wound healing, certain skin diseases,
CC cancer, and by treatment of the skin with the phorbol ester PMA.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; K02108; AAA39395.1; -; mRNA.
DR EMBL; AB012033; BAA34178.1; -; Genomic_DNA.
DR EMBL; BC080820; AAH80820.1; -; mRNA.
DR PIR; I59009; I59009.
DR HSP; P08670; LGK7.
DR IntAct; P50446; -.
DR Ensembl; ENSMUSG0000058354; Mus musculus.
DR MGI; MGI:1100845; Krt2-6a.
DR GO; GO:0005882; C:intermediate filament; ISS.
DR GO; GO:0005198; F:structural molecule activity; ISS.
DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; ISS.
DR InterPro; IPR001664; IF.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893:SFS; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
FT Coiled coil; Intermediate filament; Keratin; Phosphorylation.
FT INIT_MET 0 0 By similarity.
FT CHAIN 1 552 Keratin, type II cytoskeletal 6A.
FT /FtId=PRO_0000063736.
FT REGION 1 150 Head.
FT REGION 151 460 Rod.
FT REGION 151 186 Coil 1A.
FT REGION 187 205 Linker 1.
FT REGION 206 297 Coil 1B.
FT REGION 298 321 Linker 12.
FT REGION 322 460 Coil 2.
FT REGION 461 552 Tail.
FT SITE 402 402 Stutter.
FT MOD RES 57 57 Phosphoserine (By similarity).
FT CONFLICT 23 23 P -> L (in Ref. 1).
FT CONFLICT 120 120 P -> L (in Ref. 1).

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FT CONFLICT 172 172 L -> M (in Ref. 1).
FT CONFLICT 179 179 L -> M (in Ref. 1).
FT CONFLICT 190 190 G -> D (in Ref. 1).
FT CONFLICT 198 198 L -> M (in Ref. 1).
FT CONFLICT 223 224 LD -> MN (in Ref. 1).
FT CONFLICT 232 239 DTVEDYKS -> ELVEELRN (in Ref. 1).
FT CONFLICT 250 250 A -> D (in Ref. 1).
FT CONFLICT 311 311 D -> V (in Ref. 1).
FT CONFLICT 317 317 D -> V (in Ref. 1).
FT CONFLICT 329 331 YED -> FEV (in Ref. 1).
FT CONFLICT 343 343 W -> L (in Ref. 1).
FT CONFLICT 431 431 R -> L (in Ref. 1).
FT CONFLICT 437 437 Q -> H (in Ref. 1).
FT CONFLICT 497 497 L -> M (in Ref. 1).
SQ SEQUENCE 552 AA; 59204 MW; DEB2AG45EBA8DAF CRC64;

Query Match 81.4%; Score 35; DB 1; Length 552;
Best Local Similarity 87.5%; Pred. No. 4.5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQVEDYAO 8
Db 327 AQVEDYAO 334

RESULT 13
Q3UV11_MOUSE PRELIMINARY; PRT; 554 AA.
AC Q3UV11;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Adult female vagina cDNA, RIKEN full-length enriched library,
DE clone:930033010 product:keratin complex 2, basic, gene 6b, full
DE insert sequence.
GN Name=Krt2-6b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Vagina;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Vagina;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Imbondato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhury V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgil-Henning P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi K., Hensch T.K., Hirokawa N.,
RA Hill D., Huminecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,

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RA Petrovsky N., Piazza S., Reed J., Reid J.P., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Suglura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashina T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
[3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Vagina;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
[4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Vagina;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyszewski-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Vagina;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Iwama M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

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RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann J., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima M., Mazzaelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.,
RA "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
RN [6]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Vagina; DOI=10.1101/gr.145100;
RX MEDLINE=20499374; PubMed=11042159; Sugahara Y., Shibata K., Itoh M.,
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Vagina;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Azawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa K., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Vagina;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watanishi A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AK137688; BAE23462.1; -; mRNA.
DR MGI; MGI:1333768; Krt2-6b.
DR GO; GO:0016021; C:integral to membrane; RCA.
DR GO; GO:0005739; C:mitochondrion; IDA.
DR GO; GO:0045109; P:intermediate filament organization; IGI.
DR GO; GO:0031424; P:keratinization; IGI.
DR GO; GO:0002009; P:morphogenesis of an epithelium; IGI.
DR InterPro; IPR001664; IF.
DR InterPro; IPR003054; Keratin_II.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
SQ SEQUENCE 554 AA; 59526 MW; 440DE8AE3984B8AA CRC64;

Query Match 81.4%; Score 35; DB 2; Length 554;
Best Local Similarity 87.5%; Pred. No. 4.5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDYAQ 8
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Db 328 AQYEDIAQ 335

* RESULT 14

K2C6B MOUSE
ID K2C6B_MOUSE STANDARD; PRT; 561 AA.
AC Q92331;
DT 15-FEB-2005, integrated into UniProtKB/Swiss-Prot.
DT 15-FEB-2005, sequence version 2.
DT 07-FEB-2006, entry version 33.
DE Keratin, type II cytoskeletal 6B (Cytokeratin-6B) (CK 6B) (K6b
DE keratin) (Keratin-6 beta) (mk6-beta).
GN Name=krt6b; Synonyms=k6-beta, Krt2-6b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION.
RX STRAIN=129/SV; TISSUE=Skin;
RX MEDLINE=99009332; PubMed=9790766; DOI=10.1006/geno.1998.5476;
RA Takahashi K., Yan B., Yamashita K., Imamura S., Coulombe P.A.;
RT "The two functional keratin 6 genes of mouse are differentially
RT regulated and evolved independently from their human orthologs.";
RL Genomics 53:170-183(1998).
CC -!- FUNCTION: There are two types of cytoskeletal and microfibrillar
CC keratin: I (acidic; 40-55 kDa) [K9 to K20] and II (neutral to
CC basic; 56-70 kDa) [K1 to K8]. Both a basic and an acidic keratin
CC are required for filament assembly.
CC -!- SUBUNIT: Heterodimer of a type I and a type II keratin. KRT6
CC isomers associate with KRT16 and/or KRT17.
CC -!- TISSUE SPECIFICITY: Expressed in adult epithelia including the
CC tongue, esophagus/trachea, eye and skin. Localized preferentially
CC to the suprabasal layers of thickened epidermis in injured and
CC chemically treated skin.
CC -!- INDUCTION: By injury, and treatment of the skin with the phorbol
CC ester PMA.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB012042; BAA34179.1; -; Genomic_DNA.
DR HSSP; P08670; 1GK7.
DR MGI; MGI:1333768; Krt2-6b.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005882; C:intermediate filament; ISS.
DR GO; GO:0005739; C:mitochondrion; IDA.
DR GO; GO:0005198; F:structural molecule activity; ISS.
DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; ISS.
DR InterPro; IPR001664; IF.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR18893; SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Coiled coil; Intermediate filament; Keratin; Phosphorylation.
FT INIT MET 0
FT CHAIN 1 561
FT REGION 1 158
FT REGION 159 468
FT REGION 159 194
FT REGION 195 213
FT REGION 214 305
FT REGION 306 329
FT REGION 330 468
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FT SITE 410 410
FT MOD RES 57 57
FT SITE 57 57
SQ SEQUENCE 561 AA; 60191 MW; 65B71CAB7F9564E1 CRC64;

Query Match 81.4%; Score 35; DB 1; Length 561;
Best Local Similarity 87.5%; Pred. No. 4.5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDYQAQ 8
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Db 335 AQYEDIAQ 342

RESULT 15
Q6IFZ5 RAT
ID Q6IFZ5 RAT PRELIMINARY; PRT; 581 AA.
AC Q6IFZ5;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Type II keratin K89.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=23257644; PubMed=15085952; DOI=10.1078/0171-9335-00354;
RA Hesse M., Zimek A., Weber K., Magin T.M.;
RT "Comprehensive analysis of keratin gene clusters in humans and
rodents.";
RL Eur. J. Cell Biol. 83:19-26(2004).
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
EMBL/GenBank/DBJ third party annotation (TPA) entry.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC
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CC
CC EMBL; BK003994; DAA02235.1; -; mRNA.
DR Ensembl; ENSRNOG00000031785; Rattus norvegicus.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin I.
DR InterPro; IPR003054; Keratin II.
DR PANTHER; PTHR18893.SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
SQ SEQUENCE 581 AA; 61758 MW; 13B0F3D23BDF4E49 CRC64;

Query Match 81.4%; Score 35; DB 2; Length 581;
Best Local Similarity 87.5%; Pred. No. 4.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDYQAQ 8
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Db 337 AQYEDIAQ 344

Search completed: July 5, 2006, 19:01:29
Job time : 83.9641 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 18:28:26 ; Search time 69.5146 Seconds
(without alignments)
52.618 Million cell updates/sec

Title: US-10-774-928a-10

Perfect score: 43

Sequence: 1 AQYEDYQA 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_8.*

1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*
10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	43	100.0	8	AAO26390	Aao26390 Psoriasis
2	43	100.0	8	ADV04415	Adv04415 Leishmani
3	35	81.4	9	AAO26382	Aao26382 Psoriasis
4	35	81.4	9	ADV04407	Adv04407 Leishmani
5	35	81.4	30	AAV14568	Aav14568 Partial a
6	35	81.4	420	ADP29879	Adp29879 Human sec
7	35	81.4	541	AAU75491	Aau75491 S. aureus
8	35	81.4	629	AEA15502	Aea15502 Human pol
9	35	81.4	636	AAU34342	Aau34342 Staphyloc
10	35	81.4	636	AAU37415	Aau37415 Staphyloc
11	35	81.4	636	ADA89509	Ada89509 Staphyloc
12	35	81.4	636	ABJ18985	Abj18985 Pathogen
13	35	81.4	636	ABM72027	Abm72027 Staphyloc
14	35	81.4	644	AEA15501	Aea15501 Human pol
15	34	79.1	315	ADF06590	Adf06590 Bacterial
16	34	79.1	661	AAR63226	Aar63226 Mycoplasma
17	34	79.1	661	AAZ79910	Aaz79910 M.gallise
18	33	76.7	688	AAO75559	Aao75559 Protein e
19	33	76.7	1178	ABM70281	Abm70281 Photorhab
20	33	76.7	2011	ABM70279	Abm70279 Photorhab
21	33	76.7	3241	ABU22000	Abu22000 Protein e
22	32	74.4	176	ABB67136	Abb67136 Drosophil
23	32	74.4	252	ABE41195	Abe41195 L. pneumo

24	32	74.4	253	9	ABE37890	Abe37890 L. pneumo
25	32	74.4	587	4	AAU34198	Aau34198 Staphyloc
26	32	74.4	603	4	AAU37074	Aau37074 Staphyloc
27	32	74.4	603	6	ABU16392	Abu16392 Protein e
28	32	74.4	603	6	ABM72619	Abm72619 Staphyloc
29	31	72.1	11	5	ABG73045	Abg73045 Cryptococ
30	31	72.1	49	8	ADO39763	Ado39763 Caenorhab
31	31	72.1	82	4	AAU20776	Aau20776 Peptide #
32	31	72.1	82	4	ABB42330	Abb42330 Peptide #
33	31	72.1	82	4	AAU36136	Aau36136 Peptide #
34	31	72.1	82	4	ABB25821	Abb25821 Protein #
35	31	72.1	82	4	AAU76029	Aau76029 Human bon
36	31	72.1	82	4	AAU63216	Aau63216 Human bra
37	31	72.1	82	4	ABG57755	Abg57755 Human liv
38	31	72.1	82	5	ABG45427	Abg45427 Human pep
39	31	72.1	106	4	AAU27962	Aau27962 Human con
40	31	72.1	125	7	ADH86301	Adh86301 Enterococ
41	31	72.1	131	4	AAU82389	Aau82389 S. epider
42	31	72.1	134	9	ADX58875	Adx58875 Human pig
43	31	72.1	150	5	ABP38873	Abp38873 Staphyloc
44	31	72.1	150	8	ADS06504	Ads06504 Staphyloc
45	31	72.1	179	4	ABB62918	Abb62918 Drosophil

ALIGNMENTS

RESULT 1
AAO26390
ID AAO26390 standard; peptide; 8 AA.
XX
AC AAO26390;
XX
DT 30-JAN-2003 (first entry)
XX
DB Psoriasis treating immunotherapeutic peptide, SEQ ID No 10.
XX
KW Antipsoriatic; immunostimulant; gene therapy; pharmaceutical composition;
KW vaccine; immunogenic variant; immunotherapeutic agent; psoriasis;
KW gene therapy.
XX
OS Leishmania sp.
XX
PN WO200274239-A2.
XX
PD 26-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006496.
XX
PR 16-MAR-2001; 2001US-00809003.
XX
(AKIV-) AKIVA LLC.
XX
O'daly JA;
XX
WPI; 2003-018763/01.
XX
New polypeptide and immunogenic variants comprising amino acid sequences of particulate antigens, useful for the treatment and clinical remission of psoriasis.
XX
Claim 1; Page 43; 56pp; English.
XX
The invention relates to a polypeptide comprising an isolated amino acid sequence or immunogenic variants selected from any of 14 fully defined sequences of 7-16 amino acids, given in the specification. The immunotherapeutic agents and a pharmaceutical compositions comprising polynucleotides and vectors of the invention are useful for the treatment and clinical remission of psoriasis. The isolated nucleic acids are useful as probes. The sequences of the invention can be used in the treatment of disorders by gene therapy. This sequence represents one of the 14 immunotherapeutic peptides of the invention

```
SQ Sequence 8 AA;
Query Match 100.0%; Score 43; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQYEDYQAQ 8
   |||||
Db 1 AQYEDYQAQ 8

RESULT 2
ADV04415
ID ADV04415 standard; peptide; 8 AA.
XX
AC ADV04415;
XX
DT 24-FEB-2005 (first entry)
XX
DE Leishmania immunotherapeutic peptide SEQ ID NO:10.
XX
KW T-lymphocyte; immunogenicity; antigen; antipsoriatic; immunostimulant;
KW psoriasis.
XX
OS Leishmania sp.
XX
PN US2004241168-A1.
XX
PD 02-DEC-2004.
XX
PF 09-FEB-2004; 2004US-00774928.
XX
PR 16-MAR-2001; 2001US-00809003.
PR 17-OCT-2003; 2003US-00867892.
XX
PA (ODAL/) ODALY J A.
XX
PI Odaly JA;
XX
DR WPI; 2005-011563/01.
XX
PT Inhibiting selectively T-cell rolling in human, by administering compound
PT interfering with cutaneous lymphocyte antigen-E selectin interaction and
PT leukocyte function associated antigen-1 interaction.
XX
PS Claim 18; SEQ ID NO 10; 21pp; English.
XX
CC The invention relates to a novel method for selectively inhibiting T-cell
CC rolling in a human host, comprising administering a compound that
CC selectively interferes with the cutaneous lymphocyte antigen (CLA)-E
CC selectin interaction and leukocyte function associated antigen (LFA)-
CC 1/intercellular adhesion molecule (ICAM) and very late antigen
CC (VLA)/vascular cell adhesion molecule (VCAM) interactions. The compound
CC includes an immunotherapeutic agent, which comprises a purified protein
CC extract that is isolated by diethylaminoethyl Sephadex chromatography of
CC a Nonidet P-40 insoluble particulate antigen fraction derived from
CC isolated killed cells of amastigotes from one or more species of the
CC Leishmania genus, where the particulate antigen fraction is solubilized
CC with 8M urea and 0.025 M Tris(hydroxymethyl)aminomethane pH 8.3, and
CC to diethylaminoethyl Sephadex and is eluted with a solution comprising
CC 0.1 M sodium chloride, 8 M urea and 0.025 M
CC Tris(hydroxymethyl)aminomethane pH 8.3, and the purified protein extract
CC includes polypeptides having apparent molecular weights of 73, 80 and 82
CC kDa, after total reduction and alkylation. The species is L. amazonensis,
CC L. venezuelensis, L. brasiliensis and/or L. chagasi. A compound of the
CC invention has antipsoriatic and immunostimulant activity, and inhibits T-
CC cell rolling by interfering with CLA-E selectin interaction and LFA-
CC 1/ICAM and VLA/VCAM interactions. The method is useful for selectively
CC inhibiting T-cell rolling in a human host, and for treating psoriasis.
CC The present sequence represents a Leishmania peptide used in the
XX invention.
XX Sequence 8 AA;

Query Match 100.0%; Score 43; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQYEDYQAQ 8
   |||||
Db 1 AQYEDYQAQ 8

RESULT 3
AAO26382
ID AAO26382 standard; peptide; 9 AA.
XX
AC AAO26382;
XX
DT 30-JAN-2003 (first entry)
XX
DE Psoriasis treating immunotherapeutic peptide, SEQ ID NO 2.
XX
KW Antipsoriatic; immunostimulant; gene therapy; pharmaceutical composition;
KW vaccine; immunogenic variant; immunotherapeutic agent; psoriasis;
KW gene therapy.
XX
OS Leishmania sp.
XX
PN WO200274239-A2.
XX
PD 26-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006496.
XX
PR 16-MAR-2001; 2001US-00809003.
XX
PA (AKIV-) AKIVA LLC.
XX
PI O'daly JA;
XX
DR WPI; 2003-018763/01.
XX
PT New polypeptide and immunogenic variants comprising amino acid sequences
PT of particulate antigens, useful for the treatment and clinical remission
PT of psoriasis.
XX
PS Claim 1; Page 43; 56pp; English.
XX
CC The invention relates to a polypeptide comprising an isolated amino acid
CC sequence or immunogenic variants selected from any of 14 fully defined
CC sequences of 7-16 amino acids, given in the specification. The
CC immunotherapeutic agents and a pharmaceutical compositions comprising
CC polynucleotides and vectors of the invention are useful for the treatment
CC and clinical remission of psoriasis. The isolated nucleic acids are
CC useful as probes. The sequences of the invention can be used in the
CC treatment of disorders by gene therapy. This sequence represents one of
CC the 14 immunotherapeutic peptides of the invention
XX Sequence 9 AA;

Query Match 81.4%; Score 35; DB 6; Length 9;
Best Local Similarity 87.5%; Pred. No. 2.1e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDYQAQ 8
   |||||
Db 1 AQYEDYQAQ 8

RESULT 4
ADV04407
ID ADV04407 standard; peptide; 9 AA.
XX
AC ADV04407;
XX
```

DT 24-FEB-2005 (first entry)
XX Leishmania immunotherapeutic peptide SEQ ID NO:2.
XX
KW T-lymphocyte; immunogenicity; antigen; antipsoriatic; immunostimulant;
KW psoriasis.
XX
OS Leishmania sp.
XX
PN US2004241168-A1.
XX
PD 02-DEC-2004.
XX
XX 09-FEB-2004; 2004US-00774928.
PF 16-MAR-2001; 2001US-00809003.
XX 17-OCT-2003; 2003US-00687892.
PR
XX (ODAL/) ODALY J A.
PA
PI Odaly JA;
XX
XX WPI; 2005-011563/01.
DR
XX Inhibiting selectively T-cell rolling in human, by administering compound
PT interfering with cutaneous lymphocyte antigen-E selectin interaction and
PT leukocyte function associated antigen-1 interaction.
XX
PS Claim 9; SEQ ID NO 2; 21pp; English.
XX
CC The invention relates to a novel method for selectively inhibiting T-cell
CC rolling in a human host, comprising administering a compound that
CC selectively interferes with the cutaneous lymphocyte antigen (CLA)-E
CC selectin interaction and leukocyte function associated antigen (LFA)-
CC 1/intercellular adhesion molecule (ICAM) and very late antigen
CC (VLA)/vascular cell adhesion molecule (VCAM) interactions. The compound
CC includes an immunotherapeutic agent, which comprises a purified protein
CC extract that is isolated by diethylaminoethyl Sephadex chromatography of
CC a Nonidet P-40 insoluble particulate antigen fraction derived from
CC isolated killed cells of amastigotes from one or more species of the
CC Leishmania genus, where the particulate antigen fraction is solubilized
CC with 8M urea and 0.025 M Tris(hydroxymethyl)aminomethane pH 8.3 applied
CC to diethylaminoethyl Sephadex and is eluted with a solution comprising
CC 0.1 M sodium chloride, 8 M urea and 0.025 M
CC Tris(hydroxymethyl)aminomethane pH 8.3, and the purified protein extract
CC includes polypeptides having apparent molecular weights of 73, 80 and 82
CC kDa, after total reduction and alkylation. The species is L. amazonensis,
CC L. venezuelensis, L. brasiliensis and/or L. chagasi. A compound of the
CC invention has antipsoriatic and immunostimulant activity, and inhibits T-
CC cell rolling by interfering with CLA-E selectin interaction and LFA-
CC 1/ICAM and VLA/VCAM interactions. The method is useful for selectively
CC inhibiting T-cell rolling in a human host, and for treating psoriasis.
CC The present sequence represents an Leishmania peptide used in the
CC invention.
XX
SQ Sequence 9 AA;
Query Match 81.4%; Score 35; DB 9; Length 9;
Best Local Similarity 87.5%; Pred. No. 2.1e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AQVEDYQAQ 8
Db 1 AQVEDIAQ 8
RESULT 5
ID AAY14568
XX AAY14568 standard; peptide; 30 AA.
XX
AC AAY14568;
XX
DT 14-SEP-1999 (first entry)

XX Partial amino acid sequence of D-sequence binding protein.
DE
XX D-sequence; binding protein; phosphorylation; adeno-associated virus;
KW AAV; transgene; expression; DNA synthesis; cancer; EMSA; detection;
KW competitive electrophoretic mobility shift assay.
XX
OS Synthetic.
XX
PN WO9911652-A1.
XX
PD 11-MAR-1999.
XX
XX 01-SEP-1998; 98WO-US018194.
PF
XX 02-SEP-1997; 97US-0056052P.
PR
XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.
PA
XX Srivastava A, Qing K, Wang X, Ponnazhagan S, Bajpai A;
PI WPI; 1999-394757/33.
XX
XX New isolated D sequence binding protein.
PT
XX Disclosure; Page 23; 163pp; English.
PS
XX The invention relates to an isolated and purified D sequence binding
CC protein (D-BP) having a molecular weight of about 53 kD. This peptide
CC represents a partial amino acid sequence of the complete D-BP. The D-BP
CC is phosphorylated at tyrosine residues and blocks AAV-mediated transgene
CC expression in infected cells by inhibiting the leading strand viral DNA
CC synthesis. Inhibiting the function of D-BP in host cells can increase
CC expression of selected nucleic acids from an AAV, particularly for
CC increasing therapeutic nucleic acids for treating a disease such as
CC cancer.
XX
SQ Sequence 30 AA;
Query Match 81.4%; Score 35; DB 2; Length 30;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AQVEDYQAQ 8
Db 17 AQVEDIAQ 24
RESULT 6
ADP29879
ID ADP29879 standard; protein; 420 AA.
XX
XX ADP29879;
AC
XX 01-DEC-2005 (revised)
DT 12-AUG-2004 (first entry)
XX
XX Human secreted protein SEQ ID #1877.
DE
XX Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW cancer; inflammatory; immune; human secreted protein.
XX
XX Homo sapiens.
OS
XX WO2004035732-A2.
PN
XX 29-APR-2004.
PD
XX 28-AUG-2003; 2003WO-US026780.
PF
XX 29-AUG-2002; 2002US-0406576P.
PR 29-AUG-2002; 2002US-0406579P.
PR 29-AUG-2002; 2002US-0406585P.
PR

PR 29-AUG-2002; 2002US-0406588P.
PR 29-AUG-2002; 2002US-0406608P.
PR 29-AUG-2002; 2002US-0406611P.
PR 29-AUG-2002; 2002US-0406612P.
PR 29-AUG-2002; 2002US-0406616P.
PR 29-AUG-2002; 2002US-0406640P.
PR 29-AUG-2002; 2002US-0406642P.
PR 29-AUG-2002; 2002US-0406646P.
PR 29-AUG-2002; 2002US-0406653P.
PR 29-AUG-2002; 2002US-0406655P.
PR 29-AUG-2002; 2002US-0406666P.
PR 17-SEP-2002; 2002US-0410946P.
PR 17-SEP-2002; 2002US-0410947P.
PR 17-SEP-2002; 2002US-0410948P.
PR 17-SEP-2002; 2002US-0410949P.
PR 17-SEP-2002; 2002US-0410953P.
PR 17-SEP-2002; 2002US-0410957P.
PR 17-SEP-2002; 2002US-0410958P.
PR 17-SEP-2002; 2002US-0410959P.
PR 17-SEP-2002; 2002US-0410960P.
PR 17-SEP-2002; 2002US-0410961P.
PR 17-SEP-2002; 2002US-0410962P.
PR 17-SEP-2002; 2002US-0411019P.
PR 17-SEP-2002; 2002US-0411022P.
PR 17-SEP-2002; 2002US-0411023P.
PR 17-SEP-2002; 2002US-0411024P.
PR 17-SEP-2002; 2002US-0411032P.
PR 17-SEP-2002; 2002US-0411035P.
PR 17-SEP-2002; 2002US-0411037P.
PR 17-SEP-2002; 2002US-0411041P.
PR 17-SEP-2002; 2002US-0411045P.
PR 17-SEP-2002; 2002US-0411046P.
PR 17-SEP-2002; 2002US-0411048P.
PR 17-SEP-2002; 2002US-0411052P.
PR 17-SEP-2002; 2002US-0411055P.
PR 17-SEP-2002; 2002US-0411073P.
PR 17-SEP-2002; 2002US-0411082P.
PR 17-SEP-2002; 2002US-0411101P.
PR 17-SEP-2002; 2002US-0411111P.
PR 18-APR-2003; 2003US-0463700P.
PR 18-APR-2003; 2003US-0463708P.
PR 18-APR-2003; 2003US-0463716P.
PR 18-APR-2003; 2003US-0463732P.
PR 02-MAY-2003; 2003US-0467199P.
PR 02-MAY-2003; 2003US-0467201P.
PR 02-MAY-2003; 2003US-0467203P.
PR 02-MAY-2003; 2003US-0467230P.
PR 19-MAY-2003; 2003US-0471306P.
PR 19-MAY-2003; 2003US-0471336P.
PR 22-MAY-2003; 2003US-0472420P.
PR 22-MAY-2003; 2003US-0472430P.
PR 09-JUN-2003; 2003US-0476609P.
PR 09-JUN-2003; 2003US-0476641P.
PR 08-JUL-2003; 2003US-0485218P.
PR 08-JUL-2003; 2003US-0485223P.
PR 08-JUL-2003; 2003US-0485224P.
PR 08-JUL-2003; 2003US-0485325P.
PR 14-JUL-2003; 2003US-0486446P.
PR 14-JUL-2003; 2003US-0486480P.
PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486960P.
PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.
XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX WPI; 2004-348438/32.
XX

XX New nucleic acid molecule for diagnosing, preventing or treating diseases
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
XX genetic, bacterial and viral diseases.
XX Claim 1; SEQ ID NO 1877; 428pp; English.
XX The present invention relates to an isolated nucleic acid molecule
CC encoding a polypeptide which is believed to be cytostatic,
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein. The present sequence is
CC available on WIFOWEB and is not in the specification.
CC Revised record issued on 01-DEC-2005 : Sequence description line
CC corrected
XX Sequence 420 AA;
SQ

Query Match 81.4%; Score 35; DB 8; Length 420;
Best Local Similarity 87.5%; Pred. No. 2.8e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AQVEDYQAQ 8
Dy |||||
Dy 271 AQVEDYQAQ 278

RESULT 7
AAU75491
ID AAU75491 standard; protein; 541 AA.
XX AAU75491;
XX 23-APR-2002 (first entry)
XX S. aureus antigenic protein associated protein #11.
XX Antigenic protein; vaccine; SEREX; antibacterial; antiinflammatory;
XX dermatological; antiulcer; tuberculostatic; immunosuppressive;
XX septicaemia; food poisoning; skin disorders; peritonitis; endocarditis;
XX tuberculosis; blood infection; sepsis; meningitis; pneumonia;
XX stomach ulcer; gonorrhea; necrotising fasciitis; impetigo;
XX Lyme's disease; gastro-enteritis; dysentery; shigellosis.
XX Staphylococcus aureus.
OS
XX WO200198499-A1.
PN
XX 27-DEC-2001.
PD
XX 20-JUN-2001; 2001WO-GB002685.
PF
XX 20-JUN-2000; 2000GB-00014907.
PR
XX (UYSH-) UNIV SHEFFIELD.
PA (BIOS-) BIOSYNEXUS INC.
PA
XX Foster S, McDowell P, Brummell K, Clarke S;
XX WPI; 2002-106544/14.
XX
PT Identifying antigenic polypeptides expressed by pathogenic organisms
PT e.g., Staphylococcus aureus during infection, by SEREX (serological
PT identification of antigens by recombinant expression cloning) techniques.
XX
XX Disclosure; Page 74-76; 85pp; English.
XX The invention relates to a method for identifying antigenic polypeptides
CC expressed by pathogenic organisms e.g., Staphylococcus aureus during
CC infection, by SEREX (serological identification of antigens by

CC recombinant expression cloning) techniques. The method involves providing
 CC a nucleic acid library encoding genes/partial gene sequences of
 CC pathogenic organisms, transforming/transfecting the library into host
 CC cells, contacting the polypeptides expressed by the genes with autologous
 CC antisera derived from an animal infected with, or has been infected with
 CC the pathogen and purifying the nucleic acid encoding the polypeptide or
 CC partial polypeptide binding to the antisera. Also included are the
 CC nucleic acids and polypeptides isolated by the method, vectors and
 CC transformed cells expressing them, a vaccine comprising the polypeptide
 CC and the production of monoclonal antibodies against the polypeptides. The
 CC protein and vaccine are useful for immunising an animal (preferably
 CC human) against a pathogenic microbe. The proteins and antibodies are
 CC useful for manufacturing a medicament for treating Staphylococcus aureus-
 CC associated septicemia, food poisoning or skin disorders or
 CC Staphylococcus epidermidis-associated septicemia, sepsis, meningitis,
 CC endocarditis, tuberculosis, blood infections, sepsis, meningitis,
 CC pneumonia, stomach ulcers, gonorrhea, necrotising fasciitis, impetigo,
 CC Lyme's disease, gastro-enteritis, dysentery and shigellosis. The present
 CC sequence is an *S. aureus* protein sequence associated with the antigenic
 CC proteins of the invention. Note: The present sequence is included in the
 CC sequence listing but is not mentioned anywhere else in the specification
 XX
 XX
 SQ Sequence 541 AA;

Query Match 81.4%; Score 35; DB 5; Length 541;
 Best Local Similarity 75.0%; Pred. No. 3.6e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQVEDYQAQ 8
 Db :|||||
 10 SQVEDYKQ 17

RESULT 8
 AEA15502
 ID AEA15502 standard; protein; 629 AA.
 XX
 AC AEA15502;
 XX
 DT 28-JUL-2005 (first entry)
 DE Human polypeptide #121.
 XX
 KW Diagnosis; prognosis; cancer; breast tumor; ovary tumor; stomach tumor;
 KW colon tumor; esophagus tumor; bladder tumor; non-small-cell lung cancer;
 KW cytostatic; neoplasm.
 XX
 OS Homo sapiens.
 XX
 PN WO2005047534-A2.
 XX
 PD 26-MAY-2005.
 XX
 PF 15-OCT-2004; 2004WO-EP011599.
 XX
 XX 28-OCT-2003; 2003EP-00024565.
 XX
 PA (FARB) BAYER HEALTHCARE AG.
 XX
 PI Wirtz R, Munnes M;
 XX
 DR WPI; 2005-372393/38.
 DR N-PSDB; AEA15424.
 XX
 XX Predicting a response to cancer treatment by detecting at least 2
 PT markers, which are genes or genomic nucleic acid sequences that are
 PT located on one chromosomal region, which is altered in malignant
 PT neoplasia.
 XX
 XX Claim 7; SEQ ID NO 464; 464pp; English.
 PS
 PS The invention relates to a method of predicting response to cancer
 CC treatment comprising detection of at least 2 markers, where the markers

CC are genes and fragments or genomic nucleic acid sequences that are
 CC located on one chromosomal region, which is altered in malignant
 CC neoplasia. The invention also relates to a method for the prediction,
 CC diagnosis or prognosis of malignant neoplasia, methods for detecting
 CC deregulations in malignant neoplasia and breast cancer, a method of
 CC determining the phenotype of a cell or tissue, a method for identifying
 CC genomic regions which are altered on the chromosomal level and encode
 CC genes that are linked by function and are differentially expressed in
 CC malignant neoplasia and breast cancer, methods of screening for agents
 CC which regulate the activity of a polypeptide or a polynucleotide and
 CC antibodies that specifically bind to a full length or partial
 CC polypeptide. The method is useful for predicting response to cancer
 CC treatment. The methods and compositions are useful for predicting,
 CC diagnosing, prognosing, preventing or treating malignant neoplasia
 CC including breast cancer, ovarian cancer, gastric cancer, colon cancer,
 CC esophageal cancer, mesenchymal cancer, bladder cancer or non-small-cell
 CC lung cancer. This sequence represents a human polypeptide used in the
 CC scope of the invention.

SQ Sequence 629 AA;

Query Match 81.4%; Score 35; DB 9; Length 629;
 Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQVEDYQAQ 8
 Db :|||||
 376 AQVEDIAQ 383

RESULT 9
 AAU34342
 ID AAU34342 standard; protein; 636 AA.

XX
 AC AAU34342;
 XX
 DT 14-FEB-2002 (first entry)
 DE Staphylococcus aureus cellular proliferation protein #618.
 XX
 KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
 KW antibacterial; drug design.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO200170955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US009180.
 XX
 PR 21-MAR-2000; 2000US-0191078P.
 PR 23-MAY-2000; 2000US-0206848P.
 PR 26-MAY-2000; 2000US-020727P.
 PR 23-OCT-2000; 2000US-0242578P.
 PR 27-NOV-2000; 2000US-0253625P.
 PR 22-DEC-2000; 2000US-0257931P.
 PR 16-FEB-2001; 2001US-0269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 PI
 XX WPI; 2001-611495/70.
 DR N-PSDB; AAS2201.
 XX
 XX New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids.
 PT
 PS Example 3; SEQ ID NO 5838; 511pp; English.
 XX
 XX The invention relates to antisense inhibitors of genes essential to

CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 636 AA;

Query Match 81.4%; Score 35; DB 4; Length 636;
Best Local Similarity 75.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AQYEDYAQ 8
:|||||
Db 105 SQYEDYKQ 112

RESULT 10
AAU37415
ID AAU37415 standard; protein; 636 AA.

XX AAU37415;

XX 14-FEB-2002 (first entry)

DE Staphylococcus aureus cellular proliferation protein #1585.

XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.

XX Staphylococcus aureus.

XX WO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009180.

XX 21-MAR-2000; 2000US-0191078P.

XX 23-MAY-2000; 2000US-0206848P.

XX 26-MAY-2000; 2000US-0207272P.

XX 23-OCT-2000; 2000US-0242578P.

XX 27-NOV-2000; 2000US-0253625P.

XX 22-DEC-2000; 2000US-0257931P.

XX 16-FEB-2001; 2001US-0269308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haeelbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

XX WPI; 2001-611495/70.

XX N-PSDB; AAS55274.

XX New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids.

XX Example 3; SEQ ID NO 13008; 511pp; English.

CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 636 AA;

Query Match 81.4%; Score 35; DB 4; Length 636;
Best Local Similarity 75.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AQYEDYAQ 8
:|||||
Db 105 SQYEDYKQ 112

RESULT 11

ADA89509

ID ADA89509 standard; protein; 636 AA.

XX ADA89509;

XX 20-NOV-2003 (first entry)

DE Staphylococcus aureus antigenic protein #48.

XX antigenic protein; vaccine; Staphylococcus aureus; pathogenic organism;
KW antibacterial; neuroprotective; immunosuppressive; antiinflammatory;
KW antiulcer; immunostimulant; ophthalmological; pathogenic microbe;
KW bacteraemia; septic shock; organ infection; skin infection;
KW bacterial basal colonisation; bacterial eye infection; septicaemia;
KW tuberculosis; food poisoning; blood infection; peritonitis; endocarditis;
KW sepsis; meningitis; pneumonia; stomach ulcer; gonorrhoea; toxic shock;
KW necrotising fasciitis; impetigo; histoplasmosis; Lyme disease;
KW gastro-enteritis; dysentery; shigellosis; skin disorder.

XX Staphylococcus aureus.

XX WO2003011899-A2.

XX 13-FEB-2003.

XX 02-AUG-2002; 2002WO-GB003606.

XX 02-AUG-2001; 2001GB-00018825.

XX 09-JAN-2002; 2002GB-00000349.

XX (UYSH-) UNIV SHEFFIELD.

XX (BIOS-) BIOSYNEXUS INC.

XX Foster S, Mond J, Clarke S, McDowell P, Brummel K;

XX WPI; 2003-256434/25.

XX New antigenic polypeptides from Staphylococcus aureus or S. epidermidis,
PT useful as a vaccine for immunizing humans against e.g. bacteraemia, septic
PT shock, septicaemia, tuberculosis, meningitis, pneumonia, gonorrhoea or
PT impetigo.

XX Claim 4; Page 133; 189pp; English.

CC The present invention describes an antigenic protein or its part, which
 CC is for use as a vaccine. The antigenic protein is encoded by an isolated
 CC DNA molecule of *Staphylococcus aureus* or *S. epidermidis* partial gene
 CC sequences (designated dnaSA and dna SP, respectively; and which encodes a
 CC protein expressed by a pathogenic organism. Also described: (1) a vaccine
 CC composition comprising at least one antigenic protein; (2) a method of
 CC immunising an animal against a disease or condition caused by a
 CC pathogenic microbe by administering the antigenic protein or the vaccine;
 CC (3) an antibody or its binding part obtainable by the method above; (4)
 CC preparing a hybridoma cell line producing monoclonal antibodies; (5) a
 CC hybridoma cell line produced by the method of (4); and (6) identifying
 CC opsonic antigens expressed by a pathogenic microbe. The antigenic
 CC proteins have antibacterial, neuroprotective, immunosuppressive,
 CC antiinflammatory, antitumor, immunostimulant and ophthalmological
 CC activities, and can be used in vaccines. The antigenic proteins or
 CC vaccines can be used for immunising an animal (specifically a human)
 CC against a disease or condition caused by a pathogenic microbe, e.g.
 CC bacteraemia, septic shock, organ infection, skin infection, bacterial
 CC basal colonisation, bacterial eye infections, septicaemia, tuberculosis,
 CC bacteria-associated food poisoning, blood infections, peritonitis,
 CC endocarditis, sepsis, meningitis, pneumonia, stomach ulcers, gonorrhoea,
 CC strep throat, streptococcal-associated toxic shock, necrotising
 CC fasciitis, impetigo, histoplasmosis, Lyme disease, gastro-enteritis,
 CC dysentery, shigellosis, *S. aureus*-associated septicaemia, food-poisoning,
 CC skin disorders, *S. epidermidis*-associated septicaemia, peritonitis or
 CC endocarditis. The present sequence represents a *S. aureus* antigenic
 CC protein sequence from the present invention.

XX Sequence 636 AA;

Query Match 81.4%; Score 35; DB 6; Length 636;

Best Local Similarity 75.0%; Pred. No. 4.4e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 AQYEDYQAQ 8

Db 105 SQYEDYKQ 112

RESULT 12

ABJ18985

ID ABJ18985 standard; protein; 636 AA.

XX AC ABJ18985;

XX DT 06-MAR-2003 (first entry)

XX DE Pathogen specific antigen related staphylococcal protein SEQ ID No 156.

XX KW Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;

XX KW hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;

XX KW auto-immunity; vaccine; staphylococcal infection; antibody; cancer;

XX KW autoimmune disease; HIV; hepatitis.

XX OS *Staphylococcus* sp.

XX PN WO200259148-A2.

XX PD 01-AUG-2002.

XX PF 21-JAN-2002; 2002WO-EP000546.

XX PR 26-JAN-2001; 2001AT-00000130.

XX PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.

XX PI Meinke A, Nagy E, Von Ahsen U, Klade C, Henics T, Zauner W;

XX PI Minh DB, Vytvytska O, Etz H, Dryla A, Weichhart T, Hafner M;

XX PI Tempelmaier B;

XX DR WPI; 2003-075410/07.

XX PT Identifying, isolating and producing hyperimmune serum-reactive antigens

PT from a pathogen, for preparing vaccine or medicament for treating or
 PT preventing e.g. staphylococcal infections, comprises providing antibody
 PT preparation.

XX Example 7; Page 173; 252pp; English.

PS The invention relates to a novel method for identifying, isolating and
 CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
 CC allergen, a tissue or host prone to auto-immunity, where the antigens are
 CC used in a vaccine, comprises providing antibody preparation from a plasma
 CC pool of a type of animal, or individual sera with antibodies against the
 CC specific pathogen, tumour, allergen, tissue or host prone to auto-
 CC immunity. The hyperimmune serum-reactive antigens comprising any of the
 CC 62 sequences of 53-2261 amino acids fully defined in the specification,
 CC or their hyperimmune fragments are useful for the manufacture of a
 CC pharmaceutical preparation, particularly a vaccine against staphylococcal
 CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
 CC preparation of antibodies is useful for the manufacture of a medicament
 CC for treating or preventing staphylococcal infections or colonisation
 CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
 CC be used for diagnostic and imaging purposes. Other conditions that can be
 CC treated include cancer, autoimmune diseases or infections caused by viral
 CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
 CC sequence represents a staphylococcal protein relating to the method for
 CC identifying and producing pathogen specific antigens of the invention

XX Sequence 636 AA;

Query Match 81.4%; Score 35; DB 6; Length 636;

Best Local Similarity 75.0%; Pred. No. 4.4e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 AQYEDYQAQ 8

Db 105 SQYEDYKQ 112

RESULT 13

ABM72027

ID ABM72027 standard; protein; 636 AA.

XX AC ABM72027;

XX DT 20-NOV-2003 (first entry)

XX DE *Staphylococcus aureus* protein #1267.

XX KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;

XX KW enzymatic assay; antibiotic target.

XX OS *Staphylococcus aureus*.

XX PN WO200294868-A2.

XX PD 28-NOV-2002.

XX PF 27-MAR-2002; 2002WO-IB002637.

XX PR 27-MAR-2001; 2001GB-00007661.

XX PA (CHIR-) CHIRON SPA.

XX PI Massignani V, Mora M, Scarselli M;

XX DR WPI; 2003-120786/11.

XX DR N-PSDB; ACF73587.

XX PT New *Staphylococcus aureus* protein, useful as a vaccine for treating or
 PT preventing *Staphylococcal* infection, specifically an infection caused by
 PT *S. aureus*, e.g. sepsis.

XX PS Claim 1; SEQ ID NO 2534; 49pp; English.

CC The invention relates to novel genes and encoded proteins from
 CC *Staphylococcus aureus*. A composition comprising the *S. aureus* protein, a
 CC nucleic acid encoding the protein, or an antibody to the protein, is
 CC useful as a pharmaceutical, particularly as a vaccine for treating or
 CC preventing infection due to *Staphylococcus bacteria*, specifically an
 CC infection caused by *S. aureus*. The composition is particularly useful for
 CC treating or preventing sepsis in a patient. The composition can also be
 CC used for diagnostics. The protein is also used in an assay for enzymatic
 CC studies and as a target for antibiotics. This sequence represents one of
 CC the novel *S. aureus* proteins of the invention

XX SQ Sequence 636 AA;

Query Match 81.4%; Score 35; DB 6; Length 636;
 Best Local Similarity 75.0%; Pred. No. 4.4e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AQYEDYQAQ 8
 :|||||
 Db 105 SQYEDYKQ 112

RESULT 14
 AEA15501
 ID AEA15501 standard; protein; 644 AA.

XX AC AEA15501;

XX DT 28-JUL-2005 (first entry)

XX DE Human polypeptide #120.

XX KW Diagnosis; prognosis; cancer; breast tumor; ovary tumor; stomach tumor;
 XX colon tumor; esophagus tumor; bladder tumor; non-small-cell lung cancer;
 XX cytostatic; neoplasm.

XX OS Homo sapiens.

XX PN WO2005047534-A2.

XX PD 26-MAY-2005.

XX PF 15-OCT-2004; 2004WO-EP011599.

XX PR 28-OCT-2003; 2003EP-00024565.

XX PA (FARB) BAYER HEALTHCARE AG.

XX PI Wirtz R, Munnes M;

XX WPI; 2005-372393/38.

XX DR N-PSDB; AEA15423.

XX Predicting a response to cancer treatment by detecting at least 2
 PT markers, which are genes or genomic nucleic acid sequences that are
 PT located on one chromosomal region, which is altered in malignant
 PT neoplasia.

XX Claim 7; SEQ ID NO 463; 464pp; English.

XX The invention relates to a method of predicting response to cancer
 CC treatment comprising detection of at least 2 markers, where the markers
 CC are genes and fragments or genomic nucleic acid sequences that are
 CC located on one chromosomal region, which is altered in malignant
 CC neoplasia. The invention also relates to a method for the prediction,
 CC diagnosis or prognosis of malignant neoplasia, methods for detecting
 CC deregulations in malignant neoplasia and breast cancer, a method of
 CC determining the phenotype of a cell or tissue, a method for identifying
 CC genomic regions which are altered on the chromosomal level and encode
 CC genes that are linked by function and are differentially expressed in
 CC malignant neoplasia and breast cancer, methods of screening for agents
 CC which regulate the activity of a polypeptide or a polynucleotide and
 CC antibodies that specifically bind to a full length or partial

CC polypeptide. The method is useful for predicting response to cancer
 CC treatment. The methods and compositions are useful for predicting,
 CC diagnosing, prognosing, preventing or treating malignant neoplasia
 CC including breast cancer, ovarian cancer, gastric cancer, colon cancer,
 CC esophageal cancer, mesenchymal cancer, bladder cancer or non-small-cell
 CC lung cancer. This sequence represents a human polypeptide used in the
 CC scope of the invention.

XX SQ Sequence 644 AA;

Query Match 81.4%; Score 35; DB 9; Length 644;
 Best Local Similarity 87.5%; Pred. No. 4.4e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AQYEDYQAQ 8
 :|||||
 Db 356 AQYEDYQAQ 363

RESULT 15

ADF06590
 ID ADF06590 standard; protein; 315 AA.

XX AC ADF06590;

XX DT 12-FEB-2004 (first entry)

XX DE Bacterial polypeptide #2703.

XX KW Proteus mirabilis infection; bacterial infection; antibacterial;
 XX immunostimulant.

XX OS Proteus mirabilis.

XX PN US6605709-B1.

XX PD 12-AUG-2003.

XX PF 05-APR-2000; 2000US-00543681.

XX PR 09-APR-1999; 99US-0128706P.

XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX PI Breton GL;

XX WPI; 2003-895291/82.

XX DR N-PSDB; ADF02416.

XX New Proteus mirabilis polypeptides and polynucleotides, useful as
 PT reagents for diagnosis of bacterial disease, as components of
 PT antibacterial vaccines, as targets for antibacterial drugs, or as
 PT biocontrol agents for plants.

XX Disclosure; SEQ ID NO 6875; 870pp; English.

XX The invention relates to new proteus mirabilis polypeptides and
 CC polynucleotides. The invention also relates to antibodies against the
 CC polypeptides, methods for producing the polypeptides, a method of
 CC generating vaccines for immunising an individual against *P. mirabilis*, a
 CC method for evaluating a compound for the ability to bind a *P. mirabilis*
 CC polypeptide and a method for screening test compounds for anti-bacterial
 CC activity. The polypeptides and polynucleotides are useful as molecular
 CC targets for diagnosing, preventing and treating pathological conditions
 CC resulting from bacterial infection, as reagents for diagnosis of
 CC bacterial diseases, as components of antibacterial vaccines, as targets
 CC for antibacterial drugs or as bio-control agents for plants. This
 CC sequence represents a Proteus mirabilis polypeptide of the invention.

XX SQ Sequence 315 AA;

Query Match 79.1%; Score 34; DB 7; Length 315;
 Best Local Similarity 87.5%; Pred. No. 3.1e+02; .

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AQYEDYAO 8
| | | | |
Db 105 AQYEDKAO 112

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Job time : 71.5146 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 20:38:52 ; Search time 58.5631 Seconds
(without alignments)
63.277 Million cell updates/sec

Title: US-10-774-928A-10
Perfect score: 43
Sequence: 1 AQYEDYQAQ 8

Scoring table: BLOSUM62
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Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	43	100.0	8	5	US-10-774-928-10
2	38	88.4	98	4	US-10-437-963-128532
3	35	81.4	9	5	US-10-774-928-2
4	35	81.4	541	4	US-10-311-879-30
5	35	81.4	636	3	US-09-815-242-5838
6	35	81.4	636	3	US-09-815-242-13008
7	35	81.4	636	5	US-10-470-048B-156
8	35	81.4	636	5	US-10-485-517-170
9	33	76.7	3241	4	US-10-282-122A-49924
10	32	74.4	52	4	US-10-424-599-190535
11	32	74.4	143	4	US-10-425-115-362330
12	32	74.4	176	6	US-11-097-143-28200
13	32	74.4	201	4	US-10-425-115-361451
14	32	74.4	417	4	US-10-437-963-167445
15	32	74.4	587	3	US-09-815-242-5694
16	32	74.4	603	3	US-09-815-242-12667
17	32	74.4	603	4	US-10-282-122A-44316
18	32	74.4	1132	4	US-10-437-963-169428
19	31	72.1	11	3	US-09-946-678-7
20	31	72.1	43	4	US-10-437-963-121052
21	31	72.1	82	3	US-09-864-761-41119
22	31	72.1	106	5	US-10-220-335-631
23	31	72.1	131	5	US-10-793-626-1872
24	31	72.1	143	4	US-10-425-115-345358
25	31	72.1	150	4	US-10-724-972A-5799
26	31	72.1	179	6	US-11-097-143-15546
27	31	72.1	200	4	US-10-424-599-184988

28 31 72.1 202 6 US-11-097-143-26418 Sequence 26418, A
29 31 72.1 279 5 US-10-467-657-3032 Sequence 3032, Ap
30 31 72.1 280 3 US-09-815-242-12479 Sequence 12479, A
31 31 72.1 290 4 US-10-767-701-45172 Sequence 45172, A
32 31 72.1 290 4 US-10-425-115-303461 Sequence 303461, A
33 31 72.1 300 4 US-10-437-963-150328 Sequence 150328, A
34 31 72.1 312 6 US-11-188-298-18557 Sequence 18557, A
35 31 72.1 327 4 US-10-408-765A-1475 Sequence 1475, Ap
36 31 72.1 341 4 US-10-425-114-46394 Sequence 46394, A
37 31 72.1 433 6 US-11-188-298-2247 Sequence 2247, Ap
38 31 72.1 442 5 US-10-467-657-3900 Sequence 3900, Ap
39 31 72.1 444 4 US-10-282-122A-72394 Sequence 72394, A
40 31 72.1 448 6 US-11-188-298-16905 Sequence 16905, A
41 31 72.1 481 6 US-11-188-298-5542 Sequence 5542, Ap
42 31 72.1 484 6 US-11-188-298-16281 Sequence 16281, A
43 31 72.1 490 6 US-11-188-298-17034 Sequence 17034, A
44 31 72.1 504 3 US-09-765-205-40 Sequence 40, Appl
45 31 72.1 504 5 US-10-347-669-40 Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-10-774-928-10
; Sequence 10, Application US/10774928
; Publication No. US20040241168A1
; GENERAL INFORMATION:

; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 302178
; CURRENT APPLICATION NUMBER: US/10/774,928
; CURRENT FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Leishmania
US-10-774-928-10

Query Match 100.0%; Score 43; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQYEDYQAQ 8
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DB 1 AQYEDYQAQ 8

RESULT 2
US-10-437-963-128532
; Sequence 128532, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 128532
; LENGTH: 98
; TYPE: PRT

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; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_30877C.1.pep
US-10-437-963-128532

Query Match      88.4%; Score 38; DB 4; Length 98;
Best Local Similarity 87.5%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AQYEDYQAQ 8
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Db      36 ANYEDYQAQ 43

RESULT 3
US-10-774-928-2
; Sequence 2, Application US/10774928
; Publication No. US20040241168A1
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; FILE REFERENCE: Psoriasis
; CURRENT APPLICATION NUMBER: 302178
; CURRENT FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Leishmania
US-10-774-928-2

Query Match      81.4%; Score 35; DB 5; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.9e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AQYEDYQAQ 8
      | | | | |
Db      1 AQYEDYQAQ 8

RESULT 4
US-10-311-879-30
; Sequence 30, Application US/103111879
; Publication No. US20030186275A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; TITLE OF INVENTION: Antigenic Peptides
; FILE REFERENCE: toxin
; CURRENT APPLICATION NUMBER: US/10/311,879
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-311-879-30

Query Match      81.4%; Score 35; DB 4; Length 541;
Best Local Similarity 75.0%; Pred. No. 5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AQYEDYQAQ 8
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Db      10 SQYEDYKQ 17

RESULT 5
US-09-815-242-5838
; Sequence 5838, Application US/09815242
; Patent No. US20020061569A1
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; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5838
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5838

Query Match      81.4%; Score 35; DB 3; Length 636;
Best Local Similarity 75.0%; Pred. No. 5.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AQYEDYQAQ 8
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Db      105 SQYEDYKQ 112

RESULT 6
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; Sequence 13008, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
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;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; NUMBER OF SEQ ID NOS: 14110
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 13008
;; LENGTH: 636
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-09-815-242-13008

Query Match 81.4%; Score 35; DB 3; Length 636;
Best Local Similarity 75.0%; Pred. No. 5.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDYQAQ 8
:|||||
Db 105 SQYEDYKQ 112

RESULT 7

US-10-470-048B-156
;; Sequence 156, Application US/10470048B
;; Publication No. US2005003744A1
;; GENERAL INFORMATION:
;; APPLICANT: MEINKE ET AL.

;; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
;; FILE REFERENCE: ANTIGENS TO A SPECIFIC PATHOGEN
;; CURRENT APPLICATION NUMBER: US/10/470,048B
;; CURRENT FILING DATE: 2003-07-25
;; NUMBER OF SEQ ID NOS: 603
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 156
;; LENGTH: 636
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-10-470-048B-156

Query Match 81.4%; Score 35; DB 5; Length 636;
Best Local Similarity 75.0%; Pred. No. 5.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDYQAQ 8
:|||||
Db 105 SQYEDYKQ 112

RESULT 8

US-10-485-517-170
;; Sequence 170, Application US/10485517
;; Publication No. US2005025629A1
;; GENERAL INFORMATION:
;; APPLICANT: University of Sheffield
;; APPLICANT: Biosynex Incorporated
;; APPLICANT: Foster, Simon
;; APPLICANT: Mond, James
;; TITLE OF INVENTION: Antigenic Polypeptides
;; FILE REFERENCE: P100629W0
;; CURRENT APPLICATION NUMBER: US/10/485,517
;; CURRENT FILING DATE: 2004-02-02
;; PRIOR APPLICATION NUMBER: GB 0118825.9
;; PRIOR FILING DATE: 2001-08-02
;; PRIOR APPLICATION NUMBER: GB 0200349.9
;; PRIOR FILING DATE: 2002-01-09
;; NUMBER OF SEQ ID NOS: 424
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 170
;; LENGTH: 636
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-10-485-517-170

Query Match 81.4%; Score 35; DB 5; Length 636;
Best Local Similarity 75.0%; Pred. No. 5.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQYEDYQAQ 8
:|||||
Db 105 SQYEDYKQ 112

RESULT 9

US-10-282-122A-49924
;; Sequence 49924, Application US/10282122A
;; Publication No. US20040029129A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, Liangsu
;; APPLICANT: Zamudio, Carlos
;; APPLICANT: Malone, Cheryl
;; APPLICANT: Haselbeck, Robert
;; APPLICANT: Ohlsen, Kari
;; APPLICANT: Zyskind, Judith
;; APPLICANT: Wall, Daniel
;; APPLICANT: Trawick, John
;; APPLICANT: Carr, Grant
;; APPLICANT: Yamamoto, Robert
;; APPLICANT: Forsyth, R.
;; APPLICANT: Xu, H.

;; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;; FILE REFERENCE: ELITRA.034A
;; CURRENT APPLICATION NUMBER: US/10/282,122A
;; CURRENT FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: 60/191,078
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/206,848
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/230,335
;; PRIOR FILING DATE: 2000-09-06
;; PRIOR APPLICATION NUMBER: 60/230,347
;; PRIOR FILING DATE: 2000-09-09
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/267,636
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 49924
;; LENGTH: 3241
;; TYPE: PRT
;; ORGANISM: Burkholderia fungorum
US-10-282-122A-49924

Query Match 76.7%; Score 33; DB 4; Length 3241;
Best Local Similarity 85.7%; Pred. No. 6.7e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYEDYQAQ 8
:|||||
Db 795 QYADYQAQ 801

RESULT 10

US-10-424-599-190535
;; Sequence 190535, Application US/10424599
;; Publication No. US20040031072A1

; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 190535
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_143072C.1.pep
US-10-424-599-190535

Query Match 74.4%; Score 32; DB 4; Length 52;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYEDYQAQ 8
Db 40 QYEHYQAQ 46

RESULT 11
US-10-425-115-362330
; Sequence 362330, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 362330
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_93620C.1.pep
US-10-425-115-362330

Query Match 74.4%; Score 32; DB 4; Length 143;
Best Local Similarity 62.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AQYEDYQAQ 8
Db 46 SQYKDYVQ 53

RESULT 12
US-11-097-143-28200
; Sequence 28200, Application US/11097143
; Publication No. US2005020858A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04

; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28200
; LENGTH: 176
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-28200

Query Match 74.4%; Score 32; DB 6; Length 176;
Best Local Similarity 62.5%; Pred. No. 5.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AQYEDYQAQ 8
Db 162 AQYDDYVK 169

RESULT 13
US-10-425-115-361451
; Sequence 361451, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 361451
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_92821C.1.pep
US-10-425-115-361451

Query Match 74.4%; Score 32; DB 4; Length 201;
Best Local Similarity 62.5%; Pred. No. 6.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AQYEDYQAQ 8
Db 107 SQFEDYVQ 114

RESULT 14
US-10-437-963-167445
; Sequence 167445, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 167445
LENGTH: 417
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_66056C.1.pap
US-10-437-963-167445

Query Match 74.4%; Score 32; DB 4; Length 417;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYEDYQAQ 8
DB 211 QYETYQAQ 217

RESULT 15
US-09-815-242-5694
Sequence 5694, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 1410
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5694
LENGTH: 587
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5694

Query Match 74.4%; Score 32; DB 3; Length 587;
Best Local Similarity 62.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQYDYQAQ 8

Db 478 SQKDYAK 485
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Title: US-10-774-928A-10
Perfect score: 43
Sequence: 1 AQYEDYQAQ 8

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Searched: 112942 seqs, 26832045 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	35	81.4	541	7	US-11-256-173-30
2	35	81.4	636	6	US-10-471-571A-2534
3	32	74.4	143	6	US-10-449-902-53316
4	32	74.4	417	6	US-10-449-902-51027
5	32	74.4	603	6	US-10-471-571A-3718
6	31	72.1	300	6	US-10-449-902-46061
7	31	72.1	475	7	US-11-174-307B-160
8	31	72.1	548	6	US-10-449-902-29496
9	31	72.1	585	6	US-10-449-902-53167
10	31	72.1	852	6	US-10-449-902-51138
11	31	72.1	1127	6	US-10-449-902-53809
12	30	69.8	368	6	US-10-449-902-31471
13	30	69.8	368	6	US-10-449-902-54507
14	30	69.8	483	7	US-11-105-233-180
15	30	69.8	797	6	US-10-449-902-41261
16	29	67.4	386	7	US-11-256-173-16
17	29	67.4	389	7	US-11-264-558-5
18	29	67.4	467	7	US-11-264-558-4
19	29	67.4	593	7	US-11-293-697-4773
20	29	67.4	619	6	US-10-471-571A-3914
21	29	67.4	944	6	US-10-449-902-47242
22	29	67.4	2397	6	US-10-471-571A-2632
23	28	65.1	103	6	US-10-953-349-26513
24	28	65.1	110	7	US-11-342-171-4
25	28	65.1	125	6	US-10-530-879-10

26	65.1	217	6	US-10-953-349-35566	Sequence 35566, A
27	65.1	222	6	US-10-953-349-12891	Sequence 12891, A
28	65.1	245	6	US-10-953-349-35565	Sequence 35565, A
29	65.1	258	6	US-10-953-349-18067	Sequence 18067, A
30	65.1	289	6	US-10-953-349-12890	Sequence 12890, A
31	65.1	309	6	US-10-449-902-31890	Sequence 31890, A
32	65.1	309	6	US-10-449-902-49974	Sequence 49974, A
33	65.1	311	6	US-10-953-349-1338	Sequence 1338, Ap
34	65.1	312	6	US-10-953-349-1337	Sequence 1337, Ap
35	65.1	314	6	US-10-953-349-1336	Sequence 1336, Ap
36	65.1	320	6	US-10-449-902-52190	Sequence 52190, A
37	65.1	328	6	US-10-449-902-31205	Sequence 31205, A
38	65.1	349	6	US-10-953-349-12889	Sequence 12889, A
39	65.1	371	6	US-10-530-879-3	Sequence 3, Appli
40	65.1	372	6	US-10-953-349-11032	Sequence 11032, A
41	65.1	452	6	US-10-953-349-11031	Sequence 11031, A
42	65.1	453	6	US-10-953-349-11030	Sequence 11030, A
43	65.1	535	7	US-11-293-697-4336	Sequence 4336, Ap
44	65.1	623	7	US-11-342-171-64	Sequence 64, Appl
45	65.1	971	6	US-10-449-902-53062	Sequence 53062, A

ALIGNMENTS

RESULT 1

US-11-256-173-30
; Sequence 30, Application US/11256173
; Publication No. US20060140979A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; TITLE OF INVENTION: Antigenic Peptides
; FILE REFERENCE: toxin
; CURRENT APPLICATION NUMBER: US/11/256,173
; CURRENT FILING DATE: 2005-10-24
; PRIOR APPLICATION NUMBER: US/10/311,879
; PRIOR FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 30
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-11-256-173-30

Query Match 81.4%; Score 35; DB 7; Length 541;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 AQYEDYQAQ 8
DB :|||||
10 SQYEDYKQ 17

RESULT 2

US-10-471-571A-2534
; Sequence 2534, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 2534
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:

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; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(336)
; OTHER INFORMATION: staphylocoagulase precursor
US-10-471-571A-2534

Query Match      81.4%; Score 35; DB 6; Length 636;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AQYEDYQAQ 8
Db 105 SQYEDYKQ 112

RESULT 3
US-10-449-902-53316
; Sequence 53316, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53316
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-53316

Query Match      74.4%; Score 32; DB 6; Length 143;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QYEDYQAQ 8
Db 127 EYEEYQAQ 133

RESULT 4
US-10-449-902-51027
; Sequence 51027, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51027
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-51027
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Query Match      74.4%; Score 32; DB 6; Length 417;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYEDYQAQ 8
Db 211 QYETVQAQ 217

RESULT 5
US-10-471-571A-3718
; Sequence 3718, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 3718
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(603)
; OTHER INFORMATION: hypothetical protein
US-10-471-571A-3718

Query Match      74.4%; Score 32; DB 6; Length 603;
Best Local Similarity 62.5%; Pred. No. 55;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AQYEDYQAQ 8
Db 488 SQYKDYAK 495
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RESULT 6
US-10-449-902-46061
; Sequence 46061, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46061
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-46061

Query Match      72.1%; Score 31; DB 6; Length 300;
Best Local Similarity 62.5%; Pred. No. 42;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AQYEDYQAQ 8
Db 111 : : : :
```

```
Db      104 AQFEDYKE 111

RESULT 7
US-11-174-307B-160
; Sequence 160, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 160
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: AAA; Pfam Description: ATPase family associated
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 10176992; NR Description: contains similarity to
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 9294271; NR Description: mitochondrial
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 9294274; NR Description: mitochondrial
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 61656802; NR Description: Cell Division Protein
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 45735466; NR Description: putative ATPase
US-11-174-307B-160

Query Match      72.1%; Score 31; DB 7; Length 475;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 AQYEDY 6
Db      65 SQYEDY 70

RESULT 8
US-10-449-902-29496
; Sequence 29496, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29496
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-29496

Query Match      72.1%; Score 31; DB 6; Length 548;
Best Local Similarity 71.4%; Pred. No. 79;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 QYEDYQAQ 8
Db      244 QYQDYQQ 250

RESULT 9
US-10-449-902-53167
; Sequence 53167, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53167
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-53167

Query Match      72.1%; Score 31; DB 6; Length 585;
Best Local Similarity 71.4%; Pred. No. 84;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 QYEDYQAQ 8
Db      281 QYQDYQQ 287

RESULT 10
US-10-449-902-51138
; Sequence 51138, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
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; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51138
; LENGTH: 852
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-51138

Query Match      72.1%; Score 31; DB 6; Length 852;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 QYEDYQAQ 8
Db      626 QYQDYQQ 632

RESULT 11
US-10-449-902-53809
; Sequence 53809, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53809
; LENGTH: 1127
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-53809

Query Match      72.1%; Score 31; DB 6; Length 1127;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 QYEDYQAQ 8
Db      823 QYQDYQQ 829

RESULT 12
US-10-449-902-31471
; Sequence 31471, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31471
; LENGTH: 368
; TYPE: PRT
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; ORGANISM: Oryza sativa
US-10-449-902-31471

Query Match      69.8%; Score 30; DB 6; Length 368;
Best Local Similarity 71.4%; Pred. No. 81;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AQYEDYA 7
Db      62 SQWEDYA 68

RESULT 13
US-10-449-902-54507
; Sequence 54507, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54507
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-54507

Query Match      69.8%; Score 30; DB 6; Length 368;
Best Local Similarity 71.4%; Pred. No. 81;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AQYEDYA 7
Db      62 SQWEDYA 68

RESULT 14
US-11-105-233-180
; Sequence 180, Application US/11105233
; Publication No. US20060134653A1
; GENERAL INFORMATION:
; APPLICANT: Thiagalingam et al
; TITLE OF INVENTION: Differential Expression of Genes in MSI
; FILE REFERENCE: 1657/2001
; CURRENT FILING DATE: 2005-04-13
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 180
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-233-180

Query Match      69.8%; Score 30; DB 7; Length 483;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AQYEDYA 7
Db      265 AQYEDIA 271
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RESULT 15
US-10-449-902-41261
; Sequence 41261, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41261
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-41261

Query Match 69.8%; Score 30; DB 6; Length 797;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QYEDY 6
DB 491 QYEDY 495

Search completed: July 5, 2006, 20:53:01
Job time : 4.58252 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 19:09:18 ; Search time 9.70874 Seconds
(without alignments)
79.283 Million cell updates/sec

Title: US-10-774-928a-11

Perfect score: 44

Sequence: 1 YEDEINN 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*

- 1: pirl.*
- 2: pirl2.*
- 3: pirl3.*
- 4: pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	84.1	484	2 E64432	spore coat polysac
2	37	84.1	506	2 S37156	NADPH-ferrihemopro
3	37	84.1	683	2 T10720	NADPH-ferrihemopro
4	37	84.1	692	2 T05582	NADPH-ferrihemopro
5	37	84.1	692	2 S37159	NADPH-ferrihemopro
6	36	81.8	403	2 T28416	ORF MSV255 leucine
7	36	81.8	597	2 D70100	phosphoglucosylase
8	35	79.5	310	2 S43865	cytochrome P450
9	35	79.5	384	2 I61769	keratin 6d, type I
10	35	79.5	390	2 A60093	cytochrome P450
11	35	79.5	419	1 KRXL2B	keratin, 64K type
12	35	79.5	425	1 KRXL2A	keratin, 64K type
13	35	79.5	461	2 A43782	keratin, type II
14	35	79.5	469	2 S05602	keratin K7, type I
15	35	79.5	483	2 A34720	keratin 8, type II
16	35	79.5	487	2 JT0407	keratin 8, type II
17	35	79.5	489	2 B24177	keratin, 55K type
18	35	79.5	490	2 JS0658	cytochrome P450
19	35	79.5	502	2 A23547	keratin, type II c
20	35	79.5	513	2 S08381	keratin, 58K type
21	35	79.5	520	2 JS0291	intermediate filament
22	35	79.5	553	2 I59009	epidermal keratin
23	35	79.5	564	1 KRHUEA	keratin 6a, type I
24	35	79.5	564	1 KRHUEB	keratin 6b, type I
25	35	79.5	564	2 I61770	keratin 6c, type I
26	35	79.5	564	2 I61768	keratin 6c, type I
27	35	79.5	564	2 I61771	keratin 6f, type I
28	35	79.5	581	1 KRMS2	keratin, type II c
29	35	79.5	590	2 A29904	keratin 5, type II

30	35	79.5	629	2 A29666	keratin, 65K type
31	35	79.5	629	2 S42629	keratin K3 - rabbi
32	35	79.5	638	2 I53169	cytochrome P450
33	35	79.5	643	1 KRHU2	keratin 1, type II
34	35	79.5	645	2 A44861	keratin, 67K type
35	35	79.5	1029	2 F86359	hypothetical prote
36	35	79.5	1161	2 T18400	glutamate-cysteine
37	34	77.3	223	2 T00150	hypothetical prote
38	34	77.3	453	2 S31313	hypothetical prote
39	34	77.3	1254	2 S46636	hypothetical prote
40	34	77.3	2183	2 T37218	hypothetical prote
41	33	75.0	146	2 D86419	hypothetical prote
42	33	75.0	236	2 H71056	probable arylaloni
43	33	75.0	240	2 B83970	hypothetical prote
44	33	75.0	410	2 S77585	pilus assembly pro
45	33	75.0	410	2 H81210	pilus assembly pro

ALIGNMENTS

RESULT 1

E64432

spore coat polysaccharide biosynthesis protein G homolog - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: E64432

R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, C.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, H.O.; Woese, C. Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii. A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: E64432
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-484 <BUL>
A:Cross-references: UNIPROT:Q58462; UNIPARC:UPI0000139F8D; GB:U67549; GB:L77117; NID:9282; C:Genetics:
A:Map position: REV1004535-1003081

Query Match 84.1%; Score 37; DB 2; Length 484;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINN 7
|||:|
Db 211 YEDELNN 217

RESULT 2

S37156

NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - Jerusalem artichoke (fragment)
C:Species: Helianthus tuberosus (Jerusalem artichoke)
C:Date: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S37156
R:Hasenfratz, M.; Jeltsch, J.; Benveniste, I.; Lesot, A.; Durst, F. submitted to the EMBL Data Library, September 1993
A:Description: Multiple forms of NADPH-cytochrome P450 reductase in higher plants.
A:Reference number: S37156
A:Accession: S37156
A:Molecule type: mRNA
A:Residues: 1-506 <HAS>
A:Cross-references: UNIPROT:Q96560; UNIPARC:UPI000009D6B1; EMBL:Z26251; NID:g1359893; PII
C:Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein
C:Keywords: flavoprotein; NADP; oxidoreductase
F;1-506/Domain: NADPH-ferrihemoprotein reductase homology (fragment) <FEH>
F;1-52/Domain: Flavodoxin homology (fragment) <FLX>

Query Match 84.1%; Score 37; DB 2; Length 506;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINN 7
| | | | |
Db 405 YEDELNN 411

RESULT 3

T10720
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - opium poppy
N:Alternate names: ferrihemoprotein P-450 reductase; NADP-cytochrome reductase
C:Species: Papaver somniferum (opium poppy)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10720
R:Rosco, A.; Pauli, H.H.; Priesner, W.; Kutchan, T.M.
Arch. Biochem. Biophys. 348, 369-377, 1997
A:Title: Cloning and heterologous expression of NADPH-cytochrome P450 reductases from the
A:Reference number: 217096; MUID:98096363; PMID:9434750
A:Accession: T10720
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-683 <ROS>
A:Cross-references: UNIPROT:O24424; UNIPARC:UPI000009D902; EMBL:U67185; NID:g2580496; PDB:1W01
C:Function:
A:Description: catalyzes the reduction of the heme-thiolate-dependent monooxygenases; all
C:Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein
C:Keywords: flavoprotein; NADP; oxidoreductase
F:80-682/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F:82-230/Domain: flavodoxin homology <FLX>

Query Match 84.1%; Score 37; DB 2; Length 683;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINN 7
| | | | |
Db 582 YEDELNN 588

RESULT 4

T05582
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) ATR1 - Arabidopsis thaliana
N:Alternate names: protein F22K18.280
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C:Accession: T05582; S21530
R:Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hohenseil, J.; Mewes, H.W.; Mayer, K.F.
submitted to the Protein Sequence Database, February 1999
A:Reference number: T15419
A:Accession: T05582
A:Molecule type: DNA
A:Residues: 1-692 <BEV>
A:Cross-references: UNIPROT:Q9SB48; UNIPARC:UPI00000A72AC; EMBL:AL035356
A:Experimental source: cultivar Columbia; BAC clone F22K18
R:Mignote-Vieux, C.; Kazmaier, M.; Lacroute, F.; Pompon, D.M.
submitted to the EMBL Data Library, May 1992
A:Reference number: S21530
A:Accession: S21530

Query Match 84.1%; Score 37; DB 2; Length 692;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

A:Gene: ATR1

A:Map position: 4
A:Introns: 101/3; 121/3; 147/2; 166/3; 194/3; 207/1; 230/2; 294/2; 325/2; 400/3; 428/3;
A:Note: F22K18.280
C:Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein
C:Keywords: flavoprotein; NADP; oxidoreductase
F:85-691/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F:87-235/Domain: flavodoxin homology <FLX>

QY 1 YEDEINN 7
| | | | |
Db 591 YEDELNN 597

RESULT 5

S37159
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - spring vetch
C:Species: Vicia sativa (spring vetch, tare)
C:Date: 20-May-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: S37159
R:Benveniste, I.; Begue-Kirn, C.; Lesot, A.; Hasenfratz, M.; Durst, F.
submitted to the EMBL Data Library, September 1993
A:Description: Isolation and characterization of a cDNA encoding an NADPH-cytochrome P450
A:Reference number: S37159
A:Accession: S37159
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-692 <BEN>
A:Cross-references: UNIPROT:Q43235; UNIPARC:UPI00000A4241; EMBL:Z26252; NID:g400531; PDB:1W01
C:Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein
C:Keywords: flavoprotein; NADP; oxidoreductase
F:83-691/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F:85-234/Domain: flavodoxin homology <FLX>

Query Match 84.1%; Score 37; DB 2; Length 692;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINN 7
| | | | |
Db 591 YEDELNN 597

RESULT 6

T28416
ORF MSV255 leucine rich repeat gene family protein - Melanoplus sanguinipes entomopoxvirus
C:Species: Melanoplus sanguinipes entomopoxvirus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T28416
R:Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.

A:Reference number: 220484; MUID:99102612; PMID:9847359

A:Accession: T28416

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-403 <AFO>

A:Cross-references: UNIPROT:Q9YVI7; UNIPARC:UPI00000F4752; EMBL:AF063866; NID:g4049647; PDB:1W01

C:Genetics:

A:Note: MSV255

Query Match 81.8%; Score 36; DB 2; Length 403;
Best Local Similarity 87.5%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEDEINN 8
| | | | |
Db 10 YEDIINN 17

RESULT 7

D70100
phosphoglucosyltransferase (femD) homolog - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: D70100
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, son, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.

A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: D70100
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-597 <LE>
A;Cross-references: UNIPROT:O51037; UNIPARC:UPI00000572F1; GB:AE001115; GB:AE000783; NID:
A;Experimental source: strain B31

Query Match 81.8%; Score 36; DB 2; Length 597;
Best Local Similarity 75.0%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINNK 8

DB 216 YENDINNK 223

RESULT 8

S43865
cytokeratin 8, type II - potoro (fragment)
C;Species: Potorous tridactylus (potoro), long-nosed rat kangaroo
C;Date: 20-Feb-1995 #sequence_revision 06-Dec-1996 #text_change 09-Jul-2004
C;Accession: S43865; S40172
R;Boettger, V.; Lane, E.B.
J. Mol. Biol. 235, 61-67, 1994
A;Title: A monoclonal antibody epitope on keratin 8 identified using a phage peptide lib
A;Reference number: S43865; MUID:94118290; PMID:7507169
A;Accession: S43865
A;Molecule type: mRNA
A;Residues: 1-310 <BOE>
A;Cross-references: UNIPROT:Q28810; UNIPARC:UPI0000086BF0; EMBL:X70987; NID:g437902; PID:
A;Experimental source: kidney epithelium cells
C;Superfamily: cytoskeletal keratin
C;Keywords: coiled coil

Query Match 79.5%; Score 35; DB 2; Length 310;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEDEINNK 8

DB 180 YEDEINNK 187

RESULT 9

I61769
keratin 6d, type II - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: I61769
R;Takahashi, K.; Paladini, R.D.; Coulombe, P.A.
J. Biol. Chem. 270, 18581-18592, 1995
A;Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
A;Reference number: A57398; MUID:95355491; PMID:7543104
A;Accession: I61769
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-384 <RES>
A;Cross-references: UNIPROT:P48667; UNIPARC:UPI000012DB17; GB:L42602; NID:g914823; GB:L4
28; GB:L42608; NID:g914829; GB:L42609; NID:g914830; GB:L42610; NID:g1488252; PIDN:AAB606
C;Genetics:
A;Gene: KRT6D
A;Introns: 72/2; 92/3; 124/3; 179/3; 221/3; 295/2; 307/1
C;Superfamily: cytoskeletal keratin
C;Keywords: coiled coil

Query Match 79.5%; Score 35; DB 2; Length 384;
Best Local Similarity 75.0%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEDEINNK 8

||||| :

Db 73 YEDEINNK 80

RESULT 10

A60093
cyokeratin, type II, early ectodermal - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993
C;Accession: A60093
R;Charlebois, T.S.; Spencer, D.H.; Tarkington, S.K.; Henry, J.J.; Grainger, R.M.
Development 108, 33-45, 1990
A;Title: Isolation of a chick cyokeratin cDNA clone indicative of regional specialization
A;Reference number: A60093; MUID:90276238; PMID:1693557
A;Accession: A60093
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-390 <CHA>
A;Cross-references: UNIPARC:UPI00001774C6
C;Superfamily: cytoskeletal keratin
C;Keywords: intermediate filament

Query Match 79.5%; Score 35; DB 2; Length 390;
Best Local Similarity 75.0%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEDEINNK 8

DB 100 YEDEINNK 107

RESULT 11

KRXL2B
keratin, 64K type II cytoskeletal (clone pUF164) - African clawed frog (fragment)
N;Alternate names: 64-kDa type II keratin
C;Species: Xenopus laevis (African clawed frog)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: A02952
R;Hoffmann, W.; Franz, J.K.; Franke, W.W.
J. Mol. Biol. 184, 713-724, 1985
A;Title: Amino acid sequence microheterogeneities of basic (type II) cyokeratins of Xen
A;Reference number: A92914; MUID:86011576; PMID:2413219
A;Accession: A02952
A;Molecule type: mRNA
A;Residues: 1-419 <HOF>
A;Cross-references: UNIPROT:P04265; UNIPARC:UPI000012DB07; GB:X02895; GB:M13954; NID:g64f
A;Experimental source: clone pUF164
C;Superfamily: cytoskeletal keratin
C;Keywords: coiled coil; intermediate filament
F;1-275/Domain: rod (fragment) <ROD>
F;1-9/Region: linker 1
F;10-110/Region: coil 1B
F;11-127/Region: linker 12
F;128-146/Region: coil 2A
F;147-154/Region: linker 2
F;155-275/Region: coil 2B
F;213/Region: stutter
F;276-419/Domain: tail <END>
F;276-399/Region: H2 and V2 subdomains
F;400-419/Region: E2 subdomain

Query Match 79.5%; Score 35; DB 1; Length 419;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEDEINNK 8

DB 52 YEDEINNK 59

RESULT 12

KRXL2A
keratin, 64K type II cytoskeletal (clone pUF23) - African clawed frog (fragment)
N;Alternate names: 64-kDa type II keratin

C:Species: Xenopus laevis (African clawed frog)
 C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
 C:Accession: A02953
 R:Hoefmann, W.; Franz, J.K.; Franke, W.W.
 J. Mol. Biol. 184, 713-724, 1985
 A:Title: Amino acid sequence microheterogeneities of basic (type II) cytokeratins of Xenopus laevis
 A:Reference number: A92914; MUID:86011576; PMID:2413219
 A:Accession: A02953
 A:Molecule type: mRNA
 A:Residues: 1-425 <HOF>
 A:Cross-references: UNIPROT:P04266; UNIPARC:UPI000012DB06; GB:X02894; GB:M13956; NID:G64288
 A:Experimental source: clone pUP23
 C:Comment: The cytokeratin IF proteins appear to be obligate heteropolymers, composed of types of proteins is low and restricted to specific isolated regions within the rod domain. Three subdomains, each characterized by a distinctive amino acid composition, are found along the intermediate filament proteins, the arrangement of its subdomains probably distant species, suggests functional significance.
 C:Comment: There is only one group of closely related type II amphibian cytokeratins. The rate of differentiation of the amphibian epidermis, which lacks a true stratum corneum.
 C:Superfamily: 'cytoskeletal keratin'
 C:Keywords: coiled coil; intermediate filament
 F:1-296/Domain: rod (fragment) <ROD>
 F:1-16/Region: coil 1A (fragment)
 F:17-30/Region: linker 1
 F:31-131/Region: coil 1B
 F:132-148/Region: linker 12
 F:149-167/Region: coil 2A
 F:168-175/Region: linker 2
 F:176-296/Region: coil 2B
 F:234/Region: stutted
 F:297-425/Domain: tail <END>
 F:297-405/Region: H2 and V2 subdomains
 F:406-425/Region: E2 subdomain

Query Match 79.5%; Score 35; DB 1; Length 425;
 Best Local Similarity 75.0%; Pred. No. 40;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEDEINNK 8
 ||||| :
 Db 73 YEDEINKR 80

RESULT 13
 A43782
 keratin, type II - eastern newt (fragment)
 C:Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
 C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
 C:Accession: A43782
 R:Ferretti, P.; Brookes, J.P.; Brown, R.
 Development 111, 497-507, 1991
 A:Title: A new type II keratin restricted to normal and regenerating limbs and tails in the eastern newt
 A:Reference number: A43782; MUID:91372147; PMID:1716554
 A:Accession: A43782
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-461 <FER>
 A:Cross-references: UNIPROT:Q42435; UNIPARC:UPI00001774C4; GB:X57671
 C:Superfamily: cytoskeletal keratin

Query Match 79.5%; Score 35; DB 2; Length 461;
 Best Local Similarity 75.0%; Pred. No. 43;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEDEINNK 8
 ||||| :
 Db 134 YEDEINKR 141

RESULT 14
 S05602
 keratin K7, type II, epithelial, 55K - human
 C:Species: Homo sapiens (man)

C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 29-Aug-1997
 C:Accession: S05602; A31141
 R:Glass, C.; Fuchs, E.
 J. Cell Biol. 107, 1337-1350, 1988
 A:Title: Isolation, sequence, and differential expression of a human K7 gene in simple epithelial cells
 A:Reference number: S05602; MUID:89008577; PMID:2459129
 A:Accession: S05602
 A:Molecule type: DNA
 A:Residues: 1-469 <GLA>
 A:Cross-references: UNIPARC:UPI00001774C1; EMBL:X13320
 A:Note: the authors translated the codon ACC for residue 97 as Ala
 C:Genetics:
 A:Gene: GDB:KRT7
 A:Cross-references: GDB:128114; OMIM:148059
 A:Map position: 12q12-12q21
 A:Introns: 108/3; 179/2; 199/3; 231/3; 286/3; 328/3; 402/2; 414/1
 C:Superfamily: cytoskeletal keratin
 C:Keywords: coiled coil

Query Match 79.5%; Score 35; DB 2; Length 469;
 Best Local Similarity 75.0%; Pred. No. 44;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEDEINNK 8
 ||||| :
 Db 180 YEDEINRR 187

RESULT 15
 A34720
 keratin 8, type II cytoskeletal - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
 C:Accession: A34720; S06888; S12479; I37982; I37983; JS0487; A31942
 R:Yamamoto, R.; Kao, L.C.; McKnight, C.E.; Strauss III, J.F.
 Mol. Endocrinol. 4, 370-374, 1990
 A:Title: Cloning and sequence of cDNA for human placental cytokeratin 8. Regulation of transcription
 A:Reference number: A34720; MUID:90259929; PMID:1692965
 A:Accession: A34720
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-483 <YAM>
 A:Cross-references: UNIPROT:P05787; UNIPARC:UPI00001774C3; GB:M34225
 R:Leube, R.E.; Bosch, F.X.; Romano, V.; Zimbelmann, R.; Hoesfler, H.; Franke, W.W.
 Differentiation 33, 69-85, 1986
 A:Title: Cytokeratin expression in simple epithelia
 A:Reference number: S06888; MUID:87134779; PMID:2434381
 A:Accession: S06888
 A:Molecule type: mRNA
 A:Residues: 205-483 <LEU>
 A:Cross-references: UNIPARC:UPI000016ABAL; EMBL:X12882
 R:Franke, W.W.
 submitted to the EMBL Data Library, September 1988
 A:Reference number: S12479
 A:Accession: S12479
 A:Molecule type: mRNA
 A:Residues: 205-309, 'I', 311-483 <FRA>
 A:Cross-references: UNIPARC:UPI000016A769; EMBL:X12882; NID:G30312; PIDN:CAA31376.1; PID:1705144
 R:Waseem, A.; Alexander, C.M.; Steel, J.B.; Lane, E.B.
 New Biol. 2, 464-478, 1990
 A:Title: Embryonic simple epithelial keratins 8 and 18: chromosomal location emphasizes a common evolutionary origin
 A:Reference number: I37982; MUID:91145351; PMID:1705144
 A:Accession: I37982
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-76, 'V', 78-416, 'S', 418-428, 'G', 430-431, 'S', 433-483 <RES>
 A:Cross-references: UNIPARC:UPI0000161B3E; EMBL:X74329; NID:G400415; PIDN:CAAS2882.1; PID:1705144
 A:Accession: I37983
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 151-201, 'VD', 202-271 <RE2>
 A:Cross-references: UNIPARC:UPI000016ABCF; EMBL:X74981; NID:G400417; PIDN:CAAS2916.1; PID:1705144
 R:Krause, S.; Franke, W.W.

Gene 86, 241-249, 1990
A;Title: Organization and sequence of the human gene encoding cytokeratin 8.
A;Reference number: JS0487; MUID:90215304; PMID:1691124
A;Accession: JS0487
A;Molecule type: DNA
A;Residues: 1-76, 'V', 78-428, 'G', 'SQA', 434-483 <KRA>
A;Cross-references: UNIPARC:UPI000016A82B; GB:M34482; NID:g181572; PIDN:AAA5763.1; PID:
R;Kulesh, D.A.; Cecena, G.; Darmon, Y.M.; Vasseur, M.; Oshima, R.G.
Mol. Cell. Biol. 9, 1553-1565, 1989
A;Title: Posttranslational regulation of keratins: degradation of mouse and human keratin
A;Reference number: A31942; MUID:89261783; PMID:2471065
A;Accession: A31942
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-76, 'V', 78-231 <KUL>
A;Cross-references: UNIPARC:UPI000016A354; GB:M26512; NID:g177796; PIDN:AAA51542.1; PID:
C;Comment: This protein is one of the type II cytokeratins.
C;Genetics:
A;Gene: GDB:KRT8
A;Cross-references: GDB:118830; OMIM:148060
A;Map position: 12p13.2-12q24.1
A;Introns: 108/3; 178/2; 198/3; 230/3; 327/3; 401/2; 421/1
A;Superfamily: cytoskeletal keratin
C;Keywords: coiled coil; intermediate filament

Query Match 79.5%; Score 35; DB 2; Length 483;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEDEINNK 8

DB 179 YEDEINKR 186

Search completed: July 5, 2006, 19:20:25
Job time : 10.7087 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 18:28:56 ; Search time 81.8641 Seconds
(without alignments)
90.395 Million cell updates/sec

Title: US-10-774-928A-11
Perfect score: 44
Sequence: 1 YEDEINNK 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	93.2	777	Q54EF1_DICDI	Q54ef1 dictyosteli
2	40	90.9	437	Q4XNH7_PLACH	Q4xnh7 plasmodium
3	39	88.6	223	Q8X158_CLOPE	Q8x158 clostridium
4	38	86.4	171	Q4YIN2_PLABE	Q4yin2 plasmodium
5	38	86.4	541	Q4YN40_PLABE	Q4yn40 plasmodium
6	38	86.4	548	Q4LOR7_MAIZE	Q4lor7 zea mays (m
7	38	86.4	548	Q5G360_MAIZE	Q5g360 zea mays (m
8	37	84.1	121	Q33PE6_9GAMM	Q33pe6 shewanella
9	37	84.1	321	Q5UR43_MIMIV	Q5ur43 mimivirus
10	37	84.1	484	Y1062_METUA	Q58462 methanococ
11	37	84.1	506	Q96560_HELTU	Q96560 helianthus
12	37	84.1	549	Q54H37_DICDI	Q54h37 dictyosteli
13	37	84.1	559	Q8XIV8_CLOPE	Q8xiv8 clostridium
14	37	84.1	683	Q24424_PAPSO	Q24424 papaver som
15	37	84.1	692	Q29035_ARATH	Q29035 arabidopsis
16	37	84.1	692	Q43235_VICSA	Q43235 vicia sativ
17	37	84.1	692	Q9AU08_9ROSI	Q9au08 populus tri
18	37	84.1	692	Q8XB48_ARATH	Q8xb48 arabidopsis
19	37	84.1	703	Q8VX49_WHEAT	Q8vx49 triticum ae
20	37	84.1	712	Q9AU06_9ROSI	Q9au06 populus tri
21	37	84.1	712	Q9AU07_9ROSI	Q9au07 populus tri
22	37	84.1	714	Q653S9_ORYSA	Q653s9 oryza sativ
23	37	84.1	1191	Q81110_PLAF7	Q81110 plasmodium
24	36	81.8	372	Q9QAM2_WSSV	Q9qam2 white-spot
25	36	81.8	403	Q9YV17_MSEPV	Q9yv17 melanoplus
26	36	81.8	471	Q5HU43_CAMWR	Q5hu43 campylobact
27	36	81.8	570	Q6A1F5_DESPFS	Q6a1f5 desulfotale
28	36	81.8	595	Q663A8_BORGA	Q663a8 borrelia ga
29	36	81.8	597	Q51037_BORBU	Q51037 borrelia bu
30	36	81.8	627	Q6EBA6_CAMTE	Q6eba6 campylobact
31	36	81.8	725	Q934J5_VIBPA	Q934j5 vibrio para

32	36	81.8	725	2	Q87HI4_VIBPA	Q87hi4 vibrio para
33	36	81.8	882	2	Q4HDG9_CAMCO	Q4hdg9 campylobact
34	36	81.8	1410	2	Q7YYV2_CRYPV	Q7yyv2 cryptospori
35	36	81.8	3429	2	Q8IBP1_PLAF7	Q8ibp1 plasmodium
36	35	79.5	136	2	Q425W3_PLABE	Q425w3 plasmodium
37	35	79.5	156	2	Q3KZ86_SCHJA	Q3kz86 schistosoma
38	35	79.5	173	2	Q35T43_GEOMG	Q35t43 geobacter m
39	35	79.5	176	2	Q4JI23 ICTPU	Q4ji23 ictalurus p
40	35	79.5	194	2	Q4G296_TRIVA	Q4g296 trichomonas
41	35	79.5	214	2	Q7RGN1_PLAYO	Q7rgn1 plasmodium
42	35	79.5	222	2	Q4LOE7_MOUSE	Q4loe7 mus musculu
43	35	79.5	224	2	Q678L1_MOUSE	Q678l1 mus musculu
44	35	79.5	233	2	Q5DDV3_SCHJA	Q5ddv3 schistosoma
45	35	79.5	233	2	Q2WVY4_CLOPE	Q2wvy4 clostridium

ALIGNMENTS

RESULT 1
Q54EF1_DICDI PRELIMINARY; PRT; 777 AA.
ID Q54EF1_DICDI AC Q54EF1;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein.
GN ORFNames=DD0183975;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44889;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=AX4;
RX PubMed=15875012; DOI=10.1038/nature03481;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A., Xu Q.,
RA Sugang R., Berriman M., Song J., Olsen R., Konfortov B.A., Rivero F.,
RA Tungal B., Kummerfeld S., Madera M., Konfortov B.A., Davies R., Fey P.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Buson N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churche C.M.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D.M., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,
RA Buchrieser C., Wardrop A., Felder M., Thangavelu M., Johnson D.,
RA Knights A., Louised H., Mungall K.L., Oliver K., Price C.,
RA Quail M.A., Urushihara H., Hernandez J., Rabinowitsch E., Steffen D.,
RA Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,
RA Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,
RA Tanaka Y., Shaulsky G., Schleicher M., Weinstock G.M., Rosenthal A.,
RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzer M.,
RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
RA Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 435:43-57(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

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CC -----
CC EMBL; AAFI01000257; EAL61761.1; -; Genomic_DNA.
CC InterPro; IPR006089; Acyl CoA DH.
CC InterPro; IPR004813; Tetrapept_transpt.
CC Pfam; PF03169; OPT; 1.
CC TIGRfams; TIGR00728; OPT_sfam; 1.
CC PROSITE; PS00073; ACYL_COA_DH_2; UNKNOWN_1.
CC Hypothetical protein.
SQ SEQUENCE 777 AA; 85050 MW; 96BE7A19BE697E24 CRC64;
Query Match 93.2%; Score 41; DB 2; Length 777;

Best Local Similarity 87.5%; Pred. No. 68;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINNK 8
Db 201 YDDEINNK 208

RESULT 2

Q4XNH7_PLACH PRELIMINARY; PRT; 437 AA.
AC Q4XNH7;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein (Fragment).
GN ORFNames=PC00683.04.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
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DR EMBL; CAJ01004418; CAH81535.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 1
FT NON TER 437 437
SQ SEQUENCE 437 AA; 51115 MW; 45720BA01496B79A CRC64;

Query Match 90.9%; Score 40; DB 2; Length 437;
Best Local Similarity 87.5%; Pred. No. 59;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINNK 8
Db 179 YXDEINNK 186

RESULT 3

Q8X158_CLOPE PRELIMINARY; PRT; 223 AA.
AC Q8X158;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Hypothetical protein CPE2263.
GN OrderedLocustNames=CPE2263;
OS Clostridium perfringens
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,

RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
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DR EMBL; BA000016; BAB81969.1; -; Genomic_DNA.
DR Biocyc; CPER1502:CPE2263-MONOMER; -;
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Hypothetical protein;
KW Peptidoglycan-anchor.
SQ SEQUENCE 223 AA; 25063 MW; F259D8A358DD968E CRC64;

Query Match 88.6%; Score 39; DB 2; Length 223;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINN 7
Db 177 YEDEINN 183

RESULT 4

Q4YIN2_PLABE PRELIMINARY; PRT; 171 AA.
AC Q4YIN2;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Hypothetical protein (Fragment).
GN ORFNames=PB300572.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
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DR EMBL; CAJ01004738; CAI02133.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR PROSITE; PS50850; MFS; 1.
KW Hypothetical protein.
FT NON TER 171 171
SQ SEQUENCE 171 AA; 18905 MW; 4F77BBA698BE5146 CRC64;

Query Match 86.4%; Score 38; DB 2; Length 171;
Best Local Similarity 85.7%; Pred. No. 54;


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Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEDEINN 7
Db 33 YEDEVNN 39
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RESULT 5
Q4YN40_PLABE PRELIMINARY; PRT; 541 AA.
AC Q4YN40;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 21-FEB-2006, entry version 8.
DE Hypothetical protein.
GN ORFNAMES=PB001031.03.0;
OS Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
CC similarity).
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CC
CC EMBL; CAAI01003411; CAI00570.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR Pfam; PF07690; MFS 1; 1.
DR PROSITE; PS50850; MFS, 1.
KW Hypothetical protein; Membrane; Transmembrane; Transport.
SQ SEQUENCE 541 AA; 59919 MW; 865C51731BCFDE8 CRC64;
Query Match 86.4%; Score 38; DB 2; Length 541;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEDEINN 7
Db 33 YEDEVNN 39
|||||
RESULT 6
Q4LOR7_MAIZE PRELIMINARY; PRT; 548 AA.
AC Q4LOR7;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Putative sesquiterpene cyclase.
GN Name=Umi2;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Zea mays (Maize).
Query Match 86.4%; Score 38; DB 2; Length 541;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEDEINN 7
Db 33 YEDEVNN 39
|||||
RESULT 7
Q5GJ60_MAIZE PRELIMINARY; PRT; 548 AA.
AC Q5GJ60;
DT 01-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Terpene synthase 6.
GN Name=TPS6;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RA Koellner T.G., Schnee C., Gershenzon J., Degenhardt J.;
RT "Evolution and functional diversity of the terpene synthase family in
RT maize.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL; AY518315; AAS88576.1; -; mRNA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001906; Terp_synth-like.
DR InterPro; IPR005630; Tps_metal_bd.
DR Pfam; PF01397; Terpene_synth; 1.
DR Pfam; PF03936; Terpene_synth C; 1.
SQ SEQUENCE 548 AA; 63731 MW; BC55B95C9F131275 CRC64;
Query Match 86.4%; Score 38; DB 2; Length 548;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YEDEINN 8
Db 88 YEDEINEK 95
|||||
RESULT 8
Q33PE6_9GAMM PRELIMINARY; PRT; 121 AA.
ID Q33PE6_9GAMM
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AC Q33PE6;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Dihydroneopterin aldolase.
GN ORFNames=ShewDRAFT_3672;
GS Shewanella sp. PV-4
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=323850;
RN NUCLEOTIDE SEQUENCE.
  [1]
RP STRAIN=PV-4;
RC US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pittluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Shewanella sp. PV-4.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
  [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PV-4;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Shewanella sp. PV-4.";
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAL501000063; EAP00981.1; -; Genomic DNA.
DR GO; GO:0004150; F:dihydroneopterin aldolase activity; IEA.
DR GO; GO:0006760; P:folic acid and derivative metabolism; IEA.
SQ SEQUENCE 121 AA; 13946 MW; 6F808F043D66EBA1 CRC64;

  Query Match      84.1%; Score 37; DB 2; Length 121;
  Best Local Similarity 100.0%; Pred. No. 59;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EDEINNK 8
Db 23 EDEINNK 29

RESULT 9
Q5UR43_MIMIV
ID Q5UR43 MIMIV PRELIMINARY; PRT; 321 AA.
AC Q5UR43;
DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 07-DEC-2004, sequence version 1.
DE Hypothetical protein.
GN ORFNames=MIMI_RS62;
OS Mimivirus.
OC Viruses; dsDNA viruses, no RNA stage; Mimivirus.
OX NCBI_TaxID=212035;
RN NUCLEOTIDE SEQUENCE.
  [1]
RP STRAIN=Rowbotham-Bradford;
RX MEDLINE=22550848; PubMed=12663918; DOI=10.1126/science.1081867;
RA La Scola B., Audic S., Robert C., Jungang L., de Lamballerie X.,
RA Drancourt M., Bittles R., Claverie J.M., Raoult D.;
RT "A giant virus in amoebae.";
RL Science 299:2033-2033 (2003).
  [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Rowbotham-Bradford;
RX PubMed=15486256; DOI=10.1126/science.1101485;
RA Raoult D., Audic S., Robert C., Abergel C., Renesto P., Ogata H.,
RA La Scola B., Susan M., Claverie J.-M.;
RT "The 1.2-megabase genome sequence of Mimivirus.";
  [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Rowbotham-Bradford;
RX PubMed=15486256; DOI=10.1126/science.1101485;
RA Raoult D., Audic S., Robert C., Abergel C., Renesto P., Ogata H.,
RA La Scola B., Susan M., Claverie J.-M.;
RT "The 1.2-megabase genome sequence of Mimivirus.";
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RL Science 306:1344-1350 (2004).
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CC -----
DR EMBL; AY653733; AAV50826.1; -; Genomic DNA.
GN Hypothetical protein.
SQ SEQUENCE 321 AA; 37561 MW; F5D2CE4E266EBA4B CRC64;

  Query Match      84.1%; Score 37; DB 2; Length 321;
  Best Local Similarity 87.5%; Pred. No. 1.6e+02;
  Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YEDEINNK 8
Db 50 YEDEPNKK 57

RESULT 10
Y1062_METJA
ID Y1062 METJA STANDARD; PRT; 484 AA.
AC Q58462;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-MAR-2006, entry version 29.
DE Hypothetical protein MJ1062.
GN OrderedLocusNames=MJ1062;
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
  [1]
RP STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii";
RL Science 273:1058-1073 (1996).

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CC -----
DR EMBL; L77117; AAB99065.1; -; Genomic DNA.
DR PIR; E64432; E64432.
DR GenomeReviews; L77117_GR; MJ1062.
DR TIGR; MJ1062; -.
DR Biocyc; MJAN243232: MJ1062-MONOMER; -.
DR InterPro; IPR000182; GCN5acetyl Trans.
DR Pfam; PF00583; Acetyltransf 1; 1.
DR Complete proteome; Hypothetical protein.
FT CHAIN 1 484 Hypothetical protein MJ1062.
  /FTID=PRO_0000107155.
SQ SEQUENCE 484 AA; 56694 MW; E1764675A97CFEB2 CRC64;

  Query Match      84.1%; Score 37; DB 1; Length 484;
  Best Local Similarity 85.7%; Pred. No. 2.5e+02;
  Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINN 7
Db 211 YEDELNN 217

RESULT 11
Q96560_HELTU
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ID Q96560_HELTU PRELIMINARY; PRT; 506 AA.
AC Q96560;
DT 01-FEB-1997, integrated into UniProtKB/TrEMBL.
DT 01-FEB-1997, sequence version 1.
DE NADPH-ferrihemoprotein reductase (BC 1.6.2.4) (Fragment).
OS Helianthus tuberosus (Jerusalem artichoke).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; campanulids; Asterales; Asteraceae; Asteroideae;
OC Heliantheae; Helianthus.
OX NCBI_TaxID=4233;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=blanc commun; TISSUE=Parenchyma;
RA Hasenfratz M.;
RL Thesis (1992); Cellular and Molecular Enzymology, CNRS - Institut de
RL Biologie Moleculaire des Plantes.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=blanc commun; TISSUE=Parenchyma;
RA Hasenfratz M., Jeltsch J., Benveniste I., Lesot A., Durst F.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=blanc commun; TISSUE=Parenchyma;
RA Benveniste I.;
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; Z26251; CAA81210.1; -; mRNA.
DR PIR; S37156; S37156.
DR HSSP; P00388; 1AM0.
DR GO; GO:0010181; F-FMN binding; IEA.
DR GO; GO:0003958; F-NADPH-hemoprotein reductase activity; IEA.
DR GO; GO:0016491; F-oxidoreductase activity; IEA.
DR GO; GO:0006118; P-electron transport; IEA.
DR InterPro; IPR003097; FAD bd.
DR InterPro; IPR008254; Flavodoxin 1.
DR InterPro; IPR001709; FPN cvt reductase.
DR InterPro; IPR001433; Oxid FAD NAD bd.
DR Pfam; PF00667; FAD-binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD binding_1; 1.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS09002; FLAVODOXIN_LIKE; 1.
KW Oxidoreductase.
FT NON_TER 1
SQ SEQUENCE 506 AA; 56229 MW; 05F34FF248E82B08 CRC64;

Query Match 84.1%; Score 37; DB 2; Length 506;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINN 7
Db 405 YEDELNN 411

RESULT 12
Q54H37_DICDI
ID Q54H37_DICDI PRELIMINARY; PRT; 549 AA.
AC Q54H37;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DE NADPH-ferrihemoprotein reductase (BC 1.6.2.4) (Fragment).
OS Helianthus tuberosus (Jerusalem artichoke).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; campanulids; Asterales; Asteraceae; Asteroideae;
OC Heliantheae; Helianthus.
OX NCBI_TaxID=4233;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=blanc commun; TISSUE=Parenchyma;
RA Hasenfratz M.;
RL Thesis (1992); Cellular and Molecular Enzymology, CNRS - Institut de
RL Biologie Moleculaire des Plantes.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=blanc commun; TISSUE=Parenchyma;
RA Hasenfratz M., Jeltsch J., Benveniste I., Lesot A., Durst F.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=blanc commun; TISSUE=Parenchyma;
RA Benveniste I.;
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; Z26251; CAA81210.1; -; mRNA.
DR PIR; S37156; S37156.
DR HSSP; P00388; 1AM0.
DR GO; GO:0010181; F-FMN binding; IEA.
DR GO; GO:0003958; F-NADPH-hemoprotein reductase activity; IEA.
DR GO; GO:0016491; F-oxidoreductase activity; IEA.
DR GO; GO:0006118; P-electron transport; IEA.
DR InterPro; IPR003097; FAD bd.
DR InterPro; IPR008254; Flavodoxin 1.
DR InterPro; IPR001709; FPN cvt reductase.
DR InterPro; IPR001433; Oxid FAD NAD bd.
DR Pfam; PF00667; FAD-binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD binding_1; 1.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS09002; FLAVODOXIN_LIKE; 1.
KW Oxidoreductase.
FT NON_TER 1
SQ SEQUENCE 506 AA; 56229 MW; 05F34FF248E82B08 CRC64;

Query Match 84.1%; Score 37; DB 2; Length 506;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINN 7
Db 405 YEDELNN 411

RESULT 13
Q8XJV8_CLOPE
ID Q8XJV8_CLOPE PRELIMINARY; PRT; 559 AA.
AC Q8XJV8;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DE NADPH-ferrihemoprotein reductase (BC 1.6.2.4) (Fragment).
OS Helianthus tuberosus (Jerusalem artichoke).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; campanulids; Asterales; Asteraceae; Asteroideae;
OC Heliantheae; Helianthus.
OX NCBI_TaxID=4233;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=blanc commun; TISSUE=Parenchyma;
RA Hasenfratz M.;
RL Thesis (1992); Cellular and Molecular Enzymology, CNRS - Institut de
RL Biologie Moleculaire des Plantes.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=blanc commun; TISSUE=Parenchyma;
RA Hasenfratz M., Jeltsch J., Benveniste I., Lesot A., Durst F.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=blanc commun; TISSUE=Parenchyma;
RA Benveniste I.;
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; Z26251; CAA81210.1; -; mRNA.
DR PIR; S37156; S37156.
DR HSSP; P00388; 1AM0.
DR GO; GO:0010181; F-FMN binding; IEA.
DR GO; GO:0003958; F-NADPH-hemoprotein reductase activity; IEA.
DR GO; GO:0016491; F-oxidoreductase activity; IEA.
DR GO; GO:0006118; P-electron transport; IEA.
DR InterPro; IPR003097; FAD bd.
DR InterPro; IPR008254; Flavodoxin 1.
DR InterPro; IPR001709; FPN cvt reductase.
DR InterPro; IPR001433; Oxid FAD NAD bd.
DR Pfam; PF00667; FAD-binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD binding_1; 1.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS09002; FLAVODOXIN_LIKE; 1.
KW Oxidoreductase.
FT NON_TER 1
SQ SEQUENCE 506 AA; 56229 MW; 05F34FF248E82B08 CRC64;

Query Match 84.1%; Score 37; DB 2; Length 549;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EDEINN 8
Db 531 EDEINN 537

RESULT 13
Q8XJV8_CLOPE
ID Q8XJV8_CLOPE PRELIMINARY; PRT; 559 AA.
AC Q8XJV8;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DE NADPH-ferrihemoprotein reductase (BC 1.6.2.4) (Fragment).
OS Helianthus tuberosus (Jerusalem artichoke).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; campanulids; Asterales; Asteraceae; Asteroideae;
OC Heliantheae; Helianthus.
OX NCBI_TaxID=4233;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
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RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX PubMed=15875012; DOI=10.1038/nature03481;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A., Xu Q.,
RA Sugchang R., Berriman M., Song J., Olsen R., Szafranski K., Rivero P.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivolet P.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,
RA Karhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Ferbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.M.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D.M., Mourier T., Pain A., Lu M., Harper D., Lindsey R.,
RA Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,
RA Buchrieser C., Wardrop A., Felder M., Thangavelu M., Johnson D.,
RA Knights A., Loulseghe H., Mungall K.L., Oliver K., Price C.,
RA Quail M.A., Urushihara H., Hernandez J., Rabinowitsch E., Steffen D.,
RA Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,
RA Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,
RA Tanaka Y., Shaalsky G., Schleicher M., Weinstock G.M., Rosenthal A.,
RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzer M.,
RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
RA Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum."
RL Nature 435:43-57(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; AAF101000219; EAL62574.1; -; Genomic_DNA.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0004930; F-G-protein coupled receptor activity; IEA.
DR InterPro; IPR000832; GPCR secretin.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Hypothetical protein.
SQ SEQUENCE 549 AA; 63275 MW; 30F3E2E37B4E1280 CRC64;

Query Match 84.1%; Score 37; DB 2; Length 549;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EDEINN 8
Db 531 EDEINN 537

RESULT 13
Q8XJV8_CLOPE
ID Q8XJV8_CLOPE PRELIMINARY; PRT; 559 AA.
AC Q8XJV8;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DE NADPH-ferrihemoprotein reductase (BC 1.6.2.4) (Fragment).
OS Helianthus tuberosus (Jerusalem artichoke).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; campanulids; Asterales; Asteraceae; Asteroideae;
OC Heliantheae; Helianthus.
OX NCBI_TaxID=4233;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
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OM protein - protein search, using sw model

Run on: July 5, 2006, 18:28:26 ; Search time 69.5146 Seconds
(without alignments)
52.618 Million cell updates/sec

Title: US-10-774-928A-11
Perfect score: 44
Sequence: 1 YEDEINNK 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 8: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *
10: geneseqp2006s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	44	100.0	8	AAO26391	Psoriasis
2	44	100.0	8	ADV04416	Leishmani
3	37	84.1	683	AAW85682	Poppy cyt
4	37	84.1	692	AAW43581	Plant NAD
5	37	84.1	698	AEA34225	Opium pop
6	37	84.1	703	ADT59926	Plant pol
7	37	84.1	883	AAW85680	Poppy cyt
8	36	81.8	120	ABP42597	Human ova
9	36	81.8	217	AAW87629	Bovine ma
10	36	81.8	368	AAW85031	Shrimp wh
11	36	81.8	370	ADW94912	Plant ful
12	36	81.8	407	ADT57158	Plant pol
13	36	81.8	469	ABM81385	Tumour-as
14	36	81.8	546	AAW52397	Human ker
15	36	81.8	546	AAE20422	Human ker
16	35	79.5	113	ABG74871	Human cyt
17	35	79.5	132	ADR98929	Lung spec
18	35	79.5	139	AAW18011	Plasmodiu
19	35	79.5	180	ADN99441	Novel hum
20	35	79.5	186	AAW16318	Peptide #
21	35	79.5	186	ABB35310	Peptide #
22	35	79.5	186	AAW28813	Peptide #
23	35	79.5	186	ABB30140	Peptide #

24	35	79.5	186	4	ABB20752	Protein #
25	35	79.5	186	4	AAW68514	Human bon
26	35	79.5	186	4	AAW56141	Human bra
27	35	79.5	186	4	ABG50183	Human liv
28	35	79.5	186	4	AAW04056	Peptide #
29	35	79.5	186	4	ABG09410	Novel hum
30	35	79.5	186	5	ABG38095	Human pep
31	35	79.5	233	8	ADR98930	Lung spec
32	35	79.5	236	5	ABP43147	Human ova
33	35	79.5	250	8	ADQ67770	Novel hum
34	35	79.5	252	8	ADR10191	Human pro
35	35	79.5	273	4	ABG26376	Novel hum
36	35	79.5	275	4	ABG15282	Novel hum
37	35	79.5	282	8	ABM80614	Tumour-as
38	35	79.5	342	7	ADE15641	Human str
39	35	79.5	398	6	AAE38086	Human cyt
40	35	79.5	401	8	ABM80365	Tumour-as
41	35	79.5	403	8	ABM81640	Tumour-as
42	35	79.5	420	8	ADP29879	Human sec
43	35	79.5	429	4	ABG19547	Novel hum
44	35	79.5	429	4	ABG19546	Novel hum
45	35	79.5	433	3	AAW58755	Breast an

ALIGNMENTS

RESULT 1	AAO26391	AAO26391 standard; peptide; 8 AA.
XX	XX	
AC	AAO26391;	
XX	XX	
DT	30-JAN-2003 (first entry)	
XX	XX	
DE	XX	Psoriasis treating immunotherapeutic peptide, SEQ ID No 11.
XX	XX	Antipsoriatic; immunostimulant; gene therapy; pharmaceutical composition;
KW	XX	vaccine; immunogenic variant; immunotherapeutic agent; psoriasis;
KW	XX	gene therapy.
XX	XX	Leishmania sp.
OS	XX	
XX	XX	
PN	XX	WO200274239-A2.
XX	XX	
PD	XX	26-SEP-2002.
PF	XX	04-MAR-2002; 2002WO-US006496.
XX	XX	
PR	XX	16-MAR-2001; 2001US-00809003.
XX	XX	(AKIV-) AKIVA LLC.
PA	XX	O'daly JA;
PI	XX	
XX	XX	WPI; 2003-018763/01.
DR	XX	New polypeptide and immunogenic variants comprising amino acid sequences
XX	XX	of particulate antigens, useful for the treatment and clinical remission
PT	XX	of psoriasis.
PT	XX	
PT	XX	Claim 1; Page 43; 56pp; English.
PS	XX	
XX	XX	The invention relates to a polypeptide comprising an isolated amino acid
CC	XX	sequence or immunogenic variants selected from any of 14 fully defined
CC	XX	sequences of 7-16 amino acids, given in the specification. The
CC	XX	immunotherapeutic agents and a pharmaceutical compositions comprising
CC	XX	polynucleotides and vectors of the invention are useful for the treatment
CC	XX	and clinical remission of psoriasis. The isolated nucleic acids are
CC	XX	useful as probes. The sequences of the invention can be used in the
CC	XX	treatment of disorders by gene therapy. This sequence represents one of
CC	XX	the 14 immunotherapeutic peptides of the invention

SQ Sequence 8 AA;
Query Match 100.0%; Score 44; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEDEINNK 8
| | | | | | | |
Db 1 YEDEINNK 8

RESULT 2
ADV04416
ID ADV04416 standard; peptide; 8 AA.
XX
AC ADV04416;
XX
DT 24-FEB-2005 (first entry)
XX
DE Leishmania immunotherapeutic peptide SEQ ID NO:11.
XX
KW T-lymphocyte; immunogenicity; antigen; antipsoriatic; immunostimulant;
KW psoriasis.
XX
OS Leishmania sp.
XX
PN US2004241168-A1.
XX
PD 02-DEC-2004.
XX
PF 09-FEB-2004; 2004US-00774928.
XX
PR 16-MAR-2001; 2001US-00809003.
PR 17-OCT-2003; 2003US-00867892.
XX
PA (ODAL/) ODALY J A.
XX
PI Odaly JA;
XX
DR WPI; 2005-011563/01.
XX
PT Inhibiting selectively T-cell rolling in human, by administering compound
PT interfering with cutaneous lymphocyte antigen-E selectin interaction and
PT leukocyte function associated antigen-1 interaction.
XX
PS Disclosure; SEQ ID NO 11; 21pp; English.
XX
CC The invention relates to a novel method for selectively inhibiting T-cell
CC rolling in a human host, comprising administering a compound that
CC selectively interferes with the cutaneous lymphocyte antigen (CLA)-E
CC selectin interaction and leukocyte function associated antigen (LFA)-
CC 1/intercellular adhesion molecule (ICAM) and very late antigen
CC (VLA)/vascular cell adhesion molecule (VCAM) interactions. The compound
CC includes an immunotherapeutic agent, which comprises a purified protein
CC extract that is isolated by diethylaminoethyl Sephadex chromatography of
CC a Nonidet P-40 insoluble particulate antigen fraction derived from
CC isolated killed cells of anastigotes from one or more species of the
CC Leishmania genus, where the particulate antigen fraction is solubilized
CC with 8M urea and 0.025 M Tris(hydroxymethyl)aminomethane pH 8.3 applied
CC to diethylaminoethyl Sephadex and is eluted with a solution comprising
CC 0.1 M sodium chloride, 8 M urea and 0.025 M
CC Tris(hydroxymethyl)aminomethane pH 8.3, and the purified protein extract
CC includes polypeptides having apparent molecular weights of 73, 80 and 82
CC kDa, after total reduction and alkylation. The species is Leishmaniasis,
CC L. venezuelensis, L. brasiliensis and/or L. chagasi. A compound of the
CC invention has antipsoriatic and immunostimulant activity, and inhibits T-
CC cell rolling by interfering with CLA-E selectin interaction and LFA-
CC 1/ICAM and VLA/VCAM interactions. The method is useful for selectively
CC inhibiting T-cell rolling in a human host, and for treating psoriasis.
CC The present sequence represents a Leishmania peptide used in the
CC invention.
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 44; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEDEINNK 8
| | | | | | | |
Db 1 YEDEINNK 8

RESULT 3
AAW85682
ID AAW85682 standard; protein; 683 AA.
XX
AC AAW85682;
XX
DT 19-JUL-1999 (first entry)
XX
DE Poppy cytochrome P450 reductase.
XX
KW Opium poppy; alkaloid; cytochrome P450 reductase; morphine; codeine;
KW oripavine; thebaine; transformation; crop yield; probe; primer.
XX
OS Papaver somniferum.
XX
PN WO9911765-A1.
XX
PD 11-MAR-1999.
XX
PF 28-AUG-1998; 98WO-AU000705.
XX
PR 29-AUG-1997; 97AU-00008872.
XX
PA (JOHJ) JOHNSON & JOHNSON RES PTY LTD.
XX
PI Kutchan TM, Zenk MH, Atkins DG, Fiest AJ;
XX
DR WPI; 1999-214703/18.
DR N-PSDB; AAX08517.
XX
PT Nucleic acid encoding cytochrome P-450 reductase from poppy.
XX
PS Claim 19; Fig 10a; 58pp; English.
XX
CC Transforming plants with a nucleic acid molecule encoding cytochrome P450
CC reductase alters the yield and/or type of alkaloids produced in opium
CC poppies it specifically increases the yield of medically useful alkaloids
CC such as morphine, codeine, oripavine and thebaine. Sequences
CC complementary to the coding sequence of cytochrome P450 reductase are
CC useful as probes, primers and antisense sequences, or for design of
CC ribozymes. Transformation with DNA encoding the cytochrome P450 reductase
CC allows regulation of the total alkaloid content and of the relative
CC proportions of individual alkaloids. Produced. Increasing the alkaloid
CC content of poppy straw should reduce the cost of alkaloid production.
CC Cytochrome P450 reductase is the rate-limiting enzyme in biosynthesis of
CC alkaloids in poppies. Peptide fragments of the cytochrome P450 reductase
CC are described in AAW85672-W85678
XX
SQ Sequence 683 AA;

Query Match 84.1%; Score 37; DB 2; Length 683;
Best Local Similarity 85.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEDEINN 7
| | | | | | | |
Db 582 YEDELNN 588

RESULT 4
AAR43581
ID AAR43581 standard; protein; 692 AA.
XX

AC AAR43581;
XX
DT 25-MAR-2003 (revised)
DT 11-MAY-1994 (first entry)
XX
DE Plant NADPH cytochrome P450 reductase (ara B).
XX
XX NADPH cytochrome P450 reductase; functional complementation;
KW identification.
XX
OS Arabidopsis thaliana.
XX
PN W09321326-A2.
XX
PD 28-OCT-1993.
XX
XX 13-APR-1993; 93WO-FR000367.
PF 13-APR-1992; 92FR-00004491.
PR (ORSA-) ORSAN.
XX
XX Kazmaier M, Lacroute F, Mignotte-Vieux C, Minet M, Pompon D;
XX WPI; 1993-351736/44.
DR N-PSDB; AAQ51236.
XX
XX New DNA encoding plant NADPH cytochrome P450 reductase - cloned by
PT functional complementation in yeast, also recombinant enzyme useful in
PT P450 mediated bioconversion processes.
XX
PS Claim 13; Fig 9; 79pp; French.
XX
CC A new method for determining whether a DNA sequence encodes an NADPH
CC cytochrome P450 reductase involves transforming yeasts with plasmids of a
CC total cDNA bank of plant(s). The yeasts used in the procedure are
CC incapable of producing their own NADPH cytochrome P450 reductase. They
CC are then exposed to a cytochrome P450 inhibitor at a level which is
CC lethal to the yeast cells but not to cells which, because of the
CC transformation, now contain an active NADPH cytochrome P450 reductase.
CC Surviving clones are then isolated and plasmid DNA extracted. The gene is
CC inserted into the plasmid at a site which places it under the control of
CC an inducible promoter. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 692 AA;
Query Match 84.1%; Score 37; DB 2; Length 692;
Best Local Similarity 85.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEDEINN 7
Db 591 YEDELNN 597
RESULT 5
AEA34225
ID AEA34225 standard; protein; 698 AA.
XX
AC AEA34225;
XX
DT 25-AUG-2005 (first entry)
XX
DE Opium poppy cytochrome P450 reductase protein.
XX
KW Cytochrome P450 reductase; enzyme; enzyme engineering.
XX
OS Papaver somniferum.
XX
PN W02005053382-A1.
XX
PD 16-JUN-2005.
XX

PF 02-DEC-2004; 2004WO-AU001699.
XX
PR 02-DEC-2003; 2003AU-00906672.
XX
PA (JOHU) JOHNSON & JOHNSON RES PTY LTD.
XX
PI Allen R, Larkin P;
XX
DR WPI; 2005-435265/44.
DR N-PSDB; AEA34224.
XX
PT Novel polynucleotide encoding cytochrome P-450 enzyme of alkaloid
PT producing poppy plant and inhibiting accumulation of benzyloisquinoline
PT alkaloid, useful for producing poppy plant with altered alkaloid content.
XX
PS Example 1; SEQ ID NO 2; 67pp; English.
XX
CC The invention relates to a polynucleotide encoding a cytochrome P-450
CC reductase enzyme of an alkaloid producing poppy plant involved in a step
CC in an alkaloid biosynthesis pathway of the plant and which inhibits
CC accumulation of a benzyloisquinoline alkaloid above a normal level of the
CC alkaloid in the plant, or which encodes an active fragment, homolog or
CC its variant having enzymatic activity of the enzyme. The invention also
CC relates to a recombinant vector incorporating the polynucleotide, a
CC purified cytochrome P-450 reductase enzyme encoded by the polynucleotide
CC or its active fragment, homolog, analog, derivative or variant having
CC enzymatic activity of the enzyme, and a method of providing an alkaloid
CC producing poppy plant with an altered alkaloid content involving up-
CC regulating or down-regulating the activity of the reductase enzyme. The
CC polynucleotide is useful for producing an alkaloid producing poppy plant
CC with altered alkaloid content and for providing a transgenic poppy plant
CC having altered alkaloid content. This sequence represents the opium poppy
CC cytochrome P-450 reductase enzyme polypeptide of the invention.
XX
SQ Sequence 698 AA;
Query Match 84.1%; Score 37; DB 9; Length 698;
Best Local Similarity 85.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEDEINN 7
Db 597 YEDELNN 603
RESULT 6
ADT59926
ID ADT59926 standard; protein; 703 AA.
XX
AC ADT59926;
XX
DT 13-JAN-2005 (first entry)
XX
DE Plant polypeptide, SEQ ID 10003.
XX
KW Plant; transgenic; cold tolerance; growth rate; drought tolerance;
KW disease resistance; galactomannan production; plant growth regulator;
KW heat tolerance; herbicide tolerance; lignin production;
KW extreme osmotic condition tolerance; pathogens resistance;
KW pest resistance; yield improvement; seed oil yield; seed protein yield.
XX
OS Viridiplantae.
XX
PN US2004216190-A1.
XX
PD 28-OCT-2004.
XX
PF 18-DEC-2003; 2003US-00739930.
XX
PR 28-APR-2003; 2003US-00424599.
PR 28-APR-2003; 2003US-00425115.
XX
PA (KOVA/) KOVALIC D K.

XX Kovalic DK;
 FI WPI; 2004-757369/74.
 DR
 XX
 XX New recombinant DNA constructs useful in the field of biochemistry and
 PT genetics, and in particular for producing transgenic plants with improved
 PT biological characteristics.
 XX
 XX Claim 2; SEQ ID NO 10003; 14pp; English.
 PS
 XX The invention relates a recombinant DNA construct comprising a
 CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:
 CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
 CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,
 CC Arabidopsis, wheat and rape but the specification does not indicate which
 CC sequences is derived from which organism. Also included is a method of
 CC producing a plant having an improved property, comprising transforming a
 CC plant with a recombinant DNA construct comprising a promoter region
 CC functional in a plant cell operably joined to a polynucleotide encoding a
 CC polypeptide associated with the property, and growing the transformed
 CC plant. The property is selected from improving plant cold tolerance, for
 CC manipulating growth rate in plant cells by modification of the cell cycle
 CC pathway, for improving plant drought tolerance, for providing increased
 CC resistance to plant disease, for galactomannan production, for production
 CC of plant growth regulators, for improving plant heat tolerance, for
 CC improving plant tolerance to herbicides, for increasing the rate of
 CC homologous recombination in plants, for lignin production, for improving
 CC plant tolerance to extreme osmotic conditions, for improving plant
 CC tolerance to pathogens or pests, for yield improvement by modification of
 CC photosynthesis, for modifying seed oil yield and/or content, for
 CC modifying seed protein yield and/or content, for yield improvement by
 CC and for yield improvement by providing improved plant growth and
 CC development under at least one stress condition. The polynucleotide may
 CC also encode a plant transcription factor. The methods and compositions of
 CC the present invention are useful in the field of biochemistry and
 CC genetics, in particular for producing transgenic plants with improved
 CC biological characteristics such as increased yield, improved nitrogen
 CC flow, increasing plant tolerance to cold or heat, improving plant
 CC tolerance to extreme osmotic and drought conditions, and improving plant
 CC tolerance to plant pests or pathogens. They can also be used in physical
 CC arrays of molecules, plant breeding markers, computer-based storage and
 CC analysis systems. The present sequence is one of the 5544 plant protein
 CC sequences of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20040216190.
 XX
 SQ Sequence 703 AA;

Query Match 84.1%; Score 37; DB 8; Length 703;
 Best Local Similarity 85.7%; Pred. No. 3.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINN 7
 |||||
 Db 250 YEDELNN 256

RESULT 7
 AAW85680
 ID AAW85680 standard; protein; 883 AA.

XX
 AC AAW85680;

XX 19-JUL-1999 (first entry)

DE Poppy cytochrome P450 reductase.

KW Opium poppy; alkaloid; cytochrome P450 reductase; morphine; codeine;
 KW oripavine; thebaine; transformation; crop yield; probe; primer.

OS Papaver somniferum.
 XX
 FH Key Location/Qualifiers
 FT Protein 42..746
 FT /label= Cytochrome P450 reductase
 XX
 PN WO9911765-A1.
 XX
 PD 11-MAR-1999.
 XX
 XX 28-AUG-1998; 98WO-AU000705.
 PF
 XX 29-AUG-1997; 97AU-00008872.
 PR
 XX (JOHJ) JOHNSON & JOHNSON RES PTY LTD.
 PA
 XX Kutchan TM, Zenk MH, Atkins DG, Fist AJ;
 FI
 XX WPI; 1999-214703/18.
 DR
 XX N-PSDB; AAX08517.
 DR
 XX Nucleic acid encoding cytochrome P-450 reductase from poppy.
 FI
 XX Claim 19; Fig 9a; 58pp; English.

CC Transforming plants with a nucleic acid molecule encoding cytochrome P450
 CC reductase alters the yield and/or type of alkaloids produced in opium
 CC poppies it specifically increases the yield of medically useful alkaloids
 CC such as morphine, codeine, oripavine and thebaine. Sequences
 CC complementary to the coding sequence of cytochrome P450 reductase are
 CC useful as probes, primers and antisense sequences, or for design of
 CC ribozymes. Transformation with DNA encoding the cytochrome P450 reductase
 CC allows regulation of the total alkaloid content and of the relative
 CC proportions of individual alkaloids produced. Increasing the alkaloid
 CC content of poppy straw should reduce the cost of alkaloid production.
 CC Cytochrome P450 reductase is the rate-limiting enzyme in biosynthesis of
 CC alkaloids in poppies. Peptide fragments of the cytochrome P450 reductase
 CC are described in AAW85672-W85678

XX Sequence 883 AA;

Query Match 84.1%; Score 37; DB 2; Length 883;
 Best Local Similarity 85.7%; Pred. No. 4.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINN 7
 |||||
 Db 623 YEDELNN 629

RESULT 8
 ABP42597
 ID ABP42597 standard; protein; 120 AA.

XX
 AC ABP42597;

XX 22-AUG-2002 (first entry)

XX Human ovarian antigen HOGCG83, SEQ ID NO:3729.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.

OS Homo sapiens.

XX

PN WO200200677-A1.
XX 03-JAN-2002.
XX 07-JUN-2001; 2001WO-US018569.
XX 07-JUN-2000; 2000US-0209467P.
PR (HUMA-) HUMAN GENOME SCI INC.
XX Birse CE, Rosen CA;
XX WPI; 2002-147878/19.
DR N-PSDB; ABQ55674.
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
PT cancer), immune disorders, cardiovascular disorders and neurological
PT diseases.
XX Claim 11; SEQ ID NO 3729; 2922pp; English.
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 120 AA;
Query Match 81.8%; Score 36; DB 5; Length 120;
Best Local Similarity 75.0%; Pred. No. 80;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEDEINNK 8
Db 37 YEDEINHNR 44
RESULT 9
AAB87629
ID AAB87629 standard; protein; 217 AA.
XX AAB87629;
AC AAB87629;
XX 15-MAY-2001 (first entry)
DT Bovine mammary tissue derived protein #20.
DE
XX

KW Bovine; mammary gland; cancer; tumour; angiogenesis.
XX Bos taurus.
XX WO200114553-A1.
PN 01-MAR-2001.
XX 23-AUG-2000; 2000WO-NZ000166.
XX 23-AUG-1999; 99US-0150330P.
PR (GENE-) GENESIS RES & DEV CORP LTD.
PA (NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD.
XX Havukkala IJ, Gleen M, Grigor MR, Molenaar AJ;
PI WPI; 2001-226619/23.
DR New polypeptides and polynucleotides encoding the polypeptides, which are
XX expressed in bovine mammary gland tissue, useful for stimulating mammary
PT gland growth or function, or inducing differentiation of milk producing
PT cells.
XX Claim 11; Page 67-68; 97pp; English.
XX The present invention relates to proteins derived from bovine mammary
CC gland cells. The invention is useful for stimulating bovine mammary
CC cell growth and function, inhibiting the growth of various mammary gland
CC cancer cells, inhibiting angiogenesis and vascularization of tumours, or
CC modulating the growth of blood vessels in a mammal
XX
SQ Sequence 217 AA;
Query Match 81.8%; Score 36; DB 4; Length 217;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEDEINNK 8
Db 2 YEDEINHNR 9
RESULT 10
AAG85031
ID AAG85031 standard; protein; 368 AA.
XX AAG85031;
AC AAG85031;
XX 06-AUG-2003 (revised)
DT 11-SEP-2001 (first entry)
XX Shrimp white spot Bacilliform virus (WSBV) protein 122.
XX Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection;
KW antiviral agent; gene expression; antisense construct;
KW transgenic viral resistant shrimp.
XX White spot syndrome virus.
XX WO200138351-A2.
PN 31-MAY-2001.
XX 08-NOV-2000; 2000WO-US028888.
XX 24-NOV-1999; 99CN-00124717.
PR (PENY-) PE CORP NY.
XX (THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
PA (SINO-) SINOGENOMAX CO LTD.
XX Xu X, Yang F, He J, Pham L, He M, Ye Y, Shen Y, Kodira C;
PI

```

XX WPI; 2001-355877/37.
DR N-ESDB; AAH62811.
XX
XX Primary nucleotide sequence of the shrimp white spot Bacilliform virus
PT (WSBV), useful for producing viral polypeptides that can be used to
PT screen for agents that are useful for treating WSBV infection.
XX
XX Claim 1; Fig 3; 626pp; English.
XX
XX The invention provides the primary nucleotide sequence of the WSBV genome
CC (AAH62689), predicted transcript sequences (AAH62689-AAH62839) and
CC encoded proteins (AAG84910-AAG85051) and oligonucleotide sequences
CC (AAH62840-63160) suitable for use as primers or probes. The nucleic acid
CC molecules and proteins of the invention are useful for diagnosis and
CC monitoring viral infection, in screens for antiviral agents and for
CC monitoring viral gene expression or activity during a treatment regimen.
CC The nucleic acid molecules are also useful as antisense constructs to
CC control viral gene expression in infected cells and tissues and to create
CC transgenic viral resistant shrimp. (Updated on 06-AUG-2003 to correct OS
CC field.)
XX
SQ Sequence 368 AA;
Query Match 81.8%; Score 36; DB 4; Length 368;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINNK 8
Db :|||||
63 FKDEINNK 70

RESULT 11
ADX94912
ID ADX94912 standard; protein; 370 AA.
XX
XX ADX94912;
XX
XX 21-APR-2005 (first entry)
XX
XX Plant full length insert polypeptide seqid 57576.
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content.
XX
XX Unidentified.
XX
XX US2004034888-A1.
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
XX (LIU J.) LIU J.
PA (ZHOU Y.) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TAB/) TABASKA J E.
PA (CAO Y.) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
PI WPI; 2004-180133/17.

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XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX
XX Claim 1; SEQ ID NO 57576; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 370 AA;
Query Match 81.8%; Score 36; DB 8; Length 370;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINNK 8
Db :|||||
159 FEDEVNKR 166

RESULT 12
ADT57158
ID ADT57158 standard; protein; 407 AA.
XX
XX ADT57158;
XX
XX 13-JAN-2005 (first entry)
XX
XX Plant polypeptide, SEQ ID 7235.
XX
XX Plant; transgenic; cold tolerance; growth rate; drought tolerance;
KW disease resistance; galactomannan production; plant growth regulator;
KW heat tolerance; herbicide tolerance; lignin production;
KW extreme osmotic condition tolerance; pathogens resistance;
KW pest resistance; yield improvement; seed oil yield; seed protein yield.
XX
XX Viridiplantae.
XX
XX US2004216190-A1.
XX
XX 28-OCT-2004.
XX
XX 18-DEC-2003; 2003US-00739930.
XX
XX 28-APR-2003; 2003US-00424599.
PR 28-APR-2003; 2003US-00425115.
XX
XX (KOVA/) KOVALIC D K.
PA
XX Kovalic DK;
PI
XX WPI; 2004-757369/74.
XX
XX New recombinant DNA constructs useful in the field of biochemistry and
PT genetics, and in particular for producing transgenic plants with improved

```

PT biological characteristics.

PS Claim 2; SEQ ID NO 7235; 14pp; English.

XX The invention relates a recombinant DNA construct comprising a
XX polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:
CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,
CC Arabidopsis, wheat and rape but the specification does not indicate which
CC sequences is derived from which organism. Also included is a method of
CC producing a plant having an improved property, comprising transforming a
CC plant with a recombinant DNA construct comprising a promoter region
CC functional in a plant cell operably joined to a polynucleotide encoding a
CC polypeptide associated with the property, and growing the transformed
CC plant. The property is selected from improving plant cold tolerance, for
CC manipulating growth rate in plant cells by modification of the cell cycle
CC pathway, for improving plant drought tolerance, for providing increased
CC resistance to plant disease, for galactomanan production, for production
CC of plant growth regulators, for improving plant heat tolerance, for
CC improving plant tolerance to herbicides, for increasing the rate of
CC homologous recombination in plants, for lignin production, for improving
CC plant tolerance to extreme osmotic conditions, for improving plant
CC tolerance to pathogens or pests, for yield improvement by modification of
CC photosynthesis, for modifying seed oil yield and/or content, for
CC modifying seed protein yield and/or content, for yield improvement by
CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake
CC and for yield improvement by providing improved plant growth and
CC development under at least one stress condition. The polynucleotide may
CC also encode a plant transcription factor. The methods and compositions of
CC the present invention are useful in the field of biochemistry and
CC genetics, in particular for producing transgenic plants with improved
CC biological characteristics such as increased yield, improved nitrogen
CC flow, increasing plant tolerance to cold or heat, improving plant
CC tolerance to extreme osmotic and drought conditions, and improving plant
CC tolerance to plant pests or pathogens. They can also be used in physical
CC arrays of molecules, plant breeding markers, computer-based storage and
CC analysis systems. The present sequence is one of the 5544 plant protein
CC sequences of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20040216190.

XX Sequence 407 AA;

SQ Query Match 81.8%; Score 36; DB 8; Length 407;

Best Local Similarity 62.5%; Pred. No. 3.1e+02;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINNK 8

Db :|||:|:|:

196 FEDEVNRR 203

RESULT 13

ABM81385

ID ABM81385 standard; protein; 469 AA.

XX AC ABM81385;

XX 18-NOV-2004 (first entry)

DT Tumour-associated antigenic target (TAT) polypeptide PRO82152, SEQ.3587.

DE Tumour-associated antigenic target; TAT; human; overexpression; cancer;

XX Tumour; diagnosis; cell proliferative disorder; breast cancer;

KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;

KW central nervous system cancer; bladder cancer; pancreatic cancer;

KW cervical cancer; melanoma; leukaemia; hybridisation probe;

KW chromosome identification; chromosome mapping; gene mapping;

KW gene therapy; cytostatic.

XX Homo sapiens.

OS Homo sapiens.

PN WO2004030615-A2.

XX 15-APR-2004.

XX 29-SEP-2003; 2003WO-US028547.

XX 02-OCT-2002; 2002US-0414971P.

XX (GETH) GENENTECH INC.

XX Wu TD, Zhang Z, Zhou Y;

XX WPI; 2004-347921/32.

XX N-PSDB; ACN39445.

XX New tumor-associated antigenic target polypeptides and nucleic acids,
XX useful in preparing a medicament for treating or detecting a
XX proliferative disorder, e.g. breast, lung, colorectal, ovarian or
XX prostate cancer or tumor.

PS Claim 12; SEQ ID NO 3587; 7273pp; English.

XX The invention relates to human tumour-associated antigenic target (TAT)
XX polypeptides, and their related nucleic acids. The TAT polypeptides are
XX overexpressed in cancer tissues compared to normal tissues, and may thus
XX serve as effective targets for the diagnosis and treatment of cancer in
XX mammals. The invention also relates to nucleic acid and polypeptide
XX sequences at least 80% identical to the TAT nucleic acids and
XX polypeptides; expression vectors and host cells comprising a TAT nucleic
XX acid; an antibody specific for a TAT polypeptide; a peptide or organic
XX molecule which binds to a TAT polypeptide; fusion proteins comprising a
XX TAT polypeptide; and methods and compositions for the treatment or
XX diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
XX antibodies, antagonists, binding molecules and compositions are useful
XX for diagnosing or treating a cell proliferative disorder associated with
XX increased TAT expression, particularly cancers such as breast cancer,
XX colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
XX cancer, pancreatic cancer, cervical cancer, cancers of the central
XX nervous system, melanoma and leukaemia. TAT nucleic acids may further be
XX used as hybridisation probes, in chromosome and gene mapping, in
XX chromosome identification and in gene therapy. The present sequence
XX represents a TAT polypeptide of the invention

SQ Sequence 469 AA;

Query Match 81.8%; Score 36; DB 8; Length 469;

Best Local Similarity 75.0%; Pred. No. 3.6e+02;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINNK 8

Db :|||:|:|:

180 YEDEINHR 187

RESULT 14

AAV52397

ID AAV52397 standard; protein; 546 AA.

XX AC AAV52397;

XX 15-FEB-2000 (first entry)

DT Human keratin KERT-1.

XX Keratin; KERT-1; pancreatic tumour; intermediate filament; consensus;

KW keratin type II; basic; cytoskeleton; epithelial cell;

KW differential expression; differentiation; development; proliferation;

KW wound healing; psoriasis; viral infection; cancer; embryogenesis; skin;

KW nail; hair; diagnosis; prevention; treatment; epithelial disorder;

KW developmental disorder; proliferative disorder; reproductive disorder;

KW antagonist; antibody; detection.

XX Homo sapiens.

OS Homo sapiens.

PR 27-APR-1998; 98US-00067351.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Tang YT, Hillman JL, Corley NC, Baughn M;
 XX WPI; 2002-279090/32.
 DR N-PSDB; AAD32706.
 XX
 PT Novel human keratin protein designated KERT1-3, useful e.g. for
 PT diagnosing, treating and preventing vitiligo, eczema, cirrhosis,
 PT hepatitis, cerebral palsy, congenital glaucoma, cataract, prostatitis and
 XX infertility.
 PS Claim 1; Fig 1; 46pp; English.
 XX
 CC The invention relates to a substantially purified human keratin (KERT)
 CC polypeptide designated KERT1-3. KERT protein is useful for screening a
 CC library of molecules and compounds to identify a molecule or compound
 CC which specifically binds to the protein. The method involves contacting
 CC KERT polypeptide with a library of molecules or compounds e.g., a library
 CC of peptides or proteins, agonists, antagonists, antibodies, inhibitors,
 CC immunoglobulins, drug compounds, and pharmaceutical agents, under
 CC conditions that allow specific binding; and detecting specific binding,
 CC thereby identifying a molecule or compound which specifically binds the
 CC protein. KERT protein is useful for diagnosis, treatment and prevention
 CC of epithelial disorders (vitiligo, atopic dermatitis, epidermolysis
 CC bullosa simplex, eczema); cell proliferative disorder (arteriosclerosis,
 CC cirrhosis, hepatitis); developmental disorder (Cerebral palsy, Duchenne
 CC and Becker muscular dystrophy, myelodysplastic syndrome, congenital
 CC glaucoma, cataract) and reproductive disorder (infertility, endometrial
 CC and ovarian tumours, ectopic pregnancies, cancer of the testis, benign
 CC prostatic hyperplasia, prostatitis). KERT is also useful for screening
 CC libraries or libraries of compounds in drug screening techniques. The
 CC present sequence is human KERT-1 protein
 XX
 SQ Sequence 546 AA;

Query Match 81.8%; Score 36; DB 5; Length 546;
 Best Local Similarity 75.0%; Pred. No. 4.3e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEDEINNK 8
 DB 257 YEDEINHR 264

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OM protein - protein search, using sw model

Run on: July 5, 2006, 20:38:52 ; Search time 58.5631 Seconds
(without alignments)
63.277 Million cell updates/sec

Title: US-10-774-928A-11
Perfect score: 44
Sequence: 1 YEDEINNK 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	8	5	US-10-774-928-11
2	38	86.4	270	4	US-10-425-115-190930
3	38	86.4	645	4	US-10-425-115-280884
4	37	84.1	112	4	US-10-767-701-37605
5	37	84.1	246	4	US-10-425-115-315519
6	37	84.1	295	4	US-10-767-701-41541
7	37	84.1	526	4	US-10-425-115-295632
8	37	84.1	612	4	US-10-437-963-103055
9	37	84.1	703	5	US-10-739-930-10003
10	36	81.8	120	4	US-10-264-049-3729
11	36	81.8	217	4	US-10-263-828-88
12	36	81.8	352	5	US-10-617-316-244
13	36	81.8	370	4	US-10-425-114-57576
14	36	81.8	407	5	US-10-739-930-7235
15	36	81.8	488	4	US-10-425-115-268674
16	35	79.5	113	5	US-10-480-848A-5
17	35	79.5	139	3	US-09-351-794A-4
18	35	79.5	186	3	US-09-864-761-36050
19	35	79.5	186	5	US-10-450-763-39769
20	35	79.5	222	4	US-10-424-599-263693
21	35	79.5	236	4	US-10-264-049-4279
22	35	79.5	273	5	US-10-450-763-56735
23	35	79.5	275	5	US-10-450-763-45641
24	35	79.5	398	5	US-10-883-020-5
25	35	79.5	422	3	US-09-779-307-18
26	35	79.5	422	3	US-09-779-307-20
27	35	79.5	429	5	US-10-450-763-49905

28	35	79.5	429	5	US-10-450-763-49906	Sequence 49906, A
29	35	79.5	430	3	US-09-779-307-19	Sequence 19, Appl
30	35	79.5	433	3	US-09-925-298-463	Sequence 463, App
31	35	79.5	433	4	US-10-102-806-463	Sequence 463, App
32	35	79.5	469	4	US-10-093-766-59	Sequence 59, Appl
33	35	79.5	469	4	US-10-097-340-171	Sequence 171, App
34	35	79.5	469	4	US-10-097-340-173	Sequence 173, App
35	35	79.5	469	5	US-10-733-969A-52	Sequence 52, Appl
36	35	79.5	469	6	US-11-050-926-171	Sequence 171, App
37	35	79.5	469	6	US-11-050-926-173	Sequence 173, App
38	35	79.5	476	3	US-09-779-307-16	Sequence 16, Appl
39	35	79.5	476	5	US-10-821-234-1064	Sequence 1064, Ap
40	35	79.5	477	3	US-09-779-307-4	Sequence 4, Appl
41	35	79.5	481	4	US-10-080-334-54	Sequence 54, Appl
42	35	79.5	481	6	US-11-156-300-24	Sequence 24, Appl
43	35	79.5	482	3	US-09-779-307-17	Sequence 17, Appl
44	35	79.5	482	4	US-10-080-334-187	Sequence 187, App
45	35	79.5	482	5	US-10-883-020-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-10-774-928-11
; Sequence 11, Application US/10774928
; Publication No. US20040241168A1
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 302178
; CURRENT APPLICATION NUMBER: US/10/774,928
; CURRENT FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Leishmania
US-10-774-928-11

Query Match 100.0%; Score 44; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINNK 8
Db 1 YEDEINNK 8

RESULT 2
US-10-425-115-190930
; Sequence 190930, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Planes
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 190930
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(270)

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; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_105706C.1.pep
US-10-425-115-190930

Query Match      86.4%; Score 38; DB 4; Length 270;
Best Local Similarity 87.5%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YEDEINNK 8
Db 88 YEDEINEK 95
|||||

RESULT 3
US-10-425-115-280884
; Sequence 280884, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 280884
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(246)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_19268C.1.pep
US-10-425-115-280884

Query Match      86.4%; Score 38; DB 4; Length 645;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YEDEINNK 8
Db 185 YEDEINEK 192
|||||

RESULT 4
US-10-767-701-37605
; Sequence 37605, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 37605
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C3323_1.pep
US-10-767-701-37605

Query Match      84.1%; Score 37; DB 4; Length 112;
Best Local Similarity 85.7%; Pred. No. 54;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINN 7
Db 194 YEDELNN 200
|||||

OTHER INFORMATION: Clone ID: SORBI-28MAY03-C446_1.pep
US-10-767-701-41541

Query Match      84.1%; Score 37; DB 4; Length 295;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINN 7
Db 189 YEDELNN 195
|||||

RESULT 6
US-10-767-701-41541
; Sequence 41541, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 41541
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C446_1.pep
US-10-767-701-41541

Query Match      84.1%; Score 37; DB 4; Length 246;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEDEINN 7
Db 189 YEDELNN 195
|||||

RESULT 7
US-10-425-115-295632
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; Sequence 295632, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 295632
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(526)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_32695C.1.p
US-10-425-115-295632

Query Match 84.1%; Score 37; DB 4; Length 526;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINN 7
DB 424 YEDELNN 430

RESULT 8
US-10-437-963-103055
; Sequence 103055, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 103055
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(612)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_100522C.1.p
US-10-437-963-103055

Query Match 84.1%; Score 37; DB 4; Length 612;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINN 7
DB 510 YEDELNN 516

RESULT 9

US-10-739-930-10003
; Sequence 10003, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 10003
; LENGTH: 703
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(703)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: TRIAE-23APR03-C236_1.p
US-10-739-930-10003

Query Match 84.1%; Score 37; DB 5; Length 703;
Best Local Similarity 85.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINN 7
DB 250 YEDELNN 256

RESULT 10
US-10-264-049-3729
; Sequence 3729, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 3729
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (65)-
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-3729

Query Match 81.8%; Score 36; DB 4; Length 120;
Best Local Similarity 75.0%; Pred. No. 89;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINN 8
DB 37 YEDEINHR 44

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RESULT 11
US-10-823-828-88
; Sequence 88, Application US/10263828
; Publication No. US20030138905A1
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; TITLE OF INVENTION: Compositions isolated from bovine
; TITLE OF INVENTION: mammary gland and methods for their use.
; FILE REFERENCE: 11000.1044U1con
; CURRENT APPLICATION NUMBER: US/10/263,828
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Bovine
US-10-263-828-88

Query Match      81.8%; Score 36; DB 4; Length 217;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YEDEINNK 8
Db      2 YEDEINHR 9

RESULT 12
US-10-617-316-244
; Sequence 244, Application US/10617316
; Publication No. US20050130263A1
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka J
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; TITLE OF INVENTION: Compositions Isolated From Bovine
; TITLE OF INVENTION: Mammary Gland and Methods For Their Use.
; FILE REFERENCE: 11000.1046U1C1
; CURRENT APPLICATION NUMBER: US/10/617,316
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,701
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 262
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 244
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Bovine
US-10-617-316-244

Query Match      81.8%; Score 36; DB 5; Length 352;
Best Local Similarity 75.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YEDEINNK 8
Db      67 YEDEINHR 74

RESULT 13
US-10-425-114-57576
; Sequence 57576, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 57576
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMROTEOSINTE026E11_FLI.ppep
US-10-425-114-57576

Query Match      81.8%; Score 36; DB 4; Length 370;
Best Local Similarity 62.5%; Pred. No. 2.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YEDEINNK 8
Db      159 FEDEVNHR 166

RESULT 14
US-10-739-930-7235
; Sequence 7235, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 7235
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: ZEAMA-23APR03-C10961_25.p
US-10-739-930-7235

Query Match      81.8%; Score 36; DB 5; Length 407;
Best Local Similarity 62.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YEDEINNK 8
Db      196 FEDEVNHR 203

RESULT 15
US-10-425-115-268674
; Sequence 268674, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 268674
; LENGTH: 486
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; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
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; OTHER INFORMATION: Clone ID: MRT4577_17662C.1.pep
US-10-425-115-268674

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Query Match 81.8%; Score 36; DB 4; Length 488;
Best Local Similarity 62.5%; Pred. No. 3.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels

Qy 1 YEDEINNK 8

D_b 277 FEDEVN^R 284

Search completed: July 5, 2006, 20:51:55
Job time : 59.5631 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 20:39:32 ; Search time 4.58252 Seconds
(without alignments)
46.842 Million cell updates/sec

Title: US-10-774-928A-11
Perfect score: 44
Sequence: 1 YEDEINNK 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 112942

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	84.1	714	6 US-10-449-902-54951	Sequence 54951, A
2	35	79.5	469	6 US-10-505-928-457	Sequence 457, App
3	35	79.5	483	7 US-11-105-233-180	Sequence 180, App
4	34	77.3	758	6 US-10-449-902-51086	Sequence 51086, A
5	34	77.3	799	6 US-10-449-902-47602	Sequence 47602, A
6	34	77.3	1550	6 US-10-471-571A-1300	Sequence 1300, App
7	33	75.0	33	7 US-11-134-871-915	Sequence 915, App
8	33	75.0	940	6 US-10-449-902-45238	Sequence 45238, A
9	33	75.0	940	6 US-10-449-902-45669	Sequence 45669, A
10	32	72.7	26	7 US-11-134-871-1603	Sequence 1603, App
11	32	72.7	420	6 US-10-953-349-23057	Sequence 23057, A
12	32	72.7	430	6 US-10-953-349-23056	Sequence 23056, A
13	32	72.7	533	6 US-10-449-902-33245	Sequence 33245, A
14	32	72.7	533	6 US-10-449-902-43690	Sequence 43690, A
15	32	72.7	599	6 US-10-449-902-49534	Sequence 49534, A
16	32	72.7	964	7 US-11-289-102-392	Sequence 392, App
17	31	70.5	247	6 US-10-449-902-54216	Sequence 54216, A
18	31	70.5	568	6 US-10-449-902-46926	Sequence 46926, A
19	31	70.5	568	6 US-10-449-902-47019	Sequence 47019, A
20	31	70.5	574	6 US-10-953-349-12942	Sequence 12942, A
21	31	70.5	636	6 US-10-953-349-12941	Sequence 12941, A
22	31	70.5	638	6 US-10-953-349-12940	Sequence 12940, A
23	30	68.2	91	6 US-10-953-349-36767	Sequence 36767, A
24	30	68.2	107	6 US-10-953-349-13561	Sequence 13561, A
25	30	68.2	132	6 US-10-953-349-36766	Sequence 36766, A

ALIGNMENTS

RESULT 1

US-10-449-902-54951
; Sequence 54951, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205V1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54951
; LENGTH: 714
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-54951

Query Match 84.1%; Score 37; DB 6; Length 714;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINN 7
DB 613 YEDELNN 619

RESULT 2

US-10-505-928-457
; Sequence 457, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; APPLICANT: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2

Sequence 1458, Ap
Sequence 24110, A
Sequence 1457, Ap
Sequence 36765, A
Sequence 13251, A
Sequence 13560, A
Sequence 1456, Ap
Sequence 13250, A
Sequence 68, Appl
Sequence 50750, A
Sequence 24109, A
Sequence 22862, A
Sequence 48257, A
Sequence 55155, A
Sequence 22861, A
Sequence 84, Appl
Sequence 22860, A
Sequence 36104, A
Sequence 98, Appl
Sequence 2, Appl

140 6 US-10-953-349-1458
142 6 US-10-953-349-24110
147 6 US-10-953-349-1457
148 6 US-10-953-349-36765
158 6 US-10-953-349-13251
158 6 US-10-953-349-13560
164 6 US-10-953-349-1456
183 6 US-10-953-349-13250
201 7 US-11-199-489A-68
228 6 US-10-449-902-50750
245 6 US-10-953-349-24109
288 6 US-10-953-349-22862
295 6 US-10-449-902-48257
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358 6 US-10-953-349-22861
412 6 US-10-471-571A-84
434 6 US-10-953-349-22860
450 6 US-10-449-902-36104
472 6 US-10-196-749-98
472 7 US-11-190-075-2

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; SEQ ID NO 457
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-457

Query Match      79.5%; Score 35; DB 6; Length 469;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 YEDEINNK 8
Db 180 YEDEINRR 187

RESULT 3
US-11-105-233-180
; Sequence 180, Application US/11105233
; Publication No. US20060134653A1
; GENERAL INFORMATION:
; APPLICANT: Thiasalingam et al
; TITLE OF INVENTION: Differential Expression of Genes in MSI
; FILE OF INVENTION: Tumors
; FILE REFERENCE: 1657/2001
; CURRENT APPLICATION NUMBER: US/11/105,233
; CURRENT FILING DATE: 2005-04-13
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 180
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-233-180

Query Match      79.5%; Score 35; DB 7; Length 483;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 YEDEINNK 8
Db 179 YEDEINKR 186

RESULT 4
US-10-449-902-51086
; Sequence 51086, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51086
; LENGTH: 758
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-51086

Query Match      77.3%; Score 34; DB 6; Length 758;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINN 7

RESULT 5
US-10-449-902-47602
; Sequence 47602, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47602
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-47602

Query Match      77.3%; Score 34; DB 6; Length 799;
Best Local Similarity 85.7%; Pred. No. 73;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINN 7
Db 349 YEDEIND 355

RESULT 6
US-10-471-571A-1300
; Sequence 1300, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 1300
; LENGTH: 1550
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(1550)
; OTHER INFORMATION: phi pVL ORF 15 and 16
US-10-471-571A-1300

Query Match      77.3%; Score 34; DB 6; Length 1550;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINN 7
Db 1522 FEDEVNN 1528

RESULT 7
US-11-134-871-915
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; Sequence 915, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Quatification of Serum Glycoproteins
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 915
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-915

Query Match 75.0%; Score 33; DB 7; Length 940;
Best Local Similarity 71.4%; Pred. No. 3.6;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINN 7
Db 20 YEDEVNS 26

RESULT 8

US-10-449-902-45238
; Sequence 45238, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45238
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-45238

Query Match 75.0%; Score 33; DB 6; Length 940;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEIN 6
Db 413 YEDEIN 418

RESULT 9

US-10-449-902-45669
; Sequence 45669, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45669
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-45669

Query Match 75.0%; Score 33; DB 6; Length 940;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEIN 6
Db 413 YEDEIN 418

RESULT 10

US-11-134-871-1603
; Sequence 1603, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Quatification of Serum Glycoproteins
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1603
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-1603

Query Match 72.7%; Score 32; DB 7; Length 26;
Best Local Similarity 85.7%; Pred. No. 4.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEDEINN 7
Db 3 YEDEPNN 9

RESULT 11

US-10-953-349-23057
; Sequence 23057, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23057
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-23057

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Query Match          72.7%; Score 32; DB 6; Length 420;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EDEINN 7
Db 31 EDEINN 36

RESULT 12
US-10-953-349-23056
; Sequence 23056, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23056
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-23056

Query Match          72.7%; Score 32; DB 6; Length 430;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EDEINN 7
Db 41 EDEINN 46

RESULT 13
US-10-449-902-33245
; Sequence 33245, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33245
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-33245

Query Match          72.7%; Score 32; DB 6; Length 533;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DEINN 8
Db 444 DEINN 449

RESULT 14
US-10-449-902-33245
; Sequence 33245, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33245
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-33245

Query Match          72.7%; Score 32; DB 6; Length 533;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DEINN 8
Db 444 DEINN 449
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US-10-449-902-43690
; Sequence 43690, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43690
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-43690

Query Match          72.7%; Score 32; DB 6; Length 533;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DEINN 8
Db 444 DEINN 449

RESULT 15
US-10-449-902-49534
; Sequence 49534, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49534
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-49534

Query Match          72.7%; Score 32; DB 6; Length 599;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINN 7
Db 134 FQDEINN 140

Search completed: July 5, 2006, 20:53:00
Job time : 5.58252 secs
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OM protein - protein search, using sw model

Run on: July 5, 2006, 19:18:42 ; Search time 18.0194 Seconds
(without alignments)
38.861 Million cell updates/sec

Title: US-10-774-928A-11

Perfect score: 44

Sequence: 1 YEDEINNK 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	8	2 US-09-809-003A-11	Sequence 11, Appl
2	36	81.8	546	1 US-09-067-351-1	Sequence 1, Appli
3	36	81.8	546	2 US-09-360-490-1	Sequence 1, Appli
4	35	79.5	139	2 US-08-559-896B-4	Sequence 4, Appli
5	35	79.5	139	2 US-09-351-794A-4	Sequence 4, Appli
6	35	79.5	384	2 US-09-949-016-11034	Sequence 11034, A
7	35	79.5	469	2 US-09-077-606-3	Sequence 3, Appli
8	35	79.5	476	2 US-09-949-016-9096	Sequence 9096, Ap
9	35	79.5	482	2 US-09-538-092-858	Sequence 858, App
10	35	79.5	483	2 US-09-919-497-79	Sequence 79, Appl
11	35	79.5	502	2 US-09-949-016-11033	Sequence 11033, A
12	35	79.5	551	1 US-09-067-351-2	Sequence 2, Appli
13	35	79.5	551	2 US-09-360-490-2	Sequence 2, Appli
14	35	79.5	564	2 US-09-949-016-6628	Sequence 6628, Ap
15	35	79.5	567	2 US-10-104-047-3772	Sequence 3772, Ap
16	35	79.5	569	2 US-09-949-016-11035	Sequence 11035, A
17	35	79.5	569	2 US-09-949-016-11036	Sequence 11036, A
18	35	79.5	637	2 US-09-949-016-8152	Sequence 8152, Ap
19	35	79.5	643	2 US-09-538-092-844	Sequence 844, Appl
20	35	79.5	645	2 US-09-919-172-41	Sequence 41, Appl
21	35	79.5	652	2 US-08-559-896B-2	Sequence 2, Appli
22	35	79.5	652	2 US-09-351-794A-2	Sequence 2, Appli
23	34	77.3	67	2 US-09-248-796A-23567	Sequence 23567, A
24	34	77.3	220	2 US-09-134-000C-4085	Sequence 4085, Ap
25	33	75.0	7	2 US-09-809-003A-1	Sequence 1, Appli
26	33	75.0	8	2 US-09-809-003A-12	Sequence 12, Appl

27 33 75.0 389 2 US-09-495-406-20 Sequence 20, Appl
28 33 75.0 389 2 US-09-816-028A-34 Sequence 34, Appl
29 33 75.0 389 2 US-10-303-162-34 Sequence 34, Appl
30 33 75.0 389 2 US-10-303-134-34 Sequence 34, Appl
31 33 75.0 389 2 US-10-303-118-34 Sequence 34, Appl
32 33 75.0 389 2 US-10-303-128-34 Sequence 34, Appl
33 33 75.0 389 3 US-10-735-419-34 Sequence 34, Appl
34 33 75.0 443 2 US-09-949-016-10582 Sequence 10582, A
35 33 75.0 631 1 US-08-487-890A-115 Sequence 115, App
36 33 75.0 631 1 US-08-478-435-115 Sequence 115, App
37 33 75.0 631 1 US-08-337-483-115 Sequence 115, App
38 33 75.0 631 1 US-08-478-373-115 Sequence 115, App
39 33 75.0 631 2 US-08-474-671-115 Sequence 115, App
40 33 75.0 631 2 US-08-483-577A-115 Sequence 115, App
41 33 75.0 631 2 US-08-897-438-115 Sequence 115, App
42 33 75.0 631 2 US-08-637-654-115 Sequence 115, App
43 33 75.0 631 2 US-08-649-518-115 Sequence 115, App
44 33 75.0 995 2 US-09-362-842-2 Sequence 2, Appli
45 33 75.0 1348 2 US-09-949-002-517 Sequence 517, App

ALIGNMENTS

RESULT 1

US-09-809-003A-11
; Sequence 11, Application US/09809003A
; Patent No. 6673351

; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose

; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 302178

; CURRENT APPLICATION NUMBER: US/09/809,003A
; CURRENT FILING DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 11

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Leishmania

US-09-809-003A-11

Query Match 100.0%; Score 44; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 5e+03;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINNK 8

Db 1 YEDEINNK 8

RESULT 2

US-09-067-351-1
; Sequence 1, Application US/09067351
; Patent No. 5994081

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Corley, Neil C.

; APPLICANT: Baughn, Mariah

; TITLE OF INVENTION: HUMAN KERATINS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/067.351
;; FILING DATE: Herewith
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CERRONE, MICHAEL C.
;; REGISTRATION NUMBER: 39,132
;; REFERENCE/DOCKET NUMBER: PF-0511 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650) 855-0555
;; TELEFAX: (650) 845-4166
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 546 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: PANCYTUT02
;; CLONE: 1467090
US-09-067-351-1
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Query Match 81.8%; Score 36; DB 1; Length 546;
Best Local Similarity 75.0%; Pred. No. 76;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 YEDEINNK 8
Db 257 YEDEINHR 264
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RESULT 3
US-09-360-490-1
; Sequence 1, Application US/09360490
; Patent No. 6221843
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN KERATINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/360.490
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/067.351
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0511 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 546 amino acids
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;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: PANCYTUT02
;; CLONE: 1467090
US-09-360-490-1
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Query Match 81.8%; Score 36; DB 2; Length 546;
Best Local Similarity 75.0%; Pred. No. 76;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 YEDEINNK 8
Db 257 YEDEINHR 264
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```
RESULT 4
US-08-559-896B-4
; Sequence 4, Application US/08559896B
; Patent No. 6310046
; GENERAL INFORMATION:
; APPLICANT: Patrick E. Duffy
; APPLICANT: Christian P. Ockenhouse
; TITLE OF INVENTION: SEQUESTIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: USA MRC - MCMR-JA
; CITY: FORT DETRICK, FREDERICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559.896B
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
US-08-559-896B-4
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Query Match 79.5%; Score 35; DB 2; Length 139;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 YEDEINN 7
Db 84 YKDEINN 90
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RESULT 5
US-09-351-794A-4
; Sequence 4, Application US/09351794A
; Patent No. 6641815
; GENERAL INFORMATION:
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; APPLICANT: DUFFY, PATRICK E.
; APPLICANT: OCKENHOUSE, CHRISTIAN F.
; TITLE OF INVENTION: SEQUESTRIN
; FILE REFERENCE: 38644-175519
; CURRENT APPLICATION NUMBER: US/09/351,794A
; CURRENT FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: 08/559,896
; PRIOR FILING DATE: 1995-11-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-351-794A-4

Query Match 79.5%; Score 35; DB 2; Length 139;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEDEINN 7
Db 84 YKDEINN 90

RESULT 6

US-09-949-016-11034
; Sequence 11034, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11034
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11034

Query Match 79.5%; Score 35; DB 2; Length 384;
Best Local Similarity 75.0%; Pred. No. 80;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEDEINN 8
Db 276 YEDEINKR 283

RESULT 7

US-09-077-606-3
; Sequence 3, Application US/09077606
; Patent No. 6774220
; GENERAL INFORMATION:
; APPLICANT: JIANG, Pan Hong
; APPLICANT: KABA, Aboubacar
; APPLICANT: CHANY-FOURNIER, Francoise
; APPLICANT: CERUTTI, Itallina
; APPLICANT: CHANY, Charles
; TITLE OF INVENTION: COMPOUNDS HAVING LECTINIC PROPERTIES AND THEIR
; FILE REFERENCE: 040388/0113
; CURRENT APPLICATION NUMBER: US/09/077,606

; CURRENT FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: WO PCT/FR96/01937
; EARLIER FILING DATE: 1996-12-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-077-606-3

Query Match 79.5%; Score 35; DB 2; Length 469;
Best Local Similarity 75.0%; Pred. No. 99;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEDEINN 8
Db 180 YEDEINRR 187

RESULT 8

US-09-949-016-9096
; Sequence 9096, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9096
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9096

Query Match 79.5%; Score 35; DB 2; Length 476;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEDEINN 8
Db 187 YEDEINRR 194

RESULT 9

US-09-538-092-858
; Sequence 858, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatter Version 0.9
; SEQ ID NO 858
; LENGTH: 482

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P05787
US-09-538-092-858

Query Match      79.5%; Score 35; DB 2; Length 482;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 YEDEINNK 8
Db      178 YEDEINKR 185

RESULT 10
US-09-919-497-79
; Sequence 79, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-79

Query Match      79.5%; Score 35; DB 2; Length 483;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 YEDEINNK 8
Db      179 YEDEINKR 186

RESULT 11
US-09-949-016-11033
; Sequence 11033, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11033
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11033

Query Match      79.5%; Score 35; DB 2; Length 502;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
```

```
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 YEDEINNK 8
Db      198 YEDEINKR 205

RESULT 12
US-09-067-351-2
; Sequence 2, Application US/09067351
; Patent No. 5994081
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN KERATINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,351
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0511 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 551 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KERANOT02
; CLONE: 2029060
US-09-067-351-2

Query Match      79.5%; Score 35; DB 1; Length 551;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 YEDEINNK 8
Db      239 YEDEINKR 246

RESULT 13
US-09-360-490-2
; Sequence 2, Application US/09360490
; Patent No. 6221843
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN KERATINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/360,490
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/067,351
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0511 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 551 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KERANOT02
CLONE: 2029060
US-09-360-490-2

Query Match 79.5%; Score 35; DB 2; Length 551;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEDEINNK 8
DB 235 YEDEINKR 246

RESULT 14
US-09-949-016-6628
Sequence 6628, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6628
LENGTH: 564
TYPE: PRT
ORGANISM: Human
US-09-949-016-6628

Query Match 79.5%; Score 35; DB 2; Length 564;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEDEINNK 8
DB 253 YEDEINKR 260

RESULT 15
US-10-104-047-3772
Sequence 3772, Application US/10104047
Patent No. 6943241
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241el full length cdna
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3772
LENGTH: 567
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-3772

Query Match 79.5%; Score 35; DB 2; Length 567;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEDEINNK 8
DB 235 YEDEINKR 242

Search completed: July 5, 2006, 19:24:22
Job time : 18.0194 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 19:09:18 ; Search time 9.70874 Seconds
(without alignments)
79.283 Million cell updates/sec

Title: US-10-774-928A-12

Perfect score: 43

Sequence: 1 KYEDEINK 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.*

1: Pirl.*

2: Pirl.*

3: Pirl.*

4: Pirl.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	310	2 S43865	cytokeratin 8, typ
2	43	100.0	384	2 I61769	keratin 6d, type I
3	43	100.0	390	2 A60093	cytokeratin, type
4	43	100.0	419	1 KRXL2B	keratin, 64K type
5	43	100.0	425	1 KRXL2A	keratin, 64K type
6	43	100.0	461	2 A43782	keratin, type II -
7	43	100.0	483	2 A34720	keratin 8, type II
8	43	100.0	487	2 JT0407	keratin 8, type II
9	43	100.0	490	2 JS0658	cytokeratin EndoA
10	43	100.0	513	2 S08381	keratin, 58K type
11	43	100.0	520	2 JS0291	intermediate filam
12	43	100.0	553	2 I59009	epidermal keratin
13	43	100.0	564	1 KRHUEA	keratin 6a, type I
14	43	100.0	564	1 KRHUEB	keratin 6b, type I
15	43	100.0	564	2 I61770	keratin 6e, type I
16	43	100.0	564	2 I61768	keratin 6c, type I
17	43	100.0	564	2 I61771	keratin 6f, type I
18	43	100.0	581	1 KRMS2	keratin, type II c
19	43	100.0	590	2 A29904	keratin 5, type II
20	43	100.0	629	2 A29666	keratin, 65K type
21	43	100.0	629	2 S42629	keratin K3 - rabbi
22	43	100.0	638	2 I53169	cytokeratin 2, hu
23	43	100.0	643	1 KRHU2	keratin 1, type II
24	43	100.0	645	2 A44861	keratin, 67K type
25	40	93.0	469	2 S05602	keratin K7, type I
26	40	93.0	489	2 B24177	keratin, 55K type
27	40	93.0	502	2 A23547	keratin, type II c
28	39	90.7	164	2 C84777	cyclophilin-like p
29	39	90.7	524	2 A23518	keratin, 57K type

30	39	90.7	534	2 I37942	keratin 4, type II
31	37	86.0	370	2 A25004	keratin, 53K type
32	37	86.0	584	2 G71676	hypothetical prote
33	36	83.7	681	2 T14903	NADPH-ferrihemopro
34	36	83.7	1729	2 T18396	erythrocyte membra
35	36	83.7	2924	2 T18378	variant-specific s
36	35	81.4	94	2 C59094	hypothetical prote
37	35	81.4	184	2 D70362	ribosome recycling
38	35	81.4	224	2 S00959	hypothetical prote
39	35	81.4	293	2 AE2018	hypothetical prote
40	35	81.4	701	2 T07943	probable AMP-bindi
41	35	81.4	900	2 T50773	translation initia
42	35	81.4	900	2 T47732	probable translati
43	35	81.4	918	2 D71407	hypothetical prote
44	35	81.4	921	2 F81294	probable helicase
45	34	79.1	126	2 T21191	hypothetical prote

ALIGNMENTS

RESULT 1

S43865

cytokeratin 8, type II - potoroo (fragment)

C:Species: Potorous tridactylus (potoroo, long-nosed rat kangaroo)

C>Date: 20-Feb-1995 #sequence_revision 06-Dec-1996 #text_change 09-Jul-2004

C:Accession: S43865; S40172

R:Boettger, V.; Lane, E.B.

J. Mol. Biol. 235, 61-67, 1994

A>Title: A monoclonal antibody epitope on keratin 8 identified using a phage peptide lib

A:Reference number: S43865; MUID:94118290; PMID:7507169

A:Accession: S43865

A:Molecule type: mRNA

A:Residues: 1-310 <BOE>

A:Cross-references: UNIPROT:Q28810; UNIPARC:UPI0000086BFO; EMBL:X70987; NID:9437902; PIDN

A:Experimental source: kidney epithelium cells

C:Superfamily: cytoskeletal keratin

C:Keywords: coiled coil

Query Match 100.0%; Score 43; DB 2; Length 310;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8

DB 179 KYEDEINK 186

RESULT 2

I61769

keratin 6d, type II - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004

C:Accession: I61769

R:Takahashi, K.; Paladini, R.D.; Coulombe, P.A.

J. Biol. Chem. 270, 18581-18592, 1995

A>Title: Cloning and characterization of multiple human genes and cDNAs encoding highly

A:Reference number: A57398; MUID:95355491; PMID:7543104

A:Accession: I61769

A:Molecule type: DNA

A:Residues: 1-384 <RES>

A:Cross-references: UNIPROT:P48687; UNIPARC:UPI000012DB17; GB:L42602; NID:9914823; GB:L42

28; GB:L42608; NID:9914829; GB:L42609; NID:9914830; GB:L42610; NID:91488952; PIDN:AAB606

C:Genetics:

A:Gene: KRT6D

A:Introns: 72/2; 92/3; 124/3; 179/3; 221/3; 295/2; 307/1

C:Superfamily: cytoskeletal keratin

C:Keywords: coiled coil

Query Match 100.0%; Score 43; DB 2; Length 384;

Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 KYEDEINK 8
      |||||||
Db      72 KYEDEINK 79

RESULT 3
A60093
cytokeratin, type II, early ectodermal - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993
C:Accession: A60093
R:Charlebois, T.S.; Spencer, D.H.; Tarkington, S.K.; Henry, J.J.; Grainger, R.M.
Development 108, 33-45, 1990
A:Title: Isolation of a chick cytokeratin cDNA clone indicative of regional specialization
A:Reference number: A60093; MUID:90276238; PMID:1693557
A:Accession: A60093
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-390 <CHA>
A:Cross-references: UNIPARC:UPI00001774C6
C:Superfamily: cytoskeletal keratin
C:Keywords: intermediate filament

      Query Match      100.0%; Score 43; DB 2; Length 390;
      Best Local Similarity 100.0%; Pred. No. 1.3; Indels 0; Gaps 0;
      Matches 8; Conservative 0; Mismatches 0;

QY      1 KYEDEINK 8
      |||||||
Db      99 KYEDEINK 106

RESULT 4
KXKL2B
keratin, 64K type II cytoskeletal (clone pUF164) - African clawed frog (fragment)
N:Alternate names: 64-kDa type II keratin
C:Species: Xenopus laevis (African clawed frog)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C:Accession: A02952
R:Hoffmann, W.; Franz, J.K.; Franke, W.W.
J. Mol. Biol. 184, 713-724, 1985
A:Title: Amino acid sequence microheterogeneities of basic (type II) cytokeratins of Xenopus laevis
A:Reference number: A2914; MUID:86011576; PMID:2413219
A:Accession: A02952
A:Molecule type: mRNA
A:Residues: 1-419 <HOF>
A:Cross-references: UNIPROT:P04265; UNIPARC:UPI000012DB07; GB:X02895; GB:M13954; NID:964
A:Experimental source: clone pUF164
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament
F:1-275/Domain: rod (fragment) <NOD>
F:1-9/Region: linker 1
F:10-110/Region: coil 1B
F:111-127/Region: linker 12
F:128-146/Region: coil 2A
F:147-154/Region: linker 2
F:155-275/Region: coil 2B
F:213/Region: stutler
F:276-419/Domain: tail <END>
F:276-395/Region: H2 and V2 subdomains
F:400-419/Region: E2 subdomain

      Query Match      100.0%; Score 43; DB 1; Length 419;
      Best Local Similarity 100.0%; Pred. No. 1.4; Indels 0; Gaps 0;
      Matches 8; Conservative 0; Mismatches 0;

QY      1 KYEDEINK 8
      |||||||
Db      51 KYEDEINK 58

RESULT 5

```

```

KXKL2A
keratin, 64K type II cytoskeletal (clone pUF23) - African clawed frog (fragment)
N:Alternate names: 64-kDa type II keratin
C:Species: Xenopus laevis (African clawed frog)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C:Accession: A02953
R:Hoffmann, W.; Franz, J.K.; Franke, W.W.
J. Mol. Biol. 184, 713-724, 1985
A:Title: Amino acid sequence microheterogeneities of basic (type II) cytokeratins of Xenopus laevis
A:Reference number: A2914; MUID:86011576; PMID:2413219
A:Accession: A02953
A:Molecule type: mRNA
A:Residues: 1-425 <HOF>
A:Cross-references: UNIPROT:P04266; UNIPARC:UPI000012DB06; GB:X02894; GB:M13956; NID:964
A:Experimental source: clone pUF23
C:Comment: The cytokeratin if proteins appear to be obligate heteropolymers, composed of types of proteins is low and restricted to specific isolated regions within the rod domain. Three subdomains, each characterized by a distinctive amino acid composition, d length among the intermediate filament proteins, the arrangement of its subdomains preally distant species, suggests functional significance.
C:Comment: There is only one group of closely related type II amphibian cytokeratins. The rate of differentiation of the amphibian epidermis, which lacks a true stratum corneum.
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament
F:1-296/Domain: rod (fragment) <ROD>
F:1-16/Region: coil 1A (fragment)
F:17-30/Region: linker 1
F:31-131/Region: coil 1B
F:132-148/Region: linker 12
F:149-167/Region: coil 2A
F:168-175/Region: linker 2
F:176-296/Region: coil 2B
F:234/Region: stutler
F:297-425/Domain: tail <END>
F:297-405/Region: H2 and V2 subdomains
F:406-425/Region: E2 subdomain

      Query Match      100.0%; Score 43; DB 1; Length 425;
      Best Local Similarity 100.0%; Pred. No. 1.4; Indels 0; Gaps 0;
      Matches 8; Conservative 0; Mismatches 0;

QY      1 KYEDEINK 8
      |||||||
Db      72 KYEDEINK 79

RESULT 6
A43782
keratin, type II - eastern newt (fragment)
C:Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C:Accession: A43782
R:Ferretti, P.; Brookes, J.P.; Brown, R.
Development 111, 497-507, 1991
A:Title: A new type II keratin restricted to normal and regenerating limbs and tails is
A:Reference number: A43782; MUID:91372147; PMID:1716554
A:Accession: A43782
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <FER>
A:Cross-references: UNIPROT:O42435; UNIPARC:UPI00001774C4; GB:X57671
C:Superfamily: cytoskeletal keratin

      Query Match      100.0%; Score 43; DB 2; Length 461;
      Best Local Similarity 100.0%; Pred. No. 1.6; Indels 0; Gaps 0;
      Matches 8; Conservative 0; Mismatches 0;

QY      1 KYEDEINK 8
      |||||||
Db      133 KYEDEINK 140

RESULT 7

```


Qy 1 KYDEINK 8
 |||||
 Db 178 KYDEINK 185

RESULT 8
 JT0407

keratin 8, type II cytoskeletal, embryonic - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C/Accession: JT0407; A22078
 R/Ouellet, T.; Levac, P.; Royal, A.
 Gene 70, 75-84, 1988

A/Title: Complete sequence of the mouse type-II keratin EndoA: its amino-terminal region
 A/Reference number: JT0407; MUID:89196919; PMID:2467842
 A/Accession: JT0407
 A/Molecule type: mRNA
 A/Residues: 1-487 <OUE>
 A/Cross-references: UNIPROT:Q61518; UNIPARC:UPI00000B6EEO; GB:M22831; NID:G511653; PIDN:
 A/Experimental source: carcinoma cell line F9-21
 R/Vasseur, M.; Duprey, P.; Brulst, P.; Jacob, P.
 Proc. Natl. Acad. Sci. U.S.A. 82, 1155-1159, 1985

A/Title: One gene and one pseudogene for the cytokeratin endo A.
 A/Reference number: A22078; MUID:85140247; PMID:2579387
 A/Accession: A22078
 A/Molecule type: DNA
 A/Residues: 1-13 <VAS>
 A/Cross-references: UNIPARC:UPI000016CD31; GB:K02783; NID:G193019; PIDN:AAA37549.1; PID:
 C/Genetics:
 A/Gene: EndoA
 C/Superfamily: cytoskeletal keratin
 C/Keywords: coiled coil; intermediate filament
 F/1-94/Domain: head <HED>
 F/95-406/Domain: rod <ROD>
 F/95-128/Region: coil 1A
 F/129-146/Region: linker 1
 F/147-235/Region: coil 1B
 F/236-260/Region: linker 12
 F/261-406/Region: coil 2
 F/407-487/Domain: tail <TAI>

Query Match 100.0%; Score 43; DB 2; Length 487;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYDEINK 8
 |||||
 Db 181 KYDEINK 188

RESULT 9
 JS0658

cytokeratin EndoA - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C/Accession: JS0658
 R/Tamai, Y.; Takemoto, Y.; Matsumoto, M.; Morita, T.; Matsushiro, A.; Nozaki, M.
 Gene 104, 169-176, 1991

A/Title: Sequence of the EndoA gene encoding mouse cytokeratin and its methylation state
 A/Reference number: JS0658; MUID:92009210; PMID:1717348
 A/Accession: JS0658
 A/Status: translation not shown
 A/Molecule type: DNA
 A/Residues: 1-490 <TAM>
 A/Cross-references: UNIPROT:Q61463; UNIPARC:UPI00000220F8; GB:D90360; NID:G220391; PIDN:
 A/Comment: This type-II cytokeratin forms intermediate filaments together with type-I cy
 C/Genetics:
 A/Gene: EndoA
 A/Introns: 114/3; 184/2; 204/3; 236/3; 291/3; 333/3; 407/2; 427/1
 C/Superfamily: cytoskeletal keratin

Query Match 100.0%; Score 43; DB 2; Length 490;
 Best Local Similarity 100.0%; Pred. No. 1.7;

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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
    |||||||
Db 184 KYEDEINK 191

RESULT 10
S08381
keratin, 58K type II, cytoskeletal (clone pXenCK5(5/6)) - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
C:Accession: S08381
R:Fouquet, B.; Herrmann, H.; Franz, J.K.; Franke, W.W.
Development 104, 533-548, 1988
A:Title: Expression of intermediate filament proteins during development of Xenopus laevis
A:Reference number: S08381; MUID:90032362; PMID:2478354
A:Accession: S08381
A:Molecule type: mRNA
A:Residues: 1-513 <FOU>
A:Cross-references: UNIPROT:P16878; UNIPARC:UPI000017151D; EMBL:X14427; NID:G64625; PIDN:
C:Superfamily: cytoskeletal keratin

Query Match 100.0%; Score 43; DB 2; Length 513;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
    |||||||
Db 216 KYEDEINK 223

RESULT 11
JS0291
intermediate filament protein ON3 - goldfish
C:Species: Carassius auratus (goldfish)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: JS0291
R:Giordano, S.; Glasgow, E.; Tesser, P.; Schechter, N.
Neuron 2, 1507-1516, 1989
A:Title: A type II keratin is expressed in glial cells of the goldfish visual pathway.
A:Reference number: JS0291; MUID:90180470; PMID:2483326
A:Accession: JS0291
A:Molecule type: mRNA
A:Residues: 1-520 <GIO>
A:Cross-references: UNIPROT:P18520; UNIPARC:UPI000012D74A
A:Experimental source: Glial cell
C:Comment: This protein is one of the nonneuronal predominant intermediate filament prot
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; optic nerve; visual pathway
F:1-108/Domain: head <HEA>
F:109-144/Region: coil 1A
F:145-157/Region: linker
F:158-253/Region: coil 1B
F:254-273/Region: linker
F:274-420/Region: coil 2
F:421-520/Domain: tail <TAI>

Query Match 100.0%; Score 43; DB 2; Length 520;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
    |||||||
Db 196 KYEDEINK 203

RESULT 12
I59009
epidermal keratin subunit II - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I59009; A61205
```

```
R:Steinert, P.M.; Parry, D.A.D.; Racoosin, E.L.; Idler, W.W.; Steven, A.C.; Trus, B.L.; F
Proc. Natl. Acad. Sci. U.S.A. 81, 5709-5713, 1984
A:Title: The complete cDNA and deduced amino acid sequence of a type II mouse epidermal t
A:Reference number: I59009; MUID:85014838; PMID:6207530
A:Accession: I59009
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-553 <RES>
A:Cross-references: UNIPROT:P50446; UNIPARC:UPI000016C887; GB:K02108; NID:G198634; PIDN:I
R:Finch, J.; Andrews, K.; Krieg, P.; Fuerstenberger, G.; Slaga, T.; Ootsuyama, A.; Tanoo
Carcinogenesis 12, 1519-1522, 1991
A:Title: Identification of a cloned sequence activated during multi-stage carcinogenesis
A:Reference number: A61205; MUID:91316763; PMID:1713533
A:Accession: A61205
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 528-553 <FIN>
A:Cross-references: UNIPARC:UPI00001774C8
C:Genetics:
A:Gene: KER2
C:Superfamily: cytoskeletal keratin

Query Match 100.0%; Score 43; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
    |||||||
Db 241 KYEDEINK 248

RESULT 13
KXUEA
keratin 6a, type II - human
N:Alternate names: 56-kDa type II keratin; keratin cytoskeletal
C:Species: Homo sapiens (man)
C:Date: 15-Nov-1984 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: A57398; A02944
R:Takahashi, K.; Paladini, R.D.; Coulombe, P.A.
J. Biol. Chem. 270, 18581-18592, 1995
A:Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
A:Reference number: A57398; MUID:95355491; PMID:7543104
A:Accession: A57398
A:Status: translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-564 <TKX>
A:Cross-references: UNIPROT:P02538; UNIPARC:UPI000013CD4C; GB:L42575; NID:G908769; GB:L4;
74; GB:L42581; NID:G908775; GB:L42582; NID:G908776; GB:L42583; NID:G908777; PIDN:AAC4176;
R:Hanukoglu, I.; Fuchs, E.
Cell 33, 915-924, 1983
A:Title: The cDNA sequence of a type II cytoskeletal keratin reveals constant and variabl
A:Reference number: A02944; MUID:83259278; PMID:6191871
A:Accession: A02944
A:Molecule type: mRNA
A:Residues: 208-394, 'S', 396-564 <HAN>
A:Cross-references: UNIPARC:UPI000016AB87; GB:J00269; NID:G34068; PIDN:CAA24760.1; PID:gi:
C:Comment: The cytoskeletal and microfilillar keratins are classified into two types, t
atin IF protein subunit appears to be a heterotetramer of two type I and two type II prot
C:Genetics:
A:Gene: GDB:KRT6A
A:Cross-references: GDB:128111; OMIM:148041
A:Map position: 12q12-12q21
A:Introns: 180/3; 252/2; 272/3; 304/3; 359/3; 401/3; 475/2; 487/1
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament
F:2-163/Domain: head <HED>
F:2-126/Region: E1 and V1 subdomains
F:127-163/Region: H1 subdomain
F:162-476/Domain: rod <ROD>
F:199-210/Region: linker 1
F:211-311/Region: coil 1B
F:312-328/Region: linker 12
F:329-347/Region: coil 2A
```

F:348-355/Region: linker 2
F:356-476/Region: coil 2B
F:414/Region: stutter
F:477-564/Domain: tail <END>
F:477-496/Region: H2 subdomain
F:497-564/Region: V2 and E2 subdomains

Query Match 100.0%; Score 43; DB 1; Length 564;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
DB 252 KYEDEINK 259

RESULT 14

KRHUEB
keratin 6b, type II - human
N:Alternate names: 56K type II keratin; keratin, cytoskeletal
C:Species: Homo sapiens (man)
C>Date: 04-Dec-1986 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: I61767; A02945
R:Takahashi, K.; Paladini, R.D.; Coulombe, P.A.
J. Biol. Chem. 270, 18581-18592, 1995
A:Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
A:Reference number: A57398; MUID:95355491; PMID:7543104
A:Accession: I61767
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-564 <RES>
A:Cross-references: UNIPROT:P04259; UNIPARC:UPI0000167B38; GB:L42584; NID:g908780; GB:L4
85; GB:L42590; NID:g908786; GB:L42591; NID:g908787; GB:L42592; NID:g908788; PIDN:AAC4176
R:Tyner, A.L.; Eichman, M.J.; Fuchs, E.
Proc. Natl. Acad. Sci. U.S.A. 82, 4683-4687, 1985
A:Title: The sequence of a type II keratin gene expressed in human skin: conservation of
A:Reference number: A02945; MUID:85270392; PMID:2410904
A:Accession: A02945
A:Molecule type: DNA
A:Residues: 2-88, 'AG', '91-115, 'PA', '118, 'LC', '122-158, 'IG', '161-254, 'V', '256-564 <TYN>
A:Cross-references: UNIPARC:UPI0000173D58; GB:M11229; GB:L00205; NID:g186714; PIDN:AAA59
A:Note: Initiator Met not shown
C:Comment: There are two types of cytoskeletal and microfibrillar keratin, I (acidic) and
bi-gate heteropolymers, composed of complexes formed by the aggregation of at least one
C:Genetics:
A:Gene: GDB:KRT6B
A:Cross-references: GDB:128113; OMIM:148042
A:Map position: 12pter-12qter
A:Introns: 180/3; 252/2; 272/3; 304/3; 359/3; 401/3; 475/2; 487/1
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament
F:2-163/Domain: head <HED>
F:2-127/Region: E1 and V1 subdomains
F:128-163/Region: H1 subdomain
F:164-476/Domain: rod <ROD>
F:164-198/Region: coil 1A
F:199-210/Region: linker 1
F:211-311/Region: coil 1B
F:312-328/Region: linker 12
F:329-347/Region: coil 2A
F:348-355/Region: linker 2
F:356-476/Region: coil 2B
F:414/Region: stutter
F:477-564/Domain: tail <END>
F:477-496/Region: H2 subdomain
F:497-564/Region: V2 and E2 subdomains

Query Match 100.0%; Score 43; DB 1; Length 564;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
DB 252 KYEDEINK 259

Db 252 KYEDEINK 259

RESULT 15

I61770
keratin 6e, type II - human
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: I61770
R:Takahashi, K.; Paladini, R.D.; Coulombe, P.A.
J. Biol. Chem. 270, 18581-18592, 1995
A:Title: Cloning and characterization of multiple human genes and cDNAs encoding highly
A:Reference number: A57398; MUID:95355491; PMID:7543104
A:Accession: I61770
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-564 <RES>
A:Cross-references: UNIPROT:P48668; UNIPARC:UPI0000167E31; GB:L42611; NID:g908802; PIDN:
C:Genetics:
A:Gene: KRT6E
A:Note: this may not be a distinct gene
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil
Query Match 100.0%; Score 43; DB 2; Length 564;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
DB 252 KYEDEINK 259

Search completed: July 5, 2006, 19:20:29
Job time: 9.70874 secs

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GenCore version 5.1.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 18:28:56 ; Search time 81.8641 Seconds
(without alignments)
90.395 Million cell updates/sec

Title: US-10-774-928A-12
Perfect score: 43
Sequence: 1 KYEDEINK 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 7.2.*
1: uniprot_prot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	43	100.0	176	2	Q4J123 ICTPU	Q4J123 ictalurus p
2	43	100.0	222	2	Q4L0E7 MOUSE	Q4L0E7 mus musculus
3	43	100.0	224	2	Q678L1 MOUSE	Q678L1 mus musculus
4	43	100.0	310	2	Q28810 POTTR	Q28810 pottorus tr
5	43	100.0	324	2	Q80VP7 MOUSE	Q80VP7 mus musculus
6	43	100.0	346	2	Q4QV72 SPAAU	Q4QV72 sparus aura
7	43	100.0	365	2	Q96910 HUMAN	Q96910 homo sapien
8	43	100.0	384	1	K2C6D HUMAN	P48667 homo sapien
9	43	100.0	417	2	Q4SRP0 TETNG	Q4SRP0 tetraodon n
10	43	100.0	419	1	K2C2 XENLA	P04265 xenopus lae
11	43	100.0	425	1	K2C1 XENLA	P04266 xenopus lae
12	43	100.0	461	2	Q42435 NOTVI	Q42435 notophthalm
13	43	100.0	482	1	K2C8 HUMAN	P05787 homo sapien
14	43	100.0	482	1	K2C8 RAT	Q10758 rattus norv
15	43	100.0	483	2	Q53GJ0 HUMAN	Q53GJ0 homo sapien
16	43	100.0	483	2	Q6DHW5 HUMAN	Q6DHW5 homo sapien
17	43	100.0	483	2	Q6GMY0 HUMAN	Q6GMY0 homo sapien
18	43	100.0	483	2	Q5RB34 PONY	Q5RB34 pongo pygma
19	43	100.0	483	2	Q80WH8 MURI	Q80WH8 rattus sp.
20	43	100.0	486	2	Q9YH07 9CHON	Q9YH07 scyllorhinu
21	43	100.0	487	2	Q61518 MOUSE	Q61518 mus musculus
22	43	100.0	487	2	Q7SYF6 ACIBE	Q7SYF6 acipenser b
23	43	100.0	490	2	Q3KOK5 MOUSE	Q3KOK5 mus musculus
24	43	100.0	490	2	Q3TGI1 MOUSE	Q3TGI1 mus musculus
25	43	100.0	490	2	Q3TJE1 MOUSE	Q3TJE1 mus musculus
26	43	100.0	490	2	Q3TKI7 MOUSE	Q3TKI7 m blascocys
27	43	100.0	490	2	Q61463 MOUSE	Q61463 gallus gall
28	43	100.0	492	1	K2CO CHICK	Q93532 gallus gall
29	43	100.0	496	2	Q42434 NOTVI	Q42434 notophthalm
30	43	100.0	497	2	Q5K2N3 PROAT	Q5K2N3 protopteris
31	43	100.0	497	2	Q6NVE60 BRARE	Q6NVE60 brachydanio

32	43	100.0	498	2	Q9PV92 BRARE	Q9PV92 brachydanio
33	43	100.0	499	2	Q9H552 HUMAN	Q9H552 homo sapien
34	43	100.0	499	2	Q7ZT78 BRARE	Q7ZT78 brachydanio
35	43	100.0	505	2	Q6P4C7 HUMAN	Q6P4C7 homo sapien
36	43	100.0	508	2	Q6NVR6 XENTR	Q6NVR6 xenopus tro
37	43	100.0	511	2	Q90ZF7 RANCA	Q90ZF7 rana cateab
38	43	100.0	512	1	K2C5 XENLA	P16878 xenopus lae
39	43	100.0	515	2	Q8JFG4 ONCMY	Q8JFG4 oncorhynch
40	43	100.0	519	1	K2C1B RAT	Q61901 rattus norv
41	43	100.0	520	1	ION3 CARAU	P18520 carassius a
42	43	100.0	520	2	Q6NWF6 BRARE	Q6NWF6 brachydanio
43	43	100.0	521	2	Q5K2N4 PROAT	Q5K2N4 protopteris
44	43	100.0	521	2	Q5K2N5 PROAT	Q5K2N5 protopteris
45	43	100.0	529	2	Q919P5 RANCA	Q919P5 rana cateab

ALIGNMENTS

RESULT 1
Q4J123 ICTPU
ID Q4J123 ICTPU PRELIMINARY; PRT; 176 AA.
AC Q4J123;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Keratin 8 (Fragment).
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yeh H.-Y., Klesius P.H.;
RT "Differential gene expression of Ictalurus punctatus after
Edwardsiella ictaluri infection";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
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EMBL; DQ086174; AAY86957.1; -; mRNA.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002957; Keratin I.
DR InterPro; IPR003054; Keratin II.
DR PANTHER; PTHR18893:SP5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
DR Keratin.
KW KERATIN.
FT NON_TER 176 176
FT NON_TER 176 176
SQ SEQUENCE 176 AA; 20651 MW; 8EE3A88097529C33 CRC64;

Query Match 100.0%; Score 43; DB 2; Length 176;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
Db 69 KYEDEINK 76

RESULT 2
Q4L0E7 MOUSE
ID Q4L0E7 MOUSE PRELIMINARY; PRT; 222 AA.
AC Q4L0E7;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Type II cyokeratin Kb39 (Fragment).

```
GN Name=4732484G22Rik;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NMRI; TISSUE=Tail skin;
RA Zimek A.; Hesse M.;
RT "Cornea-specific cytochrome K3 seems to be absent in the rodent
lineage.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY651826; AAV85505.1; -; mRNA.
DR MGI; MGI:3588209; 4732484G22Rik.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002957; Keratin_1.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
KW Keratin.
FT NON_TER 1 222
FT NON_TER 222
SQ SEQUENCE 224 AA; 25801 MW; 483B4F589032C1D1 CRC64;

Query Match 100.0%; Score 43; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYDEINK 8
Db 69 KYDEINK 76

RESULT 3
Q578L1_MOUSE
ID Q678L1_MOUSE PRELIMINARY; PRT; 224 AA.
AC Q678L1.
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Keratin 1b (Fragment).
GN Name=4732484G22Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NMRI; TISSUE=Tail skin;
RA Zimek A.; Hesse M.; Magin T.; Weber K.;
RT "Homologies between the human, mouse and rat keratin-clusters.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; AY379112; AAR3930.1; -; mRNA.
DR Ensembl; ENSMUSG0000067594; Mus musculus.
DR MGI; MGI:3588209; 4732484G22Rik.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR InterPro; IPR003054; Keratin_II.

Query Match 100.0%; Score 43; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYDEINK 8
Db 69 KYDEINK 76

RESULT 4
Q28810_POTTR
ID Q28810_POTTR PRELIMINARY; PRT; 310 AA.
AC Q28810.
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 27.
DE Keratin 8 (Fragment).
OS Porcous tridactylus (Potoroo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Potoroidae; Potorous.
OX NCBI_TaxID=9310;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94118290; PubMed=7507169;
RA Boettger V.; Lane E.B.;
RT "A monoclonal antibody Epitope on Keratin 8 identified using a phage
peptide library.";
RL J. Mol. Biol. 235:61-67(1994).
CC -----
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CC -----
DR EMBL; X70987; CAA50316.1; -; mRNA.
DR PIR; S43865; S43865.
DR HSSP; P08670; 1GK7.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
KW Keratin.
FT NON_TER 1 310
FT NON_TER 310
SQ SEQUENCE 310 AA; 35170 MW; 31D37E0BC63BFA85 CRC64;

Query Match 100.0%; Score 43; DB 2; Length 310;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYDEINK 8
Db 179 KYDEINK 186

RESULT 5
Q80VP7_MOUSE
ID Q80VP7_MOUSE PRELIMINARY; PRT; 324 AA.
AC Q80VP7.
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
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DT 07-FEB-2006, entry version 20.
 DE Hypothetical protein MGC54654.
 GN Name=MGC54654;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Eye;
 RG NIH MGC Project;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL; BC046626; AAH46626.1; -; mRNA.
 DR HSSP; P08670; 1GK7.
 DR Ensembl; ENSMUSG00000046162; Mus musculus.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR001664; IF.
 DR PANTHER; PTHR18893:SF5; Keratin_II; 1.
 DR Pfam; PF00038; Filament; 1.
 DR PRINTS; PR01276; TYPE2KERATIN.
 DR PROSITE; PS00226; IF; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 324 AA; 35165 MW; 0E4D7E2514435DD CRC64;

 Query Match 100.0%; Score 43; DB 2; Length 324;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 KYEDEINK 8
 DB 202 KYEDEINK 209

 RESULT 6
 Q4QY72 SPAAU PRELIMINARY; PRT; 346 AA.
 ID Q4QY72
 AC Q4QY72
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DE Type II keratin E3-like protein.
 OS Sparus aurata (Gilthead sea bream).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
 OC Sparidae; Sparus.
 OX NCBI_TaxID=8175;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sarrapoulou E., Power D.M., Magoulas A., Geisler R., Kotoulas G.;
 RT "Comparative analysis and characterization of expressed sequence tags
 in gilthead sea bream (Sparus aurata) liver and embryos.";
 RL Aquaculture 243:69-81 (2005).
 CC -!- SIMILARITY: Belongs to the intermediate filament family.
 CC -----
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 CC -----
 CC EMBL; AY550955; AAT44423.1; -; mRNA.
 DR GO; GO:0005882; C:intermediate filament; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR001664; IF.
 DR InterPro; IPR002957; Keratin_I.
 DR PANTHER; PTHR18893:SF5; Keratin_II; 1.
 DR Pfam; PF00038; Filament; 1.
 DR PRINTS; PR01248; TYPE1KERATIN.
 DR PRINTS; PR01276; TYPE2KERATIN.
 DR PROSITE; PS00226; IF; 1.
 KW Intermediate filament; Keratin.
 SQ SEQUENCE 346 AA; 38624 MW; 75468AFEC8048F5 CRC64;

 Query Match 100.0%; Score 43; DB 2; Length 346;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 KYEDEINK 8
 DB 61 KYEDEINK 68

 RESULT 7
 Q96910 HUMAN PRELIMINARY; PRT; 365 AA.
 ID Q96910
 AC Q96910;
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 24-MAY-2005, sequence version 2.
 DE 07-FEB-2006, entry version 23.
 DE KRT8 protein (fragment).
 GN Name=KRT8;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human

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RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RC NUCLEOTIDE SEQUENCE.
RP TISSUE=Placenta;
RG NIH MGC Project;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC
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CC -----
CC EMBL; BC011373; AAH11373.2; -; mRNA.
DR Ensembl; ENSG00000170421; Homo sapiens.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005199; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin I.
DR InterPro; IPR003054; Keratin II.
DR PANTHER; PTHR18893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament.
FT NON TER 1
FT SEQUENCE 365 AA; 41108 MW; 57CD83091D0635E8 CRC64;
SQ
Query Match 100.0%; Score 43; DB 2; Length 365;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KYDEINK 8
DB 60 KYDEINK 67
RESULT 8
K2C6D HUMAN
ID K2C6D HUMAN STANDARD; PRT; 384 AA.
AC P48667;
DT 01-FEB-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-FEB-1996, sequence version 1.
DT 07-FEB-2006, entry version 44.
DE Keratin, type II cytoskeletal 6D (Cytokeratin-6D) (CK 6D) (K6d
DE keratin) (Fragment).
GN Name=KRT6D;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC TISSUE=Skin;
RA Takahashi K., Paladini R.D., Coulombe P.A.;
RA "Cloning and characterization of multiple human genes and cDNAs
RT encoding highly related type II keratin 6 isoforms.";
RL J. Biol. Chem. 270:18581-18592 (1995).
CC -!- FUNCTION: There are two types of cytoskeletal and microfibrillar
CC keratin: I (acidic; 40-55 kDa) [K9 to K20] and II (neutral to
CC basic; 56-70 kDa) [K1 to K8]. Both a basic and an acidic keratin
CC are required for filament assembly.
CC -!- SUBUNIT: Heterodimer of a type I and a type II keratin. KRT6
CC isomers associate with KRT16 and/or KRT17.
CC -!- TISSUE SPECIFICITY: Constitutively expressed in distinct types of
CC epithelia such as those in oral mucosa, esophagus, papillae of
CC tongue and hair follicle outer root sheath.
CC -!- MISCELLANEOUS: There are at least six isoforms of human type II
CC keratin 6 (K6).
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----

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CC -----
CC EMBL; L42610; AAB60696.1; -; Genomic DNA.
DR EMBL; L42603; AAB60696.1; JOINED; Genomic DNA.
DR EMBL; L42604; AAB60696.1; JOINED; Genomic DNA.
DR EMBL; L42605; AAB60696.1; JOINED; Genomic DNA.
DR EMBL; L42606; AAB60696.1; JOINED; Genomic DNA.
DR EMBL; L42607; AAB60696.1; JOINED; Genomic DNA.
DR EMBL; L42608; AAB60696.1; JOINED; Genomic DNA.
DR EMBL; L42609; AAB60696.1; JOINED; Genomic DNA.
DR PIR; I61769; I61769.
DR HSSP; P08670; IGK4.
DR Ensembl; ENSG00000170465; Homo sapiens.
DR HGNC; HGNC:20405; KRT6D.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; NAS.
DR GO; GO:0030154; P:cell differentiation; NAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; NAS.
DR InterPro; IPR001664; IF.
DR InterPro; IPR003054; Keratin II.
DR PANTHER; PTHR18893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Coiled coil; Intermediate filament; Keratin.
FT CHAIN <1 384
FT SEQUENCE 384 AA; 42468 MW; D69DCFD808C94E91 CRC64;
SQ
Query Match 100.0%; Score 43; DB 1; Length 384;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KYDEINK 8
DB 72 KYDEINK 79
RESULT 9
Q4SRP0 TETNG
ID Q4SRP0 TETNG PRELIMINARY; PRT; 417 AA.
AC Q4SRP0;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Chromosome undetermined SCAF14505, whole genome shotgun sequence.
OS ORFNames=GSTENG0013817001;
GN Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1549614; DOI=10.1038/nature03025;
RA Jallou O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Luttalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anhouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Bismont C., Skalli Z., Cattolico L., Poulain J., De Bernardis V.,
RA Craud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Farra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

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RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissenbach J., Roest Crolius H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RL the early vertebrate proto-karyotype."
 RN Nature 431:946-957(2004).
 RP [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -!- SIMILARITY: Belongs to the intermediate filament family.
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 CC -----
 CC EMBL: CRAE01014505; CAF96692.1; -; Genomic DNA.
 DR GO: GO:0005882; C:intermediate filament; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR InterPro: IPR001664; IF.
 DR InterPro: IPR003054; Keratin II.
 DR PANTHER: PTHR18893.SF5; Keratin_II; 1.
 DR Pfam: PF00038; Filament; 1.
 DR PRINTS: PR01276; TYPE2KERATIN.
 DR PROSITE: PS00226; IF; 1.
 DR Intermediate filament.
 KW Intermedate filament.
 SQ SEQUENCE 419 AA; 46557 MW; B2F4D4E29E625589 CRC64;

Query Match 100.0%; Score 43; DB 2; Length 417;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
 |||||
 Db 221 KYEDEINK 228

RESULT 10
 K2C2 XENLA
 ID K2C2 XENLA STANDARD; PRT; 419 AA.
 AC P04255;
 DT 20-MAR-1987, integrated into UniProtKB/Swiss-Prot.
 DT 07-FEB-2006, entry version 39.
 DE Keratin, type II cytoskeletal I (Clone PUF164) (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=86011576; PubMed=2413219;
 RA Hoffmann W., Franz J.K., Franke W.W.;
 RT "Amino acid sequence microheterogeneities of basic (type II)
 RT cytokeratins of Xenopus laevis epidermis and evolutionary
 RT conservativity of helical and non-helical domains."
 RL J. Mol. Biol. 184:713-724(1985).
 CC -!- SUBUNIT: Heterotrimer of two type I and two type II keratins.
 CC -!- MISCELLANEOUS: There are two types of cytoskeletal and
 CC microfibrillar keratin, I (acidic) and II (neutral to basic) (40-
 CC 55 and 56-70 kilodaltons, respectively).
 CC -!- SIMILARITY: Belongs to the intermediate filament family.
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 CC -----
 CC EMBL: X02895; CAA26654.1; -; mRNA.
 DR PIR: A02952; KRXL2B.
 DR HSSP: P08670; 1GK4.

DR InterPro: IPR001664; IF.
 DR InterPro: IPR003054; Keratin II.
 DR PANTHER: PTHR18893.SF5; Keratin_II; 1.
 DR Pfam: PF00038; Filament; 1.
 DR PRINTS: PR01276; TYPE2KERATIN.
 DR PROSITE: PS00226; IF; 1.
 KW Coiled coil; Intermediate filament; Keratin.
 FT CHAIN <1 419
 FT Keratin, type II cytoskeletal I.
 FT /FTID=PRO_0000063719.
 FT REGION <1 271
 FT Rod.
 FT REGION <1 16
 FT Linker 1.
 FT REGION 17 108
 FT Coiled coil 1B.
 FT REGION 109 132
 FT Linker 12.
 FT REGION 133 271
 FT Coiled coil 2.
 FT REGION 272 419
 FT Tail.
 FT SITE 215 215
 FT Stutter.
 FT NON TER 1 1
 SQ SEQUENCE 419 AA; 44595 MW; 15D79584FC31DF15 CRC64;

Query Match 100.0%; Score 43; DB 1; Length 419;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
 |||||
 Db 51 KYEDEINK 58

RESULT 11
 K2C1 XENLA
 ID K2C1 XENLA STANDARD; PRT; 425 AA.
 AC P04266;
 DT 20-MAR-1987, integrated into UniProtKB/Swiss-Prot.
 DT 20-MAR-1987, sequence version 1.
 DT 07-FEB-2006, entry version 39.
 DE Keratin, type II cytoskeletal I (Clone PUF23) (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=86011576; PubMed=2413219;
 RA Hoffmann W., Franz J.K., Franke W.W.;
 RT "Amino acid sequence microheterogeneities of basic (type II)
 RT cytokeratins of Xenopus laevis epidermis and evolutionary
 RT conservativity of helical and non-helical domains."
 RL J. Mol. Biol. 184:713-724(1985).
 CC -!- SUBUNIT: Heterotrimer of two type I and two type II keratins.
 CC -!- MISCELLANEOUS: There are two types of cytoskeletal and
 CC microfibrillar keratin, I (acidic) and II (neutral to basic) (40-
 CC 55 and 56-70 kilodaltons, respectively).
 CC -!- SIMILARITY: Belongs to the intermediate filament family.
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 CC -----
 CC EMBL: X02894; CAA26653.1; -; mRNA.
 DR PIR: A02953; KRXL2A.
 DR HSSP: P08670; 1GK4.
 DR InterPro: IPR001664; IF.
 DR InterPro: IPR002957; Keratin I.
 DR InterPro: IPR003054; Keratin II.
 DR PANTHER: PTHR18893.SF5; Keratin_II; 1.
 DR Pfam: PF00038; Filament; 1.
 DR PRINTS: PR01248; TYPE1KERATIN.
 DR PRINTS: PR01276; TYPE2KERATIN.
 DR PROSITE: PS00226; IF; 1.
 KW Coiled coil; Intermediate filament; Keratin.
 FT CHAIN <1 425
 FT Keratin, type II cytoskeletal I.
 FT /FTID=PRO_0000063718.
 FT REGION <1 292
 FT Rod.

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FT REGION <1 16 Coil 1A.
FT REGION 17 37 Linker 1.
FT REGION 38 129 Coil 1B.
FT REGION 130 153 Linker 12.
FT REGION 154 292 Coil 2.
FT REGION 293 425 Tail.
FT SITE 236 236 Stutter.
FT NON TER 1
SQ SEQUENCE 425 AA; 45725 MW; D58D15DEC8C1C4E3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 1; Length 425;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
DB 72 KYEDEINK 79

RESULT 12
ID O42435 NOTVI PRELIMINARY; PRT; 461 AA.
AC O42435;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 27.
DE Cytokeratin type II (Fragment).
GN Name=KII;
OS Notoththalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidae; Salamandridae;
OC Notoththalmus.
OX NCBI_TaxID=8316;
RN [1]_TaxID=8316;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Limb blastema;
RX MEDLINE=91372147; PubMed=1716554;
RA Ferretti P., Brookes J.P., Brown R.;
RT "A new type II keratin restricted to normal and regenerating limbs
and tails is responsive to retinoic acid.";
RL Development 111:497-507(1991).
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Limb blastema;
RA Ferretti P.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; AJ001295; CAA04655.1; -; mRNA.
DR PIR; A43782; A43782.
DR HSSP; P08670; 1GK7.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR003054; Keratin II.
DR PANTHER; PTHR18993:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
FT NON TER 1
SQ SEQUENCE 461 AA; 50638 MW; F3A018A7C10CA0FD CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 2; Length 461;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
DB 133 KYEDEINK 140

RESULT 13
K2C8 HUMAN
ID K2C8 HUMAN STANDARD; PRT; 482 AA.
AC P05787; Q14099; Q14716; Q14717; Q96J60;
DT 01-NOV-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997, sequence version 5.
DT 07-FEB-2006, entry version 72.
DE Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keraton-8) (K8).
GN Name=KRT8; Synonyms=CYK8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]_
RP NUCLEOTIDE SEQUENCE OF 1-230.
RX MEDLINE=89261783; PubMed=2471065;
RA Kulsh D.A., Cecena G., Darmon Y.M., Vasseur M., Oshima R.G.;
```

RT "Posttranslational regulation of keratins: degradation of mouse and
human keratins 18 and 8.";
Mol. Cell. Biol. 9:1553-1565 (1989).
[7]
RN NUCLEOTIDE SEQUENCE OF 204-482.
RP MEDLINE=87134779; PubMed=2434381;
RA Leube R.E., Bosch F.X., Romano V., Zimbelmann R., Hofer H.,
RA Franke W.W.;
RT "Cyokeratin expression in simple epithelia. III. Detection of mRNAs
encoding human cyokeratins nos. 8 and 18 in normal and tumor cells by
hybridization with cDNA sequences in vitro and in situ.";
Differentiation 33:69-85 (1986).
[8]
RN PARTIAL PROTEIN SEQUENCE.
RP TISSUE=Colon carcinoma;
RX MEDLINE=97295306; PubMed=9150948;
RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
RT "A two-dimensional gel database of human colon carcinoma proteins.";
Electrophoresis 18:605-613 (1997).
[9]
RN INTERACTION WITH PNN.
RP PubMed=10809736; DOI=10.1074/jbc.275.20.14910;
RA Shi J., Sugrue S.P.;
RT "Dissection of protein linkage between keratins and pinin, a protein
with dual location at desmosome-intermediate filament complex and in
the nucleus.";
J. Biol. Chem. 275:14910-14915 (2000).
[10]
RN PHOSPHORYLATION SITE SER-73.
RX MEDLINE=21909496; PubMed=11781324; DOI=10.1074/jbc.M111436200;
RA He T., Stepulak A., Holmstrom T.H., Omari M.B., Eriksson J.E.;
RT "The intermediate filament protein keratin 8 is a novel cytoplasmic
substrate for c-Jun N-terminal kinase.";
J. Biol. Chem. 277:10767-10774 (2002).
[11]
RN PHOSPHORYLATION SITE SER-73, AND MUTAGENESIS OF LEU-71 AND SER-73.
RX MEDLINE=21909510; PubMed=11788593; DOI=10.1074/jbc.M107623200;
RA Ku N.O., Azhar S., Omari M.B.;
RT "Keratin 8 phosphorylation by p38 kinase regulates cellular keratin
filament reorganization: modulation by a keratin 1-like disease
causing mutation.";
J. Biol. Chem. 277:10775-10782 (2002).
[12]
RN INTERACTION WITH HCV CORE PROTEIN.
RX PubMed=15846844; DOI=10.1002/pmhc.200401093;
RA Kang S.-M., Shin M.-J., Kim J.-H., Oh J.-W.;
RT "Proteomic profiling of cellular proteins interacting with the
hepatitis C virus core protein.";
Proteomics 5:2227-2237 (2005).
[13]
RN VARIANTS CRYPTOGENIC CIRRHOSIS VAL-52; CYS-53 AND CYS-61, AND VARIANT
VAL-62.
RX PubMed=12724528; DOI=10.1073/pnas.0936165100;
RA Ku N.-O., Darling J.M., Krams S.M., Esquivel C.O., Keefe E.B.,
RA Sibley R.K., Lee Y.M., Wright T.L., Omari M.B.;
RT "Keratin 8 and 18 mutations are risk factors for developing liver
disease of multiple etiologies.";
Proc. Natl. Acad. Sci. U.S.A. 100:6063-6068 (2003).
CC -!- SUBUNIT: Heterotrimer of two type I and two type II keratins.
CC Keratin 8 associates with keratin 18. Interacts with HCV core
protein and PNN.
CC -!- PTM: Phosphorylation on serine residues is enhanced during EGF
stimulation and mitosis. Ser-73 phosphorylation plays an important
role in keratin filament reorganization.
CC -!- DISEASE: Defects in KRT8 are a cause of cryptogenic cirrhosis
[MIM:215600].
CC -!- MISCELLANEOUS: There are two types of cytoskeletal and
microfibrillar keratin: I (acidic; 40-55 kDa) [K9 to K20] and II
(neutral to basic; 56-70 kDa) [K1 to K8].
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -!- DATABASE: NAME=Human Intermediate Filament Mutation Database;
WWW="http://www.interfil.org".

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
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CC EMBL: M34225; AAA35748.1; -; mRNA.
CC EMBL: M34482; AAA35763.1; -; Genomic_DNA.
CC EMBL: X74929; CAAS2882.1; -; mRNA.
CC EMBL: U76549; AAB18966.1; -; mRNA.
CC EMBL: X98614; CAAS67203.1; -; mRNA.
CC EMBL: M26512; AAA51542.1; -; mRNA.
CC EMBL: BC000654; AAH00654.2; ALT INIT; mRNA.
CC EMBL: X12882; CAA31376.1; -; mRNA.
CC EMBL: X74981; CAAS2916.1; -; Genomic_DNA.
CC PIR: A34720; A34720.
CC HSSP: P08670; IGK7.
CC IntAct: P05787; -.
CC GlycoSuiteDB: P05787; -.
CC SWISS-2DPAGE: P05787; HUMAN.
CC Siens-2DPAGE: P05787; -.
CC Ensembl: ENSG00000170421; Homo sapiens.
CC HGNC: HGNC:6446; KRT8.
CC MIM: 148060; Gene.
CC LinkHub: P05787; -.
CC GO: GO:0005882; C:intermediate filament; NAS.
CC GO: GO:0003198; F:structural molecule activity; NAS.
CC GO: GO:0007010; P:cytoskeleton organization and biogenesis; NAS.
CC InterPro: IPR001664; IF.
CC InterPro: IPR002957; Keratin I.
CC InterPro: PTHR18893; Keratin II.
CC Pfam: PF00038; Filament; 1.
CC PRINTS: PR01248; TYPE1KERATIN.
CC PRINTS: PR01276; TYPE2KERATIN.
CC PROSITE: PS00226; IF; 1.
CC Coiled coil; Direct protein sequencing; Disease mutation;
KW Intermediate filament; Keratin; Phosphorylation; Polymorphism.
FT INIT_MET 0 0
FT CHAIN 1 482 Keratin, type II cytoskeletal 8.
FT REGION 1 89 /FTID=PRO_0000063740.
FT REGION 90 397 Head.
FT REGION 90 125 Rod.
FT REGION 126 142 Coiled coil 1A.
FT REGION 143 234 Linker 1.
FT REGION 235 258 Coiled coil 1B.
FT REGION 259 397 Linker 12.
FT REGION 260 381 Coiled coil 2.
FT REGION 398 482 Necessary for interaction with PNN.
FT SITE 341 341 Tail.
FT MOD_RES 23 23 Stutter.
FT MOD_RES 73 73 Phosphoserine.
FT MOD_RES 431 431 Phosphoserine (by MAPK).
FT VARIANT 52 52 Phosphoserine (by CAMK2 and MAPK).
FT VARIANT 53 53 G -> V (in cryptogenic cirrhosis).
FT VARIANT 61 61 /FTID=VAR_023058.
FT Y -> C (in cryptogenic cirrhosis).
FT G -> C (in cryptogenic cirrhosis).
FT /FTID=VAR_023059.
FT /FTID=VAR_023060.
Query Match 100.0%; Score 43; DB 1; Length 482;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KYEIDEINK 8
Db 177 KYEIDEINK 184
RESULT 14
ID K2C8 RAT STANDARD; PRT; 482 AA.
AC Q10758; Q5WBP3;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.

RL Gene 200:149-156(1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Suzuki Y., Sugano S., Toroki Y., Toyoda A., Takeda T., Sakaki Y.,
RA Tanaka A., Yokoyama S.,
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----
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CC -----
DR EMBL; AK222941; BAD96661.1; -; mRNA.
DR Ensembl; ENSG00000170421; Homo sapiens.
DR GO; GO:0005982; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR InterPro; IPR003054; Keratin_II.
DR PANTHER; PTHR1893:SF5; Keratin_II; 1.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
FT NON TER 1
SQ SEQUENCE 483 AA; 53738 MW; D4F01FEB859C3D3 CRC64;

Query Match 100.0%; Score 43; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. NO. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
Db |||||
178 KYEDEINK 185

Search completed: July 5, 2006, 19:01:32
Job time : 83.9641 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 18:28:26 ; Search time 69.5146 Seconds
(without alignments)
52.618 Million cell updates/sec

Title: US-10-774-928A-12
Perfect score: 43
Sequence: 1 KYEDELNK 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 8 : *
1: geneseqp1980s : *
2: geneseqp1990s : *
3: geneseqp2000s : *
4: geneseqp2001s : *
5: geneseqp2002s : *
6: geneseqp2003as : *
7: geneseqp2003bs : *
8: geneseqp2004s : *
9: geneseqp2005s : *
10: geneseqp2006s : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	8	6	Aao26392 Psoriasis
2	43	100.0	8	9	Adv04417 Leishman
3	43	100.0	113	6	Abg74871 Human cyt
4	43	100.0	132	8	Adr98929 Lung spec
5	43	100.0	180	8	Adn99441 Novel hum
6	43	100.0	186	4	Aam16318 Peptide #
7	43	100.0	186	4	Abb35310 Peptide #
8	43	100.0	186	4	Aam28813 Peptide #
9	43	100.0	186	4	Abb30140 Peptide #
10	43	100.0	186	4	Abb20752 Protein #
11	43	100.0	186	4	Aam68514 Human bon
12	43	100.0	186	4	Aam56141 Human bra
13	43	100.0	186	4	Abg50183 Human liv
14	43	100.0	186	4	Aam04056 Peptide #
15	43	100.0	186	4	Abg09410 Novel hum
16	43	100.0	186	5	Abg38095 Human pep
17	43	100.0	233	8	Adr98930 Lung spec
18	43	100.0	273	4	Abg26376 Novel hum
19	43	100.0	275	4	Abg15282 Novel hum
20	43	100.0	278	8	Abm81219 Tumour-as
21	43	100.0	282	8	Abm80614 Tumour-as
22	43	100.0	342	7	Adel15641 Human str
23	43	100.0	347	4	Abg15636 Novel hum

24	43	100.0	347	4	ABG09411	Abg09411 Novel hum
25	43	100.0	394	4	ABG26375	Abg26375 Novel hum
26	43	100.0	398	6	AAE38086	Aae38086 Human cyt
27	43	100.0	401	8	ABM80365	Abm80365 Tumour-as
28	43	100.0	403	8	ABM81640	Abm81640 Tumour-as
29	43	100.0	420	8	ADP29879	Adp29879 Human sec
30	43	100.0	429	4	ABG19547	Abg19547 Novel hum
31	43	100.0	429	4	ABG19546	Abg19546 Novel hum
32	43	100.0	476	8	ADR66033	Adr66033 Human pro
33	43	100.0	476	8	ADR66931	Adr66931 Human pro
34	43	100.0	477	4	AAU06112	Aau06112 Novel hum
35	43	100.0	480	10	AEF92273	Aef92273 Human cyt
36	43	100.0	481	6	ABU52604	Abu52604 Human NOV
37	43	100.0	482	4	ABG08132	Abg08132 Novel hum
38	43	100.0	482	6	AAE38082	Aae38082 Human cyt
39	43	100.0	482	8	ADT51418	Adt51418 Human ker
40	43	100.0	482	8	ADT51421	Adt51421 Human ker
41	43	100.0	482	8	ADT51419	Adt51419 Human ker
42	43	100.0	482	8	ADT51422	Adt51422 Human ker
43	43	100.0	482	8	ADT51414	Adt51414 Human ker
44	43	100.0	482	8	ADT51420	Adt51420 Human ker
45	43	100.0	482	8	ADT51415	Adt51415 Human ker

ALIGNMENTS

RESULT 1
AAO26392
ID AAO26392 standard; peptide; 8 AA.
XX
AC AAO26392;
XX
DT 30-JAN-2003 (first entry)
XX
DE Psoriasis treating immunotherapeutic peptide, SEQ ID No 12.
XX
KW Antipsoriatic; immunostimulant; gene therapy; pharmaceutical composition;
KW vaccine; immunogenic variant; immunotherapeutic agent; psoriasis;
KW gene therapy.
XX
OS Leishmania sp.
XX
PN WO200274239-A2.
XX
PD 26-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006496.
XX
PR 16-MAR-2001; 2001US-00809003.
XX
PA (AKIV-) AKIVA LLC.
XX
PI O'daly JA;
XX
DR WPI; 2003-018763/01.
XX
PT New polypeptide and immunogenic variants comprising amino acid sequences
PT of particulate antigens, useful for the treatment and clinical remission
PT of psoriasis.
XX
PS Claim 1; Page 43; 56pp; English.
XX
CC The invention relates to a polypeptide comprising an isolated amino acid
CC sequence or immunogenic variants selected from any of 14 fully defined
CC sequences of 7-16 amino acids, given in the specification. The
CC immunotherapeutic agents and a pharmaceutical compositions comprising
CC polynucleotides and vectors of the invention are useful for the treatment
CC and clinical remission of psoriasis. The isolated nucleic acids are
CC useful as probes. The sequences of the invention can be used in the
CC treatment of disorders by gene therapy. This sequence represents one of
CC the 14 immunotherapeutic peptides of the invention

```
SQ Sequence 8 AA;
Query Match 100.0%; Score 43; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
   |||||
DB 1 KYEDEINK 8

RESULT 2
ADV04417
ID ADV04417 standard; peptide; 8 AA.
XX
AC ADV04417;
XX
DT 24-FEB-2005 (first entry)
XX
DE Leishmania immunotherapeutic peptide SEQ ID NO:12.
XX
KW T-lymphocyte; immunogenicity; antigen; antipsoriatic; immunostimulant;
KW psoriasis.
XX
OS Leishmania sp.
XX
PN US2004241168-A1.
XX
PD 02-DEC-2004.
XX
PF 09-FEB-2004; 2004US-00774928.
XX
PR 16-MAR-2001; 2001US-00809003.
PR 17-OCT-2003; 2003US-00687892.
XX
PA (ODAL/) ODALY J A.
XX
PI Odaly JA;
XX
DR WPI; 2005-011563/01.
XX
PT Inhibiting selectively T-cell rolling in human, by administering compound
PT interfering with cutaneous lymphocyte antigen-E selectin interaction and
PT leukocyte function associated antigen-1 interaction.
XX
PS Claim 18; SEQ ID NO 12; 21pp; English.
XX
CC The invention relates to a novel method for selectively inhibiting T-cell
CC rolling in a human host, comprising administering a compound that
CC selectively interferes with the cutaneous lymphocyte antigen (CLA)-E
CC selectin interaction and leukocyte function associated antigen (LFA)-
CC 1/intercellular adhesion molecule (ICAM) and very late antigen
CC (VLA)/vascular cell adhesion molecule (VCAM) interactions. The compound
CC includes an immunotherapeutic agent, which comprises a purified protein
CC extract that is isolated by diethylaminoethyl Sephadex chromatography of
CC a Nonidet P-40 insoluble particulate antigen fraction derived from
CC isolated killed cells of anastigotes from one or more species of the
CC Leishmania genus, where the particulate antigen fraction is solubilized
CC with 8M urea and 0.025 M Tris(hydroxymethyl)aminomethane pH 8.3 applied
CC to diethylaminoethyl Sephadex and is eluted with a solution comprising
CC 0.1 M sodium chloride, 8 M urea and 0.025 M
CC Tris(hydroxymethyl)aminomethane pH 8.3, and the purified protein extract
CC includes polypeptides having apparent molecular weights of 73, 80 and 82
CC kDa, after total reduction and alkylation. The species is L. amazonensis,
CC L. venezuelensis, L. brasiliensis and/or L. chagasi. A compound of the
CC invention has antipsoriatic and immunostimulant activity, and inhibits T-
CC cell rolling by interfering with CLA-E selectin interaction and LFA-
CC 1/ICAM and VLA/VCAM interactions. The method is useful for selectively
CC inhibiting T-cell rolling in a human host, and for treating psoriasis.
CC The present sequence represents a Leishmania peptide used in the
CC invention.
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 43; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
   |||||
DB 1 KYEDEINK 8

RESULT 3
ABG74871
ID ABG74871 standard; protein; 113 AA.
XX
AC ABG74871;
XX
DT 19-JUN-2003 (first entry)
XX
DE Human cytokeraatin-1 protein fragment.
XX
KW Cytokeratin-1; inflammation; infection; soluble; sepsis; veterinary;
KW sepsis-like systemic infection; human.
XX
OS Homo sapiens.
XX
PN WO2003002600-A1.
XX
PD 09-JAN-2003.
XX
PF 12-JUN-2002; 2002WO-EP006473.
XX
PR 27-JUN-2001; 2001DE-01030985.
XX
PA (BRAH-) BRAHMS AG.
XX
PI Bergmann A, Struck J, Uehlein M;
XX
DR WPI; 2003-201491/19.
XX
PT New use of soluble cytokeraatin-1 fragments from body fluid are tissue as
PT marker peptides or to provide therapeutics for the diagnosis, prognosis
PT and treatment of inflammatory disease and infection, including systemic
PT inflammation.
XX
PS Claim 4; Page 41; Slipp; German.
XX
CC This invention describes a novel use of soluble cytokeraatin-1 fragments
CC from body fluid or tissue as marker peptides for the detection, prognosis
CC and control of inflammation and infection or as a therapeutic target for
CC inflammation and infection. The invention also describes a method of
CC producing a soluble cytokeraatin-1 fragment in rich or pure form from a
CC human material rich in cytokeraatin-1 by enzymatically splitting the
CC cytokeraatin-1 with endoprotease to obtain the hydrolysis products and
CC purifying the resulting fragments. The novel cytokeraatin fragments are
CC useful for the differential diagnosis, early recognition and prognosis,
CC evaluation of severity of sepsis and heavy infection, particularly sepsis
CC -like systemic infection. The fragments are used in human and veterinary
CC therapy, particularly the fragment or it's specific antibody is used to
CC treat inflammatory disease or infection. This sequence represents the
CC human cytokeraatin-1 protein fragment described in the disclosure of the
CC invention
XX
SQ Sequence 113 AA;
Query Match 100.0%; Score 43; DB 6; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
   |||||
DB 84 KYEDEINK 91
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RESULT 4
ADR98929
ID ADR98929 standard; protein; 132 AA.
XX AC ADR98929;
XX DT 18-NOV-2004 (first entry)
XX DE Lung specific gene splice variant encoded protein #101.
XX KW cytostatic; gene therapy; vaccine; lung; diagnosis; cancer;
XX KW non-cancerous lung disease; lung tissue; antagonist; gene therapy;
XX KW transgenic animal; splice variant.
XX OS Homo sapiens.
XX PN WO2004074430-A2.
XX PD 02-SEP-2004.
XX PF 08-DEC-2003; 2003WO-US038896.
XX PR 06-DEC-2002; 2002US-0431307P.
XX PR 06-DEC-2002; 2002US-0431510P.
XX PR 06-DEC-2002; 2002US-0431516P.
XX PA (DIAD-) DIADEXUS INC.
XX PI Macina RA, Turner LR, Sun Y, Liu S;
XX WPI: 2004-635553/61.
XX N-PSDB; ADR98791.
XX PT New isolated human lung specific nucleic acid molecule, useful for
XX PT identifying, diagnosing, monitoring, staging, imaging and treating lung
XX PT cancer and non-cancerous diseases of the lung.
XX PS Claim 1; SEQ ID NO 214; 542pp; English.
XX CC The invention relates to a new isolated lung specific nucleic acid
XX CC molecule (1) comprising any of 113 fully defined nucleotide sequences
XX CC given in the specification, their encoded protein sequences, sequences
XX CC selectively hybridizing to the nucleotide sequences or a sequence having
XX CC at least 60% identity to the nucleotide sequences. The methods and
XX CC compositions of the present invention are useful for identifying,
XX CC diagnosing, monitoring, staging, imaging and treating lung cancer and non
XX CC -cancerous diseases of the lung. They are also used for identifying lung
XX CC tissue, monitoring and identifying and/or designing antagonists of the
XX CC polypeptide of the invention, gene therapy, production of transgenic
XX CC animals and production of engineered lung tissue for treatment and
XX CC research. Lung specific genes (LSGs) were identified by a systematic
XX CC analysis of gene expression data in the LIFESeq Gold database using the
XX CC data mining software package candidate lead automatic search program
XX CC (CLASP). Genes were grouped into gene bins where each bin is a cluster of
XX CC sequences grouped together where they share a common contig.
XX CC Differentially expressed tissue-specific genes were selected based on the
XX CC percentage level in the targeted tissue versus all the other tissues. The
XX CC expression levels for each gene in libraries of normal tissues or non-
XX CC tumour tissues from cancer patients were compared with the expression
XX CC levels in tissue libraries associated with tumour or disease. This
XX CC sequence represents a protein of the invention.
XX SQ Sequence 132 AA;
Query Match 100.0%; Score 43; DB 8; Length 132;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KYEIDEINK 8
DB 46 KYEIDEINK 53
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RESULT 5
ADR99441
ID ADR99441 standard; protein; 180 AA.
XX AC ADR99441;
XX DT 29-JUL-2004 (first entry)
XX DE Novel human protein sequence #257.
XX KW anti-inflammatory; dermatological; neuroprotective; immunomodulator;
XX KW antibacterial; virucide; antipsoriatic; cytostatic; gene therapy;
XX KW vaccine; inflammatory; CNS; immune disorder; cancer; psoriasis; diabetes;
XX KW early aging; hormonal imbalance; ischemic heart disease;
XX KW ulcerative colitis.
XX OS Homo sapiens.
XX PN WO2004038003-A2.
XX PD 06-MAY-2004.
XX PF 24-OCT-2003; 2003WO-US033947.
XX PR 25-OCT-2002; 2002US-0421061P.
XX PR 25-OCT-2002; 2002US-0421080P.
XX PR 25-OCT-2002; 2002US-0421552P.
XX PR 25-OCT-2002; 2002US-0421614P.
XX PR 30-OCT-2002; 2002US-0422177P.
XX PR 30-OCT-2002; 2002US-0422178P.
XX PR 15-NOV-2002; 2002US-0426355P.
XX PR 15-NOV-2002; 2002US-0426384P.
XX PR 15-NOV-2002; 2002US-0426394P.
XX PR 15-NOV-2002; 2002US-0426430P.
XX PR 15-NOV-2002; 2002US-0426916P.
XX PR 27-NOV-2002; 2002US-0429224P.
XX PR 27-NOV-2002; 2002US-0429275P.
XX PR 27-NOV-2002; 2002US-0429302P.
XX PR 27-NOV-2002; 2002US-0429326P.
XX PR 27-NOV-2002; 2002US-0429651P.
XX PR 04-DEC-2002; 2002US-0430645P.
XX PR 04-DEC-2002; 2002US-0430651P.
XX PR 04-DEC-2002; 2002US-0430657P.
XX PR 04-DEC-2002; 2002US-0430663P.
XX PR 04-DEC-2002; 2002US-0430668P.
XX PR 04-DEC-2002; 2002US-0430684P.
XX PR 05-DEC-2002; 2002US-0430937P.
XX PR 05-DEC-2002; 2002US-0430965P.
XX PR 05-DEC-2002; 2002US-0431458P.
XX PR 12-DEC-2002; 2002US-0433251P.
XX PR 12-DEC-2002; 2002US-0433500P.
XX PR 13-DEC-2002; 2002US-0433316P.
XX PR 13-DEC-2002; 2002US-0433318P.
XX PR 23-DEC-2002; 2002US-0436236P.
XX PR 03-JAN-2003; 2003US-0437914P.
XX PR 17-JAN-2003; 2003US-0440820P.
XX PR 17-JAN-2003; 2003US-0440821P.
XX PR 18-APR-2003; 2003US-0463700P.
XX PR 18-APR-2003; 2003US-0463708P.
XX PR 18-APR-2003; 2003US-0463716P.
XX PR 18-APR-2003; 2003US-0463732P.
XX PR 02-MAY-2003; 2003US-0467199P.
XX PR 02-MAY-2003; 2003US-0467201P.
XX PR 02-MAY-2003; 2003US-0467203P.
XX PR 02-MAY-2003; 2003US-0467230P.
XX PR 19-MAY-2003; 2003US-0471306P.
XX PR 19-MAY-2003; 2003US-0471336P.
XX PR 22-MAY-2003; 2003US-0471336P.
XX PR 22-MAY-2003; 2003US-0472420P.
XX PR 22-MAY-2003; 2003US-0472430P.
XX PR 09-JUN-2003; 2003US-0476609P.
XX PR 09-JUN-2003; 2003US-0476621P.
XX PR 09-JUN-2003; 2003US-0476632P.
XX PR 09-JUN-2003; 2003US-0476641P.
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PR	30-JUN-2000; 2000US-00608408.	
PR	03-AUG-2000; 2000US-00632366.	
PR	21-SEP-2000; 2000US-0234687P.	
PR	27-SEP-2000; 2000US-0236359P.	
PR	04-OCT-2000; 2000GB-00024263.	
XX	(MOLE-) MOLECULAR DYNAMICS INC.	
PA		
XX	Penn SG, Hanzel DK, Chen W, Rank DR;	
XX	WPI; 2001-488901/53.	
XX		
PT	Human genome-derived single exon nucleic acid probes useful for analyzing	
PT	gene expression in human cervical epithelial cells.	
XX		
PS	Claim 27; SEQ ID NO 21144; 487pp; English.	
XX		
CC	The present invention relates to human single exon nucleic acid probes	
CC	(SENPs; see AAI10069-AA128459). The present sequence is a peptide encoded	
CC	by one such probe. The SENPs are derived from human HeLa cells. The SENPs	
CC	can be used to produce a single exon microarray, which can be used for	
CC	measuring human gene expression in a sample derived from human cervical	
CC	epithelial cells. By measuring gene expression, the probes are therefore	
CC	useful in grading and/or staging of diseases of the cervix, notably	
CC	cervical cancer. Note: The sequence data for this patent did not form	
CC	part of the printed specification, but was obtained in electronic format	
CC	directly from WIPO at ftp.wipo.int/pub/published_pct_sequences	
XX		
XX	Sequence 186 AA;	
SQL		
	Query Match 100.0%; Score 43; DB 4; Length 186;	
	Best Local Similarity 100.0%; Pred. No. 4.6;	
	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
Qy	1 KYEDEINK 8	
Db	173 KYEDEINK 180	
RESULT 7		
ABB35310		
ID	ABB35310 standard; peptide; 186 AA.	
XX	ABB35310;	
XX		
DT	04-FEB-2002 (first entry)	
XX		
DE	Peptide #2816 encoded by human foetal liver single exon probe.	
XX	Human; foetal liver; gene expression; single exon nucleic acid probe.	
KW	Homo sapiens.	
OS		
XX	WO200157277-A2.	
PN		
XX	09-AUG-2001.	
PD		
XX		
XX	30-JAN-2001; 2001WO-US000659.	
XX		
PR	04-FEB-2000; 2000US-0180312P.	
PR	26-MAY-2000; 2000US-0207456P.	
PR	30-JUN-2000; 2000US-00608408.	
PR	03-AUG-2000; 2000US-00632366.	
PR	21-SEP-2000; 2000US-0234687P.	
PR	27-SEP-2000; 2000US-0236359P.	
PR	04-OCT-2000; 2000GB-00024263.	
XX		
PA	(MOLE-) MOLECULAR DYNAMICS INC.	
XX		
PI	Penn SG, Hanzel DK, Chen W, Rank DR;	
XX	WPI; 2001-483447/52.	
DR		
XX		

PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
PS Claim 27; SEQ ID NO 27945; 639pp + Sequence Listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 186 AA;

Query Match 100.0%; Score 43; DB 4; Length 186;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
Db 173 KYEDEINK 180

RESULT 8
AAM28813
ID AAM28813 standard; protein; 186 AA.
XX
AC AAM28813;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #2850 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488897/53.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488897/53.
XX
PF Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
PT
PS Claim 27; SEQ ID NO 29082; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP:
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
SQ Sequence 186 AA;

Query Match 100.0%; Score 43; DB 4; Length 186;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
Db 173 KYEDEINK 180

RESULT 8
AAM28813
ID AAM28813 standard; protein; 186 AA.
XX
AC AAM28813;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #2850 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488897/53.
XX
PF Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
PT
PS Claim 27; SEQ ID NO 29082; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP:
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
SQ Sequence 186 AA;

Query Match 100.0%; Score 43; DB 4; Length 186;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
Db 173 KYEDEINK 180

RESULT 9
ABB30140
ID ABB30140 standard; peptide; 186 AA.
XX
AC ABB30140;
XX
DT 01-FEB-2002 (first entry)
XX
DE Peptide #2791 encoded by breast cell single exon nucleic acid probe.
XX
KW Human; microarray; single exon probe; gene expression; breast; disease;
KW cancer.
XX
OS Homo sapiens.
XX
PN WO200157271-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000662.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-496933/54.
XX
PF New spatially-addressable set of single exon nucleic acid probes, useful
PT for measuring gene expression in sample derived from human breast,
PT comprises number of single exon nucleic acid probes.
XX
PS Claim 27; SEQ ID NO 13108; 327pp + Sequence Listing; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting the
CC probes with a collection of detectably labelled nucleic acids derived
CC from mRNA of human breast, and then measuring the label bound to each
CC probe of the microarray. The probes are useful for verifying the
CC expression of regions of genomic DNA predicted to encode proteins. They
CC are useful for gene discovery, and for determining predisposition and/or
CC prognosing breast disease. Gene expression analysis is useful for
CC assessing the toxicity of chemical agents on cells. The microarray of
CC this invention presents a far greater diversity of probes for measuring
CC gene expression, with far less bias than expressed sequence tag
CC microarrays. The method is suitable for rapid production of functional
CC information from genomic sequence. The present sequence is a peptide
CC encoded by a single exon nucleic acid probe of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 186 AA;

Query Match 100.0%; Score 43; DB 4; Length 186;

```
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYEDEINK 8
Db 173 KYEDEINK 180

RESULT 10
ABB20752
ID ABB20752 standard; protein; 186 AA.
XX AC ABB20752;
XX DT 23-JAN-2002 (first entry)
XX DE Protein #2751 encoded by probe for measuring heart cell gene expression.
XX KW Human; gene expression; heart; microarray; vascular system;
XX KW cardiovascular disease; hypertension; cardiac arrhythmia;
XX KW congenital heart disease.
XX OS Homo sapiens.
XX PN WO200157274-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000666.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488999/53.
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX PT hearts.
XX PS Claim 15; SEQ ID NO 22522; 530pp; English.
XX CC The present invention relates to single exon nucleic acid probes for
XX CC measuring human gene expression in a sample derived from human heart (see
XX CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
XX CC probe. The probes may be used for predicting, measuring and displaying
XX CC gene expression in samples derived from the human heart via microarrays.
XX CC By measuring gene expression, the probes are useful for predicting,
XX CC diagnosing, grading, staging, monitoring and prognosing diseases of the
XX CC human heart and vascular system e.g. cardiovascular disease,
XX CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
XX CC sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 186 AA;

Query Match 100.0%; Score 43; DB 4; Length 186;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYEDEINK 8
Db 173 KYEDEINK 180
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RESULT 11
AAM68514
ID AAM68514 standard; protein; 186 AA.
XX AC AAM68514;
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28820.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000668.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488999/53.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human bone marrow.
XX PS Example 4; SEQ ID NO 28820; 658pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC bone marrow. They can be used to measure gene expression in bone marrow
XX CC samples, which may enable the improved diagnosis and treatment of cancers
XX CC such as lymphoma, leukaemia and myeloma. The present sequence is a
XX CC protein encoded by one of the probes of the invention
XX SQ Sequence 186 AA;

Query Match 100.0%; Score 43; DB 4; Length 186;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYEDEINK 8
Db 173 KYEDEINK 180

RESULT 12
AAM56141
ID AAM56141 standard; protein; 186 AA.
XX AC AAM56141;
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe encoded protein SEQ ID NO: 28246.
XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;
XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX OS Homo sapiens.
```

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PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
XX Example 4; SEQ ID NO 28246; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is a protein encoded by one of
XX the probes of the invention
XX
XX SQ Sequence 186 AA;
XX
XX Query Match 100.0%; Score 43; DB 4; Length 186;
XX Best Local Similarity 100.0%; Pred. No. 4.6;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KYEDEINK 8
XX Db 173 KYEDEINK 180
XX
XX RESULT 13
XX ID ABG50183 standard; peptide; 186 AA.
XX
XX AC ABG50183;
XX
XX DT 25-FEB-2003 (first entry)
XX
XX DE Human liver peptide, SEQ ID No 28831.
XX
XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX hypercholesterolaemia; coronary heart disease.
XX
XX OS Homo sapiens.
XX
XX PN WO200157273-A2.
XX
XX PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-476286/51.
XX
XX Novel single exon nucleic acid probe used to measuring gene expression in
XX
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PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488898/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human adult liver.
XX
XX Claim 27; SEQ ID NO 28831; 658pp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX measuring human gene expression in a sample derived from human adult
XX liver, comprising one of 13109 defined nucleotide sequences given in the
XX specification (or complements/ fragments). The probe hybridises at high
XX stringency to a nucleic acid molecule expressed in the human adult liver.
XX (I) may be used for predicting, measuring and displaying gene expression
XX in samples derived from human adult liver. The genes identified may be
XX involved in genetic liver diseases such as cirrhosis,
XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX associated with coronary heart disease. ABG47348-ABG59930 represent human
XX liver single exon encoded peptides of the invention. Note: The sequence
XX information for this patent does not appear in the printed specification
XX but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 186 AA;
XX
XX Query Match 100.0%; Score 43; DB 4; Length 186;
XX Best Local Similarity 100.0%; Pred. No. 4.6;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KYEDEINK 8
XX Db 173 KYEDEINK 180
XX
XX RESULT 14
XX ID AAM04056 standard; protein; 186 AA.
XX
XX AC AAM04056;
XX
XX DT 09-OCT-2001 (first entry)
XX
XX DE Peptide #2738 encoded by probe for measuring breast gene expression.
XX
XX KW Probe; human; breast disease; breast cancer; development disorder;
XX inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
XX OS Homo sapiens.
XX
XX PN WO200157270-A2.
XX
XX PD 09-AUG-2001.
XX
XX 29-JAN-2001; 2001WO-US000661.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-476286/51.
XX
XX Novel single exon nucleic acid probe used to measuring gene expression in
XX
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PT a human breast.
PS Claim 27; SEQ ID NO 12796; 322pp; English.
XX
CC The present invention relates to novel single exon nucleic acid probes
CC (see AA10010-AA110067). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for measuring human gene expression in
CC a human breast sample, where the probe hybridises at high stringency to a
CC nucleic acid expressed in the human breast. The probes are useful for
CC predicting, diagnosing, grading, staging, monitoring and prognosing
CC diseases of the human breast, particularly those diseases with polygenic
CC aetiology. The diseases include: breast cancer, disorders of development,
CC inflammatory diseases of the breast, fibrocystic changes, proliferative
CC breast diseases and non-carcinoma tumours. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 186 AA;
Query Match 100.0%; Score 43; DB 4; Length 186;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KYEDEINK 8
Db 173 KYEDEINK 180
RESULT 15
ABG09410
ID ABG09410 standard; protein; 186 AA.
XX
AC ABG09410;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #9401.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
PA
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS73597.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 39769; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC patent did not appear in the invention. Note: The sequence data for this
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 186 AA;

Query Match 100.0%; Score 43; DB 4; Length 186;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYEDEINK 8
Db 11 KYEDEINK 18

Search completed: July 5, 2006, 18:43:52
Job time : 70.5146 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 20:38:52 ; Search time 58.5631 Seconds
(without alignments)
63.277 Million cell updates/sec

Title: US-10-774-928A-12

Perfect score: 43

Sequence: 1 KYEDEINK 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

1: /EMC_Celerra_SID33/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /EMC_Celerra_SID33/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SID33/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
5: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
6: /EMC_Celerra_SID33/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	43	100.0	8	5	US-10-774-928-12	Sequence 12, Appl
2	43	100.0	113	5	US-10-480-848A-5	Sequence 5, Appli
3	43	100.0	186	3	US-09-864-761-36050	Sequence 36050, A
4	43	100.0	186	3	US-10-450-763-39769	Sequence 39769, A
5	43	100.0	273	5	US-10-450-763-56735	Sequence 56735, A
6	43	100.0	275	5	US-10-450-763-45641	Sequence 45641, A
7	43	100.0	347	5	US-10-450-763-39770	Sequence 39770, A
8	43	100.0	347	5	US-10-450-763-45995	Sequence 45995, A
9	43	100.0	384	5	US-10-450-763-56734	Sequence 56734, A
10	43	100.0	398	5	US-10-883-020-5	Sequence 5, Appli
11	43	100.0	422	3	US-09-779-307-18	Sequence 18, Appl
12	43	100.0	422	3	US-09-779-307-20	Sequence 20, Appl
13	43	100.0	429	5	US-10-450-763-49905	Sequence 49905, A
14	43	100.0	429	5	US-10-450-763-49906	Sequence 49906, A
15	43	100.0	430	3	US-09-779-307-19	Sequence 19, Appl
16	43	100.0	476	3	US-09-779-307-16	Sequence 16, Appl
17	43	100.0	477	3	US-09-779-307-4	Sequence 4, Appli
18	43	100.0	481	4	US-10-080-334-54	Sequence 54, Appl
19	43	100.0	481	6	US-11-156-300-24	Sequence 24, Appl
20	43	100.0	482	3	US-09-779-307-17	Sequence 17, Appl
21	43	100.0	482	4	US-10-080-334-187	Sequence 187, App
22	43	100.0	482	5	US-10-883-020-1	Sequence 1, Appli
23	43	100.0	482	5	US-10-450-763-38491	Sequence 38491, A
24	43	100.0	483	3	US-09-919-497-79	Sequence 79, Appl
25	43	100.0	483	3	US-09-974-298-41	Sequence 41, Appl
26	43	100.0	483	3	US-09-981-353-158	Sequence 158, App
27	43	100.0	483	4	US-10-177-293-258	Sequence 258, App

Sequence 183, App
Sequence 184, App
Sequence 185, App
Sequence 186, App
Sequence 116, App
Sequence 9, Appli
Sequence 2, Appli
Sequence 39773, A
Sequence 38492, A
Sequence 8, Appli
Sequence 6, Appli
Sequence 55674, A
Sequence 421, App
Sequence 1619, Ap
Sequence 5130, App
Sequence 938, App
Sequence 27, Appl
Sequence 3772, Ap

ALIGNMENTS

RESULT 1

US-10-774-928-12
; Sequence 12, Application US/10774928
; Publication No. US20040241168A1
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 302178
; CURRENT APPLICATION NUMBER: US/10774,928
; CURRENT FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Leishmania
US-10-774-928-12

Query Match 100.0%; Score 43; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
|||
Db 1 KYEDEINK 8

RESULT 2

US-10-480-848A-5
; Sequence 5, Application US/10480848A
; Publication No. US20040219597A1
; GENERAL INFORMATION:
; APPLICANT: B.R.A.H.M.S Aktiengesellschaft
; TITLE OF INVENTION: Use of soluble cytokeatin 1 fragments in diagnosis and
; TITLE OF INVENTION: therapy
; FILE REFERENCE: 3537PCTNAT
; CURRENT APPLICATION NUMBER: US/10/480,848A
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: DE 101 30 985.6
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-480-848A-5

Query Match 100.0%; Score 43; DB 5; Length 113;

Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
Db 84 KYEDEINK 91

RESULT 3
US-09-864-761-36050
; Sequence 36050, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-09-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36050
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011309.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 72
; OTHER INFORMATION: EXPRESSED IN HB100, SIGNAL = 59
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 7.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.8
; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 44
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.5

; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 16
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5e+02
; OTHER INFORMATION: EST HUMAN HIT: BE870853.1, EVALUE 9.00e-68
; OTHER INFORMATION: SWISSPROT HIT: P05787, EVALUE 1.00e-68
US-09-864-761-36050

Query Match 100.0%; Score 43; DB 3; Length 186;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
Db 173 KYEDEINK 180

RESULT 4
US-10-450-763-39769
; Sequence 39769, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 39769
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (124)..(171)
; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL00226D, p-value=7.000e-38, raw score of 19.10
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(169)
; OTHER INFORMATION: Intermediate filament proteins domain identified by PFam,
; OTHER INFORMATION: accession name filament, E-value=4.3e-71, PFam score of 249.6
US-10-450-763-39769

Query Match 100.0%; Score 43; DB 5; Length 186;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
Db 11 KYEDEINK 18

RESULT 5
US-10-450-763-56735
; Sequence 56735, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31

;; PRIOR APPLICATION NUMBER: 09/649,167
;; PRIOR FILING DATE: 2000-08-23
;; NUMBER OF SEQ ID NOS: 60736
;; SOFTWARE: Custom
;; SEQ ID NO 56735
;; LENGTH: 273
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: DOMAIN
;; LOCATION: (177)..(225)
;; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
;; OTHER INFORMATION: accession number BL00226B, p-value=3.348e-35, raw score of 23.86
;; FEATURE:
;; NAME/KEY: DOMAIN
;; LOCATION: (78)..(271)
;; OTHER INFORMATION: Intermediate filament proteins domain identified by Pfam,
;; OTHER INFORMATION: accession number BL00226B, p-value=8.6e-101, Pfam score of 348.3
US-10-450-763-56735

Query Match 100.0%; Score 43; DB 5; Length 273;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
DB 166 KYEDEINK 173

RESULT 6
US-10-450-763-45641
;; Sequence 45641, Application US/10450763
;; Publication No. US20050196754A1
;; GENERAL INFORMATION:
;; APPLICANT: Hyseq, Inc
;; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;; FILE REFERENCE: 790CIP3/US
;; CURRENT APPLICATION NUMBER: US/10/450,763
;; CURRENT FILING DATE: 2003-06-11
;; PRIOR APPLICATION NUMBER: PCT/US01/08631
;; PRIOR FILING DATE: 2001-03-30
;; PRIOR APPLICATION NUMBER: 09/540,217
;; PRIOR FILING DATE: 2000-03-31
;; PRIOR APPLICATION NUMBER: 09/649,167
;; PRIOR FILING DATE: 2000-08-23
;; NUMBER OF SEQ ID NOS: 60736
;; SOFTWARE: Custom
;; SEQ ID NO 45641
;; LENGTH: 275
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: DOMAIN
;; LOCATION: (179)..(227)
;; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
;; OTHER INFORMATION: accession number BL00226B, p-value=3.348e-35, raw score of 23.86
;; FEATURE:
;; NAME/KEY: DOMAIN
;; LOCATION: (87)..(273)
;; OTHER INFORMATION: Intermediate filament proteins domain identified by Pfam,
;; OTHER INFORMATION: accession number BL00226B, p-value=3.2e-89, Pfam score of 309.8
US-10-450-763-45641

Query Match 100.0%; Score 43; DB 5; Length 275;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
DB 168 KYEDEINK 175

RESULT 7

US-10-450-763-39770
;; Sequence 39770, Application US/10450763
;; Publication No. US20050196754A1
;; GENERAL INFORMATION:
;; APPLICANT: Hyseq, Inc
;; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;; FILE REFERENCE: 790CIP3/US
;; CURRENT APPLICATION NUMBER: US/10/450,763
;; CURRENT FILING DATE: 2003-06-11
;; PRIOR APPLICATION NUMBER: PCT/US01/08631
;; PRIOR FILING DATE: 2001-03-30
;; PRIOR APPLICATION NUMBER: 09/540,217
;; PRIOR FILING DATE: 2000-03-31
;; PRIOR APPLICATION NUMBER: 09/649,167
;; PRIOR FILING DATE: 2000-08-23
;; NUMBER OF SEQ ID NOS: 60736
;; SOFTWARE: Custom
;; SEQ ID NO 39770
;; LENGTH: 347
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: DOMAIN
;; LOCATION: (180)..(228)
;; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
;; OTHER INFORMATION: accession number BL00226B, p-value=1.643e-31, raw score of 23.86
;; FEATURE:
;; NAME/KEY: DOMAIN
;; LOCATION: (77)..(342)
;; OTHER INFORMATION: Intermediate filament proteins domain identified by Pfam,
;; OTHER INFORMATION: accession name filament, E-value=1.1e-78, Pfam score of 274.8
US-10-450-763-39770

Query Match 100.0%; Score 43; DB 5; Length 347;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
DB 169 KYEDEINK 176

RESULT 8
US-10-450-763-45995
;; Sequence 45995, Application US/10450763
;; Publication No. US20050196754A1
;; GENERAL INFORMATION:
;; APPLICANT: Hyseq, Inc
;; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;; FILE REFERENCE: 790CIP3/US
;; CURRENT APPLICATION NUMBER: US/10/450,763
;; CURRENT FILING DATE: 2003-06-11
;; PRIOR APPLICATION NUMBER: PCT/US01/08631
;; PRIOR FILING DATE: 2001-03-30
;; PRIOR APPLICATION NUMBER: 09/540,217
;; PRIOR FILING DATE: 2000-03-31
;; PRIOR APPLICATION NUMBER: 09/649,167
;; PRIOR FILING DATE: 2000-08-23
;; NUMBER OF SEQ ID NOS: 60736
;; SOFTWARE: Custom
;; SEQ ID NO 45995
;; LENGTH: 347
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: DOMAIN
;; LOCATION: (180)..(228)
;; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
;; OTHER INFORMATION: accession number BL00226B, p-value=1.643e-31, raw score of 23.86
;; FEATURE:
;; NAME/KEY: DOMAIN
;; LOCATION: (77)..(342)
;; OTHER INFORMATION: Intermediate filament proteins domain identified by Pfam,

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; OTHER INFORMATION: accession name filament, E-value=1.1e-78, Pfam score of 274.8
US-10-450-763-45995

Query Match      100.0%; Score 43; DB 5; Length 347;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYEDEINK 8
Db 169 KYEDEINK 176

RESULT 9
US-10-450-763-56734
; Sequence 56734, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: HySeq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56734
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (164)..(212)
; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL00226B, p-value=4.656e-29, raw score of 23.86
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (80)..(312)
; OTHER INFORMATION: Intermediate filament proteins domain identified by Pfam,
; OTHER INFORMATION: accession name filament, E-value=4e-88, Pfam score of 306.2
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(394)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-56734

Query Match      100.0%; Score 43; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYEDEINK 8
Db 153 KYEDEINK 160

RESULT 10
US-10-883-020-5
; Sequence 5, Application US/10883020
; Publication No. US20050048070A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, Henrik
; APPLICANT: Jensenius, Jens
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: Cancer-Associated Epitope
; FILE REFERENCE: 1361.017US1
; CURRENT APPLICATION NUMBER: US/10/883,020
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: PCT/US03/00297
; PRIOR FILING DATE: 2003-01-03
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; PRIOR APPLICATION NUMBER: US 60/345,208
; PRIOR FILING DATE: 2002-01-03
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-883-020-5

Query Match      100.0%; Score 43; DB 5; Length 398;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYEDEINK 8
Db 93 KYEDEINK 100

RESULT 11
US-09-779-307-18
; Sequence 18, Application US/09779307
; Patent No. US20020137675A1
; GENERAL INFORMATION:
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Majumder, Kumud
; APPLICANT: Vernet, Corine
; APPLICANT: Prayaga, Sudhirdas
; TITLE OF INVENTION: Polynucleotides and Polypeptides Encoded Thereby
; FILE REFERENCE: 15966-662 US
; CURRENT APPLICATION NUMBER: US/09/779,307
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/180,880
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/181,044
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/181,656
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/182,795
; PRIOR FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 18
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-307-18

Query Match      100.0%; Score 43; DB 3; Length 422;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYEDEINK 8
Db 177 KYEDEINK 184

RESULT 12
US-09-779-307-20
; Sequence 20, Application US/09779307
; Patent No. US20020137675A1
; GENERAL INFORMATION:
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Majumder, Kumud
; APPLICANT: Vernet, Corine
; APPLICANT: Prayaga, Sudhirdas
; TITLE OF INVENTION: Polynucleotides and Polypeptides Encoded Thereby
; FILE REFERENCE: 15966-662 US
; CURRENT APPLICATION NUMBER: US/09/779,307
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/180,880
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/181,044
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; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/181,656
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/182,795
; PRIOR FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-779-307-20

Query Match 100.0%; Score 43; DB 3; Length 422;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
|||
Db 177 KYEDEINK 184

RESULT 13
US-10-450-763-49905
; Sequence 49905, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 49905
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (183)..(231)
; OTHER INFORMATION: Intermediate filament proteins domain identified by eMATRIX.
; OTHER INFORMATION: accession number BL00226B, p-value=2.714e-23, raw score of 23.86
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (107)..(348)
; OTHER INFORMATION: Intermediate filament proteins domain identified by PFam.
; OTHER INFORMATION: accession name filament, E-value=4.2e-90, PFam score of 312.7
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(429)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-49905

Query Match 100.0%; Score 43; DB 5; Length 429;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
|||
Db 172 KYEDEINK 179

RESULT 14
US-10-450-763-49906
; Sequence 49906, Application US/10450763
; Publication No. US20050196754A1

; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 49906
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (183)..(231)
; OTHER INFORMATION: Intermediate filament proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL00226B, p-value=2.714e-23, raw score of 23.86
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (107)..(348)
; OTHER INFORMATION: Intermediate filament proteins domain identified by PFam,
; OTHER INFORMATION: accession name filament, E-value=4.2e-90, PFam score of 312.7
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(429)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-49906

Query Match 100.0%; Score 43; DB 5; Length 429;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
|||
Db 172 KYEDEINK 179

RESULT 15
US-09-779-307-19
; Sequence 19, Application US/09779307
; Patent No. US20020137675A1
; GENERAL INFORMATION:
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Majumder, Kumud
; APPLICANT: Vernet, Corine
; APPLICANT: Prayaga, Sudhirdas
; TITLE OF INVENTION: Polynucleotides and Polypeptides Encoded Thereby
; FILE REFERENCE: 15966-662 US
; CURRENT APPLICATION NUMBER: US/09/779,307
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/180,880
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/181,044
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/181,656
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/182,795
; PRIOR FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-779-307-19

Query Match 100.0%; Score 43; DB 3; Length 430;

Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYEDEINK 8
|||
Db 184 KYEDEINK 191

Search completed: July 5, 2006, 20:51:59
Job time : 58.5631 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 20:39:32 ; Search time 4.58252 Seconds
(without alignments)
46.842 Million cell updates/sec

Title: US-10-774-928A-12

Perfect score: 43

Sequence: 1 KYEDEINK 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 112942

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

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- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pap.*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	483	7	US-11-105-233-180
2	40	93.0	469	6	US-10-505-928-457
3	39	90.7	140	6	US-10-953-349-1458
4	39	90.7	147	6	US-10-953-349-1457
5	39	90.7	164	6	US-10-953-349-1456
6	34	79.1	940	6	US-10-449-902-45238
7	34	79.1	940	6	US-10-449-902-45669
8	33	76.7	242	6	US-10-449-902-46212
9	33	76.7	256	7	US-11-174-307B-4514
10	33	76.7	456	6	US-10-706-435A-26
11	33	76.7	457	6	US-10-706-435A-4
12	33	76.7	758	6	US-10-449-902-51086
13	33	76.7	799	6	US-10-449-902-47602
14	33	76.7	964	7	US-11-289-102-392
15	32	74.4	33	7	US-11-134-871-915
16	32	74.4	163	6	US-10-449-902-38644
17	32	74.4	225	6	US-10-471-571A-5244
18	32	74.4	251	6	US-10-449-902-47327
19	32	74.4	275	6	US-10-449-902-48344
20	32	74.4	436	6	US-10-471-571A-5632
21	32	74.4	691	6	US-10-953-349-1322
22	32	74.4	705	6	US-10-953-349-1321
23	32	74.4	713	6	US-10-953-349-1320
24	32	74.4	723	6	US-10-449-902-53379
25	31	72.1	44	7	US-11-199-489A-136

26	31	72.1	107	6	US-10-953-349-13561	Sequence 13561, A
27	31	72.1	158	6	US-10-953-349-13560	Sequence 13560, A
28	31	72.1	196	6	US-10-953-349-19059	Sequence 19059, A
29	31	72.1	238	6	US-10-953-349-19058	Sequence 19058, A
30	31	72.1	247	6	US-10-449-902-54216	Sequence 54216, A
31	31	72.1	273	7	US-11-101-316-168	Sequence 168, App
32	31	72.1	568	6	US-10-449-902-46926	Sequence 46926, A
33	31	72.1	568	6	US-10-449-902-47019	Sequence 47019, A
34	31	72.1	607	6	US-10-449-902-45927	Sequence 45927, A
35	31	72.1	714	6	US-10-449-902-54951	Sequence 54951, A
36	31	72.1	2871	6	US-10-505-928-100	Sequence 100, App
37	30	69.8	228	6	US-10-449-902-50750	Sequence 50750, A
38	30	69.8	247	6	US-10-953-349-17634	Sequence 17634, A
39	30	69.8	251	6	US-10-449-902-30710	Sequence 30710, A
40	30	69.8	251	6	US-10-449-902-32230	Sequence 32230, A
41	30	69.8	257	6	US-10-953-349-4598	Sequence 4598, Ap
42	30	69.8	263	6	US-10-953-349-33086	Sequence 33086, A
43	30	69.8	283	6	US-10-953-349-33085	Sequence 33085, A
44	30	69.8	286	6	US-10-953-349-4597	Sequence 4597, Ap
45	30	69.8	304	6	US-10-953-349-33084	Sequence 33084, A

ALIGNMENTS

RESULT 1

US-11-105-233-180
; Sequence 180, Application US/11105233
; Publication No. US20060134653A1
; GENERAL INFORMATION:
; APPLICANT: Thiagalingam et al
; TITLE OF INVENTION: Differential Expression of Genes in MSI
; FILE OF INVENTION: Tumors
; FILE REFERENCE: 1657/2001
; CURRENT APPLICATION NUMBER: US/11/105,233
; CURRENT FILING DATE: 2005-04-13
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 180
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-233-180

Query Match 100.0%; Score 43; DB 7; Length 483;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
DB 178 KYEDEINK 185

RESULT 2

US-10-505-928-457
; Sequence 457, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 457
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-457

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Query Match      93.0%; Score 40; DB 6; Length 469;
Best Local Similarity 87.5%; Pred. No. 2.9;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYEDEINK 8
Db 179 KYEDEINR 186

RESULT 3
US-10-953-349-1458
; Sequence 1458, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1458
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1458

Query Match      90.7%; Score 39; DB 6; Length 140;
Best Local Similarity 87.5%; Pred. No. 1.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYEDEINK 8
Db 55 KFEDEINK 62

RESULT 4
US-10-953-349-1457
; Sequence 1457, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1457
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1457

Query Match      90.7%; Score 39; DB 6; Length 147;
Best Local Similarity 87.5%; Pred. No. 1.3;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYEDEINK 8
Db 62 KFEDEINK 69

RESULT 5
US-10-953-349-1456
; Sequence 1456, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
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; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1456
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1456

Query Match      90.7%; Score 39; DB 6; Length 164;
Best Local Similarity 87.5%; Pred. No. 1.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYEDEINK 8
Db 79 KFEDEINK 86

RESULT 6
US-10-449-902-45238
; Sequence 45238, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45238
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-45238

Query Match      79.1%; Score 34; DB 6; Length 940;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YEDEINK 8
Db 413 YEDEINE 419

RESULT 7
US-10-449-902-45669
; Sequence 45669, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 45669
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-45669

Query Match 79.1%; Score 34; DB 6; Length 940;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YEDEINK 8
|||||
Db 413 YEDEINE 419

RESULT 8

US-10-449-902-46212
; Sequence 46212, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46212
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-46212

Query Match 76.7%; Score 33; DB 6; Length 242;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YEDEINK 8
|||||
Db 84 YEDEANK 90

RESULT 9

US-11-174-307B-4514
; Sequence 4514, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; FILE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 4514
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:

; NAME/KEY: misc_feature

; LOCATION:
; OTHER INFORMATION: GI Number: 50947575; NR Description: thylakoid lumen protein,
; OTHER INFORMATION: chloroplast precursor-like [Oryza sativa (japonica cultivar-group)]
; OTHER INFORMATION: >gi|42408803|dbj|BAD10064.1| thylakoid lumen protein, chloroplast
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION:

; OTHER INFORMATION: GI Number: 21537211; NR Description: thylakoid lumen protein,
; FEATURE:

; NAME/KEY: misc_feature

; LOCATION:

; OTHER INFORMATION: GI Number: 32815945; NR Description: Atig76450 [Arabidopsis
; OTHER INFORMATION: thaliana] >gi|18203439|sp|Q9S720|THU1_ARATH Unknown thylakoid lumen
; OTHER INFORMATION: protein, chloroplast precursor >gi|18411110|ref|NP_565131.1|
; FEATURE:

; NAME/KEY: misc_feature

; LOCATION:

; OTHER INFORMATION: GI Number: 61826057; NR Description: PREDICTED: similar to
; OTHER INFORMATION: serine/arginine repetitive matrix 1, partial [Bos taurus]
; OTHER INFORMATION: gi|61818041|ref|XP_593433.1| PREDICTED: similar to serine/arginin
; FEATURE:

; NAME/KEY: misc_feature

; LOCATION:

; OTHER INFORMATION: GI Number: 7949115; NR Description: Ser/Arg-related nuclear
; OTHER INFORMATION: matrix protein; plenty-of-prolines-101; serine/arginine repetitive
; OTHER INFORMATION: matrix protein 1 [Mus musculus] >gi|3153821|gb|AAC17422.1|
US-11-174-307B-4514

Query Match 76.7%; Score 33; DB 7; Length 256;

Best Local Similarity 85.7%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YEDEINK 8
|||||
Db 98 YEDEANK 104

RESULT 10

US-10-706-435A-26
; Sequence 26, Application US/10706435A
; Publication No. US20060088547A1
; GENERAL INFORMATION:
; APPLICANT: Walter Reed Army Institute of Research
; APPLICANT: Lanar, David E.
; APPLICANT: Hillier, Collette J.
; APPLICANT: Lyon, Jeffrey A.
; APPLICANT: Angov, Evelina
; APPLICANT: Kumar, Sanjai
; APPLICANT: Rogers, William
; APPLICANT: Barbosa, Arnaldo
; TITLE OF INVENTION: Expression, Purification, and Uses of a Plasmodium
; TITLE OF INVENTION: falciparum Liver Stage Antigen 1 Polypeptide
; FILE REFERENCE: 003/285/SAP
; CURRENT APPLICATION NUMBER: US/10/706,435A
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 60/425,719
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Word XP
; SEQ ID NO 26
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: LSA-NRC(H) protein
US-10-706-435A-26

Query Match 76.7%; Score 33; DB 6; Length 456;

Best Local Similarity 85.7%; Pred. No. 59;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEIN 7

```
Db          294 KYEDEL 300
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RESULT 11
US-10-706-435A-4
; Sequence 4, Application US/10706435A
; Publication No. US20060088547A1
; GENERAL INFORMATION:
; APPLICANT: Walter Reed Army Institute of Research
; APPLICANT: Lanar, David B.
; APPLICANT: Hillier, Collette J.
; APPLICANT: Lyon, Jeffrey A.
; APPLICANT: Angov, Evelina
; APPLICANT: Kumar, Sanjai
; APPLICANT: Rogers, William
; APPLICANT: Barbosa, Arnoldo
; TITLE OF INVENTION: Expression, Purification, and Uses of a Plasmodium
; FILE REFERENCE: 003/285/SAP
; CURRENT APPLICATION NUMBER: US/10/706,435A
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 60/425,719
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Word XP
; SEQ ID NO 4
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: LSA-NRC (H) Mut
US-10-706-435A-4

Query Match          76.7%; Score 33; DB 6; Length 457;
Best Local Similarity 85.7%; Pred. No. 59;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 KYEDEL 7
|||||:
Db          294 KYEDEL 300

RESULT 12
US-10-449-902-51086
; Sequence 51086, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51086
; LENGTH: 758
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-51086

Query Match          76.7%; Score 33; DB 6; Length 758;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 YEDEL 7
|||||:
Db          230 YEDEL 235
|||||:
RESULT 13
US-10-449-902-47602
; Sequence 47602, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47602
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-47602

Query Match          76.7%; Score 33; DB 6; Length 799;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 YEDEL 7
|||||:
Db          349 YEDEL 354

RESULT 14
US-11-289-102-392
; Sequence 392, Application US/11289102
; Publication No. US20060121511A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Hyerim
; APPLICANT: Shaw, Peter M.
; APPLICANT: Clark, Edwin
; TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO
; FILE REFERENCE: 10338 NP
; CURRENT APPLICATION NUMBER: US/11/289,102
; CURRENT FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US 60/631,993
; PRIOR FILING DATE: 2004-11-30
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 392
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-289-102-392

Query Match          76.7%; Score 33; DB 7; Length 964;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY          2 YEDEL 8
|||||:
Db          524 YEDEL 530

RESULT 15
US-11-134-871-915
; Sequence 915, Application US/11134871
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/ Publication No. US20060141528A1
/ GENERAL INFORMATION:
/ APPLICANT: Aebersold, Rudolf H.
/ APPLICANT: Zhang, Hui
/ TITLE OF INVENTION: Compositions and Methods for
/ TITLE OF INVENTION: Qualification of Serum Glycoproteins
/ FILE REFERENCE: 66661-116
/ CURRENT APPLICATION NUMBER: US/11/134,871
/ CURRENT FILING DATE: 2005-05-20
/ PRIOR APPLICATION NUMBER: 60/573,593
/ PRIOR FILING DATE: 2004-05-21
/ NUMBER OF SEQ ID NOS: 3602
/ SOFTWARE: PASTSEQ for Windows Version 4.0
/ SEQ ID NO 915
/ LENGTH: 33
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-134-871-915

Query Match 74.4%; Score 32; DB 7; Length 33;
Best Local Similarity 83.3%; Pred. No. 5.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YEDEIN 7
Db 20 YEDEVN 25

Search completed: July 5, 2006, 20:53:02
Job time : 4.58252 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 19:18:42 ; Search time 18.0194 Seconds
(without alignments)
38.861 Million cell updates/sec

Title: US-10-774-928A-12
Perfect score: 43
Sequence: 1 KYDEINK 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	8	2	US-09-809-003A-12
2	43	100.0	384	2	US-09-949-016-11034
3	43	100.0	443	2	US-09-949-016-10582
4	43	100.0	482	2	US-09-538-092-858
5	43	100.0	483	2	US-09-919-497-79
6	43	100.0	502	2	US-09-949-016-11033
7	43	100.0	564	2	US-09-949-016-6628
8	43	100.0	567	2	US-10-104-047-3772
9	43	100.0	569	2	US-09-949-016-11035
10	43	100.0	569	2	US-09-949-016-11036
11	43	100.0	637	2	US-09-949-016-8152
12	43	100.0	643	2	US-09-538-092-844
13	43	100.0	645	2	US-09-919-172-41
14	40	93.0	469	2	US-09-077-606-3
15	40	93.0	476	2	US-09-949-016-9096
16	40	93.0	551	1	US-09-067-351-2
17	40	93.0	551	2	US-09-360-490-2
18	39	90.7	608	2	US-10-094-749-2446
19	38	88.4	7	2	US-09-809-003A-1
20	38	88.4	216	2	US-09-248-796A-14967
21	38	88.4	546	1	US-09-067-351-1
22	38	88.4	546	2	US-09-360-490-1
23	34	79.1	234	2	US-09-270-767-32857
24	34	79.1	234	2	US-09-270-767-48074
25	34	79.1	608	2	US-09-270-767-32937
26	34	79.1	608	2	US-09-270-767-48154

27	33	76.7	8	2	US-09-809-003A-11	Sequence 11, Appl
28	33	76.7	229	2	US-09-454-204A-41	Sequence 41, Appl
29	33	76.7	315	2	US-09-248-796A-18213	Sequence 18213, A
30	33	76.7	369	2	US-09-248-796A-18582	Sequence 18582, A
31	33	76.7	407	2	US-09-248-796A-15463	Sequence 15463, A
32	33	76.7	426	2	US-09-538-092-7	Sequence 7, Appl
33	33	76.7	533	2	US-09-248-796A-17526	Sequence 17526, A
34	33	76.7	699	2	US-08-851-843A-52	Sequence 52, Appl
35	33	76.7	699	2	US-08-974-549A-188	Sequence 188, App
36	33	76.7	699	2	US-08-854-050-52	Sequence 52, Appl
37	33	76.7	699	2	US-09-430-323-52	Sequence 52, Appl
38	33	76.7	699	2	US-09-402-181B-188	Sequence 188, App
39	33	76.7	699	2	US-09-721-456-188	Sequence 188, App
40	33	76.7	699	2	US-09-766-253-52	Sequence 52, Appl
41	33	76.7	699	2	US-10-054-295-52	Sequence 52, Appl
42	33	76.7	699	2	US-09-438-486A-52	Sequence 52, Appl
43	33	76.7	699	3	US-10-054-611-52	Sequence 52, Appl
44	33	76.7	719	2	US-08-851-843A-7	Sequence 7, Appl
45	33	76.7	719	2	US-08-974-549A-219	Sequence 219, App

ALIGNMENTS

RESULT 1

US-09-809-003A-12
; Sequence 12, Application US/09809003A
; Patent No. 6673351
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; FILE REFERENCE: 302178
; CURRENT APPLICATION NUMBER: US/09/809,003A
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Leishmania
US-09-809-003A-12

Query Match 100.0%; Score 43; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYDEINK 8
DB 1 KYDEINK 8

RESULT 2

US-09-949-016-11034
; Sequence 11034, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11034
; LENGTH: 384

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; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11034

Query Match      100.0%; Score 43; DB 2; Length 384;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYEDEINK 8
Db 275 KYEDEINK 282

RESULT 3
US-09-949-016-10582
; Sequence 10582, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10582
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10582

Query Match      100.0%; Score 43; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYEDEINK 8
Db 138 KYEDEINK 145

RESULT 4
US-09-538-092-858
; Sequence 858, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatter Version 0.9
; SEQ ID NO 858
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)-(0)
; OTHER INFORMATION: Polypeptide Accession Number P05787
US-09-538-092-858

Query Match      100.0%; Score 43; DB 2; Length 482;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYEDEINK 8
Db 177 KYEDEINK 184

RESULT 5
US-09-919-497-79
; Sequence 79, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-79

Query Match      100.0%; Score 43; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYEDEINK 8
Db 178 KYEDEINK 185

RESULT 6
US-09-949-016-11033
; Sequence 11033, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11033
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11033

Query Match      100.0%; Score 43; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYEDEINK 8
Db 197 KYEDEINK 204
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RESULT 7
US-09-949-016-6628
; Sequence 6628, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6628
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6628

Query Match      100.0%; Score 43; DB 2; Length 564;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KYEDEINK 8
Db      252 KYEDEINK 259

RESULT 8
US-10-104-047-3772
; Sequence 3772, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3772
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3772

Query Match      100.0%; Score 43; DB 2; Length 567;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KYEDEINK 8
Db      234 KYEDEINK 241

RESULT 9
US-09-949-016-11035
; Sequence 11035, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11035
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11035

Query Match      100.0%; Score 43; DB 2; Length 569;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KYEDEINK 8
Db      258 KYEDEINK 265

RESULT 10
US-09-949-016-11036
; Sequence 11036, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11036
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11036

Query Match      100.0%; Score 43; DB 2; Length 569;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KYEDEINK 8
Db      258 KYEDEINK 265

RESULT 11
US-09-949-016-8152
; Sequence 8152, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8152
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8152

Query Match      100.0%; Score 43; DB 2; Length 569;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KYEDEINK 8
Db      258 KYEDEINK 265
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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8152
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8152

Query Match      100.0%; Score 43; DB 2; Length 637;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 KYEDEINK 8
DB      269 KYEDEINK 276

RESULT 12
US-09-538-092-844
; Sequence 844, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Mansfield, Traci A.
; APPLICANT: Giot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15366-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 844
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P04264
US-09-538-092-844

Query Match      100.0%; Score 43; DB 2; Length 643;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 KYEDEINK 8
DB      268 KYEDEINK 275

RESULT 13
US-09-919-172-41
; Sequence 41, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 41
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Human

Query Match      100.0%; Score 43; DB 2; Length 645;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 KYEDEINK 8
DB      273 KYEDEINK 280

RESULT 14
US-09-077-606-3
; Sequence 3, Application US/09077606
; Patent No. 6774220
; GENERAL INFORMATION:
; APPLICANT: JIANG, Pan Hong
; APPLICANT: KABA, Aboubacar
; APPLICANT: CHANY-FOURNIER, Francoise
; APPLICANT: CERUTTI, Italina
; APPLICANT: CHANY, Charles
; TITLE OF INVENTION: COMPOUNDS HAVING LECTINIC PROPERTIES AND THEIR
; TITLE OF INVENTION: BIOLOGICAL APPLICATIONS
; FILE REFERENCE: 040388/0113
; CURRENT APPLICATION NUMBER: US/09/077,606
; CURRENT FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: WO PCT/FR96/01937
; EARLIER FILING DATE: 1996-12-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-077-606-3

Query Match      93.0%; Score 40; DB 2; Length 469;
Best Local Similarity 87.5%; Pred. No. 14;
Matches      7; Conservative      1; Mismatches      0; Indels      0; Gaps      0;

QY      1 KYEDEINK 8
DB      179 KYEDEINK 186

RESULT 15
US-09-949-016-9096
; Sequence 9096, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9096
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9096
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Query Match 93.0%; Score 40; DB 2; Length 476;
Best Local Similarity 87.5%; Pred. NO. 14;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYEDEINK 8
Db 186 KYEDEINR 193

Search completed: July 5, 2006, 19:24:26
Job time : 19.0194 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 19:20:41 ; Search time 14.6667 Seconds
(without alignments)
104.964 Million cell updates/sec

Title: US-10-774-928a-13

Perfect score: 79
Sequence: 1 EIEQYNLLLLASYLDF 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*

- 1: PIR1.*
- 2: PIR2.*
- 3: PIR3.*
- 4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	58.2	336	2 T22322	hypothetical prote
2	43	54.4	309	2 T33888	hypothetical prote
3	42	53.2	408	2 T24114	hypothetical prote
4	42	53.2	471	2 E86192	hypothetical prote
5	42	53.2	1613	2 G64488	reverse gyrase (in
6	42	53.2	1624	2 C71129	probable reverse g
7	41	51.9	105	2 E97862	hypothetical prote
8	41	51.9	220	2 S51444	hypothetical prote
9	41	51.9	1092	1 S37676	glutamate dehydrog
10	40	50.6	299	2 F69785	fructokinase homol
11	40	50.6	341	2 S31571	cinnamyl-alcohol d
12	40	50.6	357	2 T09141	cinnamyl-alcohol d
13	40	50.6	358	2 S31572	hypothetical prote
14	40	50.6	771	2 T01315	DNA topoisomerase
15	40	50.6	804	1 ISECTB	DNA gyrase subunit
16	40	50.6	804	2 B91208	hypothetical prote
17	40	50.6	804	2 D86054	membrane antigen p
18	40	50.6	1318	1 QQB51	P140 protein - hum
19	40	50.6	1318	2 S29606	TATA box binding p
20	40	50.6	2049	2 T47587	adherence factor T
21	40	50.6	3335	2 H81702	hypothetical prote
22	39	49.4	185	2 C90063	response regulator
23	39	49.4	225	2 F97349	conserved hypotet
24	39	49.4	233	1 C70106	hypothetical prote
25	39	49.4	257	2 F75084	keratin Ha3-II, ty
26	39	49.4	362	2 I37459	keratin, 47.6K typ
27	39	49.4	404	2 JS0073	keratin, 48K type
28	39	49.4	412	1 KRSHL1	keratin Ha1, type
29	39	49.4	416	2 S60034	

30	39	49.4	786	2 E87565	conserved hypotet
31	39	49.4	828	2 D81522	DNA mismatch repai
32	39	49.4	828	2 C86608	DNA mismatch repai
33	39	49.4	828	2 G72017	DNA mismatch repai
34	39	49.4	1892	2 T18314	hypothetical prote
35	38	48.1	105	2 G71645	hypothetical prote
36	38	48.1	185	2 H96988	transcription regu
37	38	48.1	322	2 G64694	arginase - Helicob
38	38	48.1	324	2 B84150	hypothetical prote
39	38	48.1	362	2 S45094	cinnamyl-alcohol d
40	38	48.1	411	2 S45318	keratin 12 - rabbi
41	38	48.1	422	2 S59319	probable membrane
42	38	48.1	430	2 S05481	keratin 18, type I
43	38	48.1	476	2 S64425	hypothetical prote
44	38	48.1	488	2 JQ2257	nuclear antigen 21
45	38	48.1	488	2 T02207	protein 21D7 - com

ALIGNMENTS

RESULT 1

T22322
hypothetical protein F46G10.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22322
R:Colles, L.
submitted to the EMBL Data Library, July 1995
A:Reference number: Z19548
A:Accession: T22322
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-336 <WIL>
A:Cross-references: UNIPROT:O20478; UNIPARC:UPI000007A8AC; EMBL:Z50177; PIDN:CAA90544.1;
A:Experimental source: clone F46G10
C:Genetics:
A:Gene: CESP:F46G10.4
A:Map position: X
A:Introns: 16/3; 50/1; 80/3; 129/1; 162/2; 195/3; 216/3; 257/2; 290/3

Query Match 58.2%; Score 46; DB 2; Length 336;
Best Local Similarity 60.0%; Pred. No. 4.8;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIEQYNLLLLASYLD 15
|||:|||||:
Db 34 EAEQFLNLAAYAD 48

RESULT 2

T33888
hypothetical protein Y39F10A.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T33888
R:Leonard, S.; Graves, T.; Wilson, C.
submitted to the EMBL Data Library, February 1999
A:Description: The sequence of C. elegans cosmid Y39F10A.
A:Reference number: Z21432
A:Accession: T33888
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-309 <LEO>
A:Cross-references: UNIPROT:Q9TYN8; UNIPARC:UPI000007DF80; EMBL:AFI25450; PIDN:AAD12817.
A:Experimental source: strain Bristol N2; clone Y39F10A
C:Genetics:
A:Gene: CESP:Y39F10A.3
A:Map position: 2
A:Introns: 33/1; 73/3; 139/2; 170/3
C:Superfamily: Caenorhabditis elegans hypothetical protein K06H6.2

Query Match 54.4%; Score 43; DB 2; Length 309;

```

Best Local Similarity 53.3%; Pred. No. 14;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IEQYNLLLSASYLDF 16
DB 293 VEKYGKLVANVYDF 307

RESULT 3
T24114
Hypochemical protein R10D12.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24114
R:Percy, C.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19842
A:Accession: T24114
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-408 <WIL>
A:Cross-references: UNIPROT:Q9XVK1; UNIPARC:UPI000008028D; EMBL:Z81109; PIDN:CAB03244.1;
A:Experimental source: clone R10D12
C:Genetics:
A:Gene: CESP:R10D12.2
A:Map position: 5
A:Introns: 44/1; 101/1; 123/1; 151/1; 284/2; 351/3

Query Match 53.2%; Score 42; DB 2; Length 408;
Best Local Similarity 53.8%; Pred. No. 28;
Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIEQYNLLLSASY 13
DB 26 EIEKWNLILVSF 38

RESULT 4
E86192
Hypochemical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86192
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-471 <STO>
A:Cross-references: UNIPROT:Q9MA46; UNIPARC:UPI00000A8FAC; GB:AE005172; NID:G6850308; PI
C:Genetics:
A:Map position: 1

Query Match 53.2%; Score 42; DB 2; Length 471;
Best Local Similarity 62.5%; Pred. No. 32;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIEQYNLLLSASYLDF 16
DB 107 EITRYGNLLSASYKGF 122

RESULT 5
G64488
reverse gyrase (intein-containing) - Methanococcus jannaschii
N:Contains: intein
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: G64488
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, A.;
Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
raon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: G64488
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1613 <BUL>
A:Cross-references: UNIPROT:Q58907; UNIPARC:UPI0000068850; GB:U67592; GB:L77117; NID:928;
C:Genetics:
A:Map position: FOR1483759-1488600
C:Keywords: ATP; nucleotide binding; P-loop; protein splicing
E:100-107/Region: nucleotide-binding motif A (P-loop)
F:219-224/Region: nucleotide-binding motif B
F:225-228/Region: DEAD/H motif #status atypical

Query Match 53.2%; Score 42; DB 2; Length 1613;
Best Local Similarity 53.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 EQYNLLLSAYLD 15
DB 1145 ESYINALIAGYFD 1157

RESULT 6
C71129
probable reverse gyrase - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C:Accession: C71129
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: C71129
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1624 <KAW>
A:Cross-references: UNIPROT:O58530; UNIPARC:UPI000006680C; GB:AP000003; NID:G3236130; PI
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0800

Query Match 53.2%; Score 42; DB 2; Length 1624;
Best Local Similarity 46.2%; Pred. No. 1.1e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 EQYNLLLSAYLD 15
DB 1179 EYINAMIAGYFD 1191

RESULT 7
E97862
Hypochemical protein RC1301 [imported] - Rickettsia conorii (strain Malish 7)
C:Species: Rickettsia conorii
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: E97862
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893

```

A:Accession: E97862
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-105 <KUR>
A:Cross-references: UNIPROT:Q92G24; UNIPARC:UPI000000CC074; GB:AE006914; PIDN:AAL03839.1;
C:Genetics:
A:Gene: RC1301

Query Match 51.9%; Score 41; DB 2; Length 105;
Best Local Similarity 58.3%; Pred. No. 10;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 EOYLNLLASYL 14
Db 93 EDYLNLIINSYI 104
| | | | | : | | | | |
| | | | | : | | | | |

RESULT 8
S51444
hypothetical protein YLR221c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein L8083.7
C:Species: Saccharomyces cerevisiae
C:Date: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
A:Accession: S51444
R:Hallsworth, K.
submitted to the EMBL Data Library, December 1994
A:Reference: The sequence of *S. cerevisiae* cosmid 8083.
A:Reference number: S51443
A:Accession: S51444
A:Molecule type: DNA
A:Residues: 1-220 <HAL>
A:Cross-references: UNIPROT:Q05942; UNIPARC:UPI0000052DF0; EMBL:U19027; NID:g609363; PIDN:
C:Genetics:
A:Gene: SGD:RSA3; MIPS:YLR221c
A:Cross-references: SGD:S0004211
A:Map position: 12R

Query Match 51.9%; Score 41; DB 2; Length 220;
Best Local Similarity 61.5%; Pred. No. 22;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 EOYLNLLASYLD 15
Db 162 EBYLNLFENYGD 174
| | | | | : | | | | |
| | | | | : | | | | |

RESULT 9
S37676
glutamate dehydrogenase (EC 1.4.1.2) - yeast (Saccharomyces cerevisiae)
N:Alternate names: glutamic dehydrogenase; NAD-specific glutamate dehydrogenase; protein
C:Species: Saccharomyces cerevisiae
C:Date: 31-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 05-Oct-2004
A:Accession: S37676; S22282; S67774; S67778
R:Boles, E.; Lehnert, W.; Zimmermann, F.K.
Eur. J. Biochem. 217, 469-477, 1993

A:Title: The role of the NAD-dependent glutamate dehydrogenase in restoring growth on glucose
A:Reference number: S37676; MUID:94039072; PMID:7901008
A:Accession: S37676
A:Molecule type: DNA
A:Residues: 1-1092 <BOL>
A:Cross-references: UNIPROT:P33327; UNIPARC:UPI00001292E2; EMBL:X72015; NID:g396750; PIDN:
R:Miller, S.M.; Magasanik, B.
Mol. Cell. Biol. 11, 6229-6247, 1991

A:Title: Role of the complex upstream region of the GDH2 gene in nitrogen regulation of
A:Reference number: S22282; MUID:92049354; PMID:1682801
A:Accession: S22282
A:Molecule type: DNA
A:Residues: 1-79 <ML>
A:Cross-references: UNIPARC:UPI00001689AE; GB:S66436; NID:g238959; PIDN:AAB20327.1; PIDN:
R:Schmidt, E.R.; Bahr, A.; Kraemer, C.; Hankeln, T.; Moeller-Rieker, S.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67756
A:Accession: S67774

A:Molecule type: DNA
A:Residues: 1-1092 <SCH>
A:Cross-references: UNIPARC:UPI00001292E2; EMBL:Z74263; NID:g1431359; PIDN:CAA98793.1; PIDN:
A:Experimental source: strain S288C
R:Rasmussen, S.W.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67778
A:Accession: S67778
A:Molecule type: DNA
A:Residues: 849-1092 <RAS>
A:Cross-references: UNIPARC:UPI0000172054; EMBL:Z74263; GSPDB:GN00004; MIPS:YDL215C
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:GDH2; MIPS:YDL215C
A:Cross-references: SGD:S0002374; MIPS:YDL215C
A:Map position: 4L
C:Superfamily: NAD-dependent glutamate dehydrogenase
C:Keywords: NAD; oxidoreductase
F:536,626/Binding site: substrate (Lys) #status predicted

Query Match 51.9%; Score 41; DB 1; Length 1092;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 EOYLNLLASYL 14
Db 1049 ESYLKVLSSYL 1060
| | | | | : | | | | |
| | | | | : | | | | |

RESULT 10
F69785
fructokinase homolog ydhr - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
A:Accession: F69785
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron,
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: F69785
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-299 <KUN>
A:Cross-references: UNIPROT:Q05510; UNIPARC:UPI000005FFB8; GB:Z99107; GB:AL009126; NID:g
A:Experimental source: strain 168
C:Genetics:
A:Gene: ydhr
C:Superfamily: fructokinase; glucose kinase homology
F:50-186/Domain: glucose kinase homology <GKH>

Query Match 50.6%; Score 40; DB 2; Length 299;
Best Local Similarity 53.3%; Pred. No. 44;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IEQYVFKIMNSYLD 16
Db 241 IQYVFKIMNSYLD 255
| | | | | : | | | | |
| | | | | : | | | | |

RESULT 11
S31571

cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) - cottonwood (fragment)
C:Species: Populus deltoides (cottonwood)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C:Accession: S31571
R:van Doorselaere, J.; van Montagu, M.; Inze, D.
submitted to the EMBL Data Library, January 1993
A:Description: Isolation and characterization of poplar and alfalfa cinnamyl alcohol dehydrogenase homology
A:Reference number: S31571
A:Accession: S31571
A:Molecule type: mRNA
A:Residues: 1-341 <VAN>
A:Cross-references: UNIPROT:P31657; UNIPARC:UPI0000174E44; EMBL:Z19568
A:Experimental source: leaf
C:Function:
A:Pathway: lignin biosynthesis
A:Note: last step in pathway
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C:Keywords: lignin biosynthesis; metalloprotein; oxidoreductase; zinc
F:32-340/Domain: long-chain alcohol dehydrogenase homology <LADH>
F:47,69,163/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted

Query Match 50.6%; Score 40; DB 2; Length 341;
Best Local Similarity 60.0%; Pred. No. 50;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EIEQYLNLLASYLD 15
||||| : |||
Db 109 EIEQYCNKKIWSYND 123

RESULT 12
T09141
cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) - cottonwood
C:Species: Populus deltoides (cottonwood)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T09141
R:van Doorselaere, J.; Baucher, M.; Feuillet, C.; Boudet, A.M.; van Montagu, M.; Inze, Plant Physiol. Biochem. 33, 105-109, 1995
A:Title: Isolation of cinnamyl alcohol dehydrogenase cDNAs from two important economic species
A:Reference number: Z16583
A:Accession: T09141
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-357 <VAN>
A:Cross-references: UNIPROT:P31657; UNIPARC:UPI0000126DBA; EMBL:Z19568; NID:g288752; PID:100,103,106,114/Binding site: zinc, noncatalytic (Cys, His, Cys) #status predicted
C:Function:
A:Description: catalyzes the reversible oxidation of cinnamyl alcohol to cinnamaldehyde
A:Pathway: lignin biosynthesis
A:Note: last step in pathway
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C:Keywords: lignin biosynthesis; metalloprotein; oxidoreductase; zinc
F:32-340/Domain: long-chain alcohol dehydrogenase homology <LADH>
F:183-212/Region: beta-alpha-beta NADP nucleotide-binding fold
F:47,69,163/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted
F:100,103,106,114/Binding site: zinc, noncatalytic (Cys) #status predicted

Query Match 50.6%; Score 40; DB 2; Length 357;
Best Local Similarity 60.0%; Pred. No. 53;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EIEQYLNLLASYLD 15
||||| : |||
Db 109 EIEQYCNKKIWSYND 123

RESULT 13
S31572
cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) - alfalfa
C:Species: Medicago sativa (alfalfa)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S31572
R:van Doorselaere, J.; van Montagu, M.; Inze, D.

submitted to the EMBL Data Library, January 1993
A:Description: Isolation and characterization of poplar and alfalfa cinnamyl alcohol dehydrogenase homology
A:Reference number: S31571
A:Accession: S31572
A:Molecule type: mRNA
A:Residues: 1-358 <VAN>
A:Cross-references: UNIPROT:P31656; UNIPARC:UPI0000126DB7; EMBL:Z19573; NID:g19594; PID:NID:g19594; PID:NID:g19594
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C:Keywords: alcohol metabolism; metalloprotein; oxidoreductase; zinc
F:33-341/Domain: long-chain alcohol dehydrogenase homology <LADH>
F:48,70,164/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted

Query Match 50.6%; Score 40; DB 2; Length 358;
Best Local Similarity 60.0%; Pred. No. 53;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EIEQYLNLLASYLD 15
||||| : |||
Db 110 EIEQYCNKKIWSYND 124

RESULT 14
T01315
hypothetical protein T14P8.16 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01315
R:Kalicki, J.; Elliott, G.; Cloud, J.
submitted to the EMBL Data Library, May 1998
A:Description: The sequence of A. thaliana T14P8.
A:Reference number: Z14290
A:Accession: T01315
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-771 <KAL>
A:Cross-references: UNIPROT:O81298; UNIPARC:UPI000009E31F; EMBL:AF069298; NID:g3193282; PID:g3193282; PID:g3193282
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Introns: 328/3; 396/2
A:Note: T14P8.16

Query Match 50.6%; Score 40; DB 2; Length 771;
Best Local Similarity 61.5%; Pred. No. 1.2e+02;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIEQYLNLLASY 13
||||| : |||
Db 694 EIQMINLLSSH 706

RESULT 15
ISECTB
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) chain B - Escherichia coli (strain K-12)
N:Alternate names: DNA gyrase B chain; type II DNA topoisomerase B chain
C:Species: Escherichia coli
C:Date: 30-Sep-1988 #sequence_revision 31-Oct-1997 #text_change 05-Oct-2004
C:Accession: D65172; A26444; A36953; C22168; A38344
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: D65172
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-804 <BLAT>
A:Cross-references: UNIPROT:P06982; UNIPARC:UPI00001681E5; GB:AE000447; GB:U00096; NID:g288752
A:Experimental source: strain K-12, substrain MG1655
R:Adachi, T.; Mizuuchi, M.; Robinson, E.A.; Appella, E.; O'Dea, M.H.; Gellert, M.; Mizuuchi, Nucleic Acids Res. 15, 771-784, 1987
A:Title: DNA sequence of the E. coli gyrB gene: application of a new sequencing strategy.
A:Reference number: A93674; MUID:87146392; PMID:3029692

A;Accession: A26444
A;Molecule type: DNA
A;Residues: 1-384, 'A', 386-804 <ADA>
A;Cross-references: UNIPARC:UPI000016552C; GB:X04341; GB:X00870; NID:G41643; PIDN:CAA278
R;Menzel, R.; Gellert, M.
J. Bacteriol. 169, 1272-1278, 1987
A;Title: Fusions of the Escherichia coli gyrA and gyrB control regions to the galactokinase gene.
A;Reference number: A26953; MUID:87137287; PMID:3029031
A;Accession: A26953
A;Molecule type: DNA
A;Residues: 1-23 <MEN>
A;Cross-references: UNIPARC:UPI000016F1BF; GB:M15548; NID:G146307; PIDN:AAA23949.1; PID:
R;Adachi, T.; Mizunuchi, K.; Menzel, R.; Gellert, M.
Nucleic Acids Res. 12, 6389-6395, 1984
A;Title: DNA sequence and transcription of the region upstream of the E. coli gyrB gene.
A;Reference number: A22168; MUID:84237235; PMID:6089112
A;Accession: C22168
A;Molecule type: DNA
A;Residues: 1-50, 'R', 52-55, 'L', 57-106 <AD2>
A;Cross-references: UNIPARC:UPI00001730B3
R;Tamura, J.K.; Gellert, M.
J. Biol. Chem. 265, 21342-21349, 1990
A;Title: Characterization of the ATP binding site on Escherichia coli DNA gyrase. Affinity
A;Reference number: A38344; MUID:91065955; PMID:2174443
A;Accession: A38344
A;Molecule type: protein
A;Residues: 93-126, 'X', 128-129 <TAM>
A;Cross-references: UNIPARC:UPI00001730B4
A;Note: Lys-103 and Lys-110 were shown to bind covalently to the ATP analog and DNA gyrase.
C;Comment: DNA gyrase, which catalyzes DNA supercoiling and relaxing, is made up of two
C;Genetics:
A;Gene: gyrB
A;Map position: 83 min
C;Superfamily: Type II topoisomerase, subunit B
C;Keywords: antibiotic resistance; ATP; DNA supercoiling; isomerase
F;93-129/Region: ATP-binding

Query Match 50.6%; Score 40; DB 1; Length 804;
Best Local Similarity 61.5%; Pred. No. 1.2e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IEQYLNLLASYL 14
Db 349 VEQQMNELLAEYL 361

Search completed: July 5, 2006, 19:25:15
Job time : 16.6667 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 19:01:48 ; Search time 186 Seconds
(without alignments)
79.571 Million cell updates/sec

Title: US-10-774-928A-13
Perfect score: 79
Sequence: 1 EIEQVNLNLLASYLDF 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 7.2.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	60.8	458	Q7NB33 MYCGA	Q7nb33 mycoplasma
2	47	59.5	2982	Q4RXP0 TETNG	Q4rxp0 tetraodon n
3	46	58.2	336	Q20478 CAENORHABDI	Q20478 caenorhabdi
4	46	58.2	688	Q54MG6 DICTYOSTELI	Q54mg6 dictyosteli
5	45	57.0	266	Q4B3Q0 POLAROMONAS	Q4b3q0 polaromonas
6	45	57.0	988	Q813L6 PLAF7	Q813l6 plasmodium
7	44	55.7	245	Q4HIG6 CAMCO	Q4hig6 campylobact
8	44	55.7	519	Q5ZMD9 CHICK	Q5zmd9 gallus gall
9	44	55.7	619	Q7RD05 PLAYO	Q7rd05 plasmodium
10	44	55.7	1684	Q4UA79 THEAN	Q4ua79 theileria a
11	44	55.7	2543	Q8IBR8 PLAF7	Q8ibr8 plasmodium
12	43	54.4	248	Q5HUA7 CAMJR	Q5hua7 campylobact
13	43	54.4	309	Q9TYN8 CAEL	Q9ty n8 caenorhabdi
14	43	54.4	375	Q65280 ASF	Q65280 african swi
15	43	54.4	493	Q6KITS PICTO	Q6kity5 picophilus
16	43	54.4	565	Q33JY3 METHU	Q33jy3 methanospir
17	43	54.4	641	Q2NIG3 9MOLU	Q2nig3 aster yello
18	43	54.4	1793	YCF1 LOTJA	Q9bbn6 lotus japon
19	42	53.2	253	Q2XC9 PSEPU	Q2xc9 pseudomonas
20	42	53.2	253	Q88F14 PSEPK	Q88pf14 pseudomonas
21	42	53.2	256	Q52745 RUMPL	Q52745 ruminococcu
22	42	53.2	258	Q3NDQ2 9PROT	Q3ndq2 nitrosomona
23	42	53.2	267	Q7VJP4 HELHP	Q7vjp4 helicobacte
24	42	53.2	408	Q9XVK1 CAEL	Q9xvk1 caenorhabdi
25	42	53.2	471	Q9MA46 ARATH	Q9ma46 arabidopsis
26	42	53.2	558	Q4P454 USTWA	Q4p454 ustilago ma
27	42	53.2	602	Q35P20 9BRAD	Q35p20 bradyrhizob
28	42	53.2	837	Q67R65 SYMTH	Q67r65 symbiobacte
29	42	53.2	1613	1 RGYR METJA	Q58907 methanococc
30	42	53.2	1624	1 RGYR PYRHO	Q58530 pyrococcus
31	42	53.2	1711	1 RGYR PYRKO	Q6f598 pyrococcus

32 42 53.2 1898 2 Q54KP2 DICDI Q54kp2 dictyosteli
33 42 53.2 3583 2 Q9V3N4 DROME Q9v3n4 drosophila
34 42 53.2 3584 2 Q9U999 DROME Q9u999 drosophila
35 41 51.9 105 1 Y1301 RICCN Q92924 rickettsia
36 41 51.9 105 2 Q7PA41 RICSI Q7pa41 rickettsia
37 41 51.9 105 2 Q68Y09 RICTY Q68y09 rickettsia
38 41 51.9 110 2 Q4UJV6 RICFE Q4ujv6 rickettsia
39 41 51.9 161 2 Q6MU33 MYCMS Q6mu33 mycoplasma
40 41 51.9 220 1 RSA3 YEAST Q05942 saccharomyc
41 41 51.9 233 2 Q36L25 MARHY Q36l25 marinobacte
42 41 51.9 270 2 Q2IED0 9DELT Q2ied0 anaeromyxob
43 41 51.9 332 2 Q2US99 ASPOR Q2us99 aspergillus
44 41 51.9 332 2 Q61NZ5 CAERB Q61nz5 caenorhabdi
45 41 51.9 355 2 Q6RCS7 9ROSI Q6rcs7 corchorus c

ALIGNMENTS

RESULT 1

Q7NB33 MYCGA PRELIMINARY; PRT; 458 AA.
ID Q7NB33 MYCGA AC Q7NB33;
DT 15-DEC-2003, integrated into UniProtKB/T-EMBL.
DT 15-DEC-2003, sequence version 1.
DT 21-FEB-2006, entry version 15.
DE ARCA.
GN Name=arCA; OrderedLocusNames=MYCGA4470; ORFNames=MGA_0105;
OS Mycoplasma gallisepticum.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2096;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=R(low);
RX MEDLINE=22830409; PubMed=12949158; DOI=10.1099/mic.0.26427-0;
RA Papazisi L., Gorton T.S., Kutish G., Markham P.F., Browning G.F.,
RA Nguyen D.K., Swartzell S., Madan A., Mahairas G., Geary S.J.;
RT "The complete genome sequence of the avian pathogen Mycoplasma
RT gallisepticum strain R(low).";
RL Microbiology 149:2307-2316(2003).

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CC -----
CC EMBL; AB015450; AAP56797.1; -; Genomic DNA.
DR BioCyc; MGAL233150:MGA_0105-MONOMER; -;
DR GO; GO:0016990; P-arginine deiminase activity; IEA.
DR GO; GO:0006527; P-arginine catabolism; IEA.
DR InterPro; IPR003198; Amidino trans.
DR InterPro; IPR003876; Arg.deiminase.
DR Pfam; PF02274; Amidinotransf.; 1.
DR PRINTS; PR01466; ARGDEIMINASE.
KW Complete proteome.
SQ SEQUENCE 458 AA; 52887 MW; 69CD34ED174AC2D CRC64;

Query Match 60.8%; Score 48; DB 2; Length 458;

Best Local Similarity 83.3%; Pred. No. 17;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QYLNLLASLYLD 15
Db 112 QYLNLLASLYLD 123

*RESULT 2

Q4RXP0 TETNG PRELIMINARY; PRT; 2982 AA.
ID Q4RXP0 TETNG AC Q4RXP0;
DT 19-JUL-2005, integrated into UniProtKB/T-EMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Chromosome 11 SCAF14979, whole genome shotgun sequence.
GN ORFNames=GSTENG00027341001;


```
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidia; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Tuncgali B., Berriman M., Song J., Olsen R., Szatranski K., Xu Q.,
RA Suganb A., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loulseghe H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schlegel M., Weinstein G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Bartell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
CC -!- CAUTION: The sequence shown here is derived from an
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CC -----
CC EMBL; AAF10100124; EAL64732.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 688 688
SQ SEQUENCE 688 AA; 78241 MW; 33C58408004A0CC7 CRC64;

Query Match 58.2%; Score 46; DB 2; Length 688;
Best Local Similarity 75.0%; Pred. No. 60;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EQYNLLLSYL 14
DB 146 ENYLLLVNVL 157

RESULT 5
Q4B3Q0_9BURK PRELIMINARY; PRT; 266 AA.
AC Q4B3Q0;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Twin-arginine translocating C-subunit.
GN ORFNames=BprodRAFT_4563;
OS Polaromonas sp. JS666.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Polaromonas.
OX NCBI_TaxID=296591;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JS666;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Pliuck S., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pliuck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Polaromonas sp.
RT JS666.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JS666;
RA Hall N., Bowman S., Churcher C., Quail M., Barrall B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC
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RA Larimer F., Land M.;
RT "Annotation of the draft assembly of Polaromonas sp. JS666.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JS666;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Pliuck S., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pliuck S., Richardson P.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; AAF02000002; EAM40774.1; -; Genomic_DNA.
DR InterPro; IPR002033; Translocase.
DR Pfam; PF00902; TatC; 1.
DR PRINTS; PR01840; TATCFAMILY.
DR TIGRFAMs; TIGR00945; tatC; 1.
SQ SEQUENCE 266 AA; 28879 MW; F060941BBAA301D2 CRC64;

Query Match 57.0%; Score 45; DB 2; Length 266;
Best Local Similarity 50.0%; Pred. No. 33;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIEQVLLLSYLD 16
DB 162 DIEEVNVLGNFLAF 177

RESULT 6
Q8I3L6_PLAF7 PRELIMINARY; PRT; 988 AA.
AC Q8I3L6;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Hypothetical protein PFE1240w.
GN Name=PFE1240w;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=3D7;
RX MEDLINE=22255708; PubMed=12368867; DOI=10.1038/nature01095;
RA Hall N., Pain A., Berriman M., Churcher C.M., Harris B., Harris D.,
RA Mungall K.L., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R.M., Davis P., Dear P., Dearden F., Doggett J.,
RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sulston J.E., Craig A., Newbold C., Barrall B.G.;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
RL Nature 419:527-531(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=3D7;
RA Devlin K., Baker S., Davies P., Mungall K., Berriman M., Pain A.,
RA Hall N., Bowman S., Churcher C., Quail M., Barrall B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC
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DR EMBL; AL929354; CAD51612.1; -; Genomic DNA.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0005506; F: iron ion binding; IEA.
DR InterPro; IPR007197; Radical SAM.
DR Pfam; PF04055; Radical_SAM; I.
KW Hypothetical protein.
SQ SEQUENCE 988 AA; 116754 MW; 356FB2B826AB8335 CRC64;
Query Match 57.0%; Score 45; DB 2; Length 988;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 EIEQYLNLLASLYLDF 16
Db 841 EIDSYNILQLGYPDF 856
RESULT 7
QHIG6_CAMCO PRELIMINARY; PRT; 245 AA.
AC Q4HIG6;
DT 16-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein.
GN ORFNames=CC0927;
OS Campylobacter coli RM2228.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=306254;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RM2228;
RA Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Rasko D.A.,
RA Jacques R.J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,
RA Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U.,
RA Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,
RA Nelson K.E.;
RT "Major structural and novel potential virulence mechanisms from the
RT genomes of multiple Campylobacter species.";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
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-----
DR EMBL; AAF10100001; EAL57653.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 245 AA; 29199 MW; E6387DA72E8F1F47 CRC64;
Query Match 55.7%; Score 44; DB 2; Length 245;
Best Local Similarity 47.4%; Pred. No. 45;
Matches 9; Conservative 4; Mismatches 2; Indels 4; Gaps 1;
QY 2 IEQYLNLL----LASLYLDF 16
Db 104 ISEYNILQLFLAGYIDF 122
RESULT 8
Q5ZMD9_CHICK PRELIMINARY; PRT; 519 AA.
ID Q5ZMD9;
AC Q5ZMD9;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 21-FEB-2006, entry version 9.
DE Hypothetical protein.
GN ORFNames=RCJMB04_2h4;
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```
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
RA Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
RA Plachy J., Carninci P., Hayaishizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT gene function analysis.";
RL Genome Biol. 6:R6-R6(2005).
CC
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-----
DR EMBL; AJ719445; CAG31104.1; -; mRNA.
DR GO; GO:0005488; F: binding; IEA.
DR InterPro; IPR013143; PAM.
DR InterPro; IPR000717; PCI.
DR InterPro; IPR011990; TPR-like_helical.
DR Pfam; PF01399; PCI; 1.
DR SMART; SM00088; PINT; 1.
KW Hypothetical protein.
SQ SEQUENCE 519 AA; 59397 MW; 8D22F0307B685465 CRC64;
Query Match 55.7%; Score 44; DB 2; Length 519;
Best Local Similarity 64.3%; Pred. No. 1e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 EIEQYLNLLASLYL 14
Db 147 EVEAYLQLLEVIYL 160
RESULT 9
Q7RD05_PLAYO PRELIMINARY; PRT; 619 AA.
ID Q7RD05_PLAYO PRELIMINARY; PRT; 619 AA.
AC Q7RD05;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Homo sapiens RIKEN cDNA 1600015H11 gene-related.
GN ORFNames=PY05621;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=17XNL;
RA MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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DR EMBL; AABL01001803; EAA17664.1; -; Genomic_DNA.
DR HSSP; O43172; 1MZV.
DR InterPro; IPR003648; SFM.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINRPT.
DR SMART; SM00320; WD40; 6.
DR PROSITE; PS00678; WD REPEATS 1; UNKNOWN_1.
DR PROSITE; PS0082; WD REPEATS 2; 3.
DR PROSITE; PS0294; WD REPEATS REGION; 1.
KW Complete proteome; Repeat; WD repeat.
SQ SEQUENCE 619 AA; 72467 MW; 7287DC126095BCEA CRC64;

Query Match 55.7%; Score 44; DB 2; Length 619;
Best Local Similarity 43.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIEOYNLLASLYLDF 16
Db 104 EVBEFNILKKYIDF 119

RESULT 10
Q4UA79 THEAN PRELIMINARY; PRT; 1684 AA.
AC Q4UA79;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
GN ORFNames=TA07330;
OS Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OC NCBI_TaxID=5874;
RN [1];
RC STRAIN=Ankara isolate clone C9;
RP PubMed=15994597; DOI=10.1258/jrsm.98.7.320;
RA Pain A., Renauld H., Berriman M., Murphy L., Yeats C.A., Weir W.,
RA Kerhornou A., Aslett M., Bishop R., Bouchier C., Cochet M.,
RA Coulson R.M.R., Cronin A., de Villiers E.P., Fraser A., Fosker N.,
RA Gardner M., Goble A., Griffiths-Jones S., Harris D.E., Katzer F.,
RA Larke N., Lord A., Maser P., McKellar S., Mooney P., Morton F.,
RA Nene V., O'Neill S., Price C., Quail M.A., Rabinowitsch E.,
RA Rawlings N.D., Rutter S., Saunders D., Seeger K., Shah T., Squares R.,
RA Squares S., Tivey A., Walker A.R., Woodward J., Dobbelaere D.A.E.,
RA Langsley G., Rajandream M.A., McKeever D., Shields B., Tait A.,
RA Barrell B., Hall N.;
RA "Genome of the host-cell transforming parasite Theileria annulata
RT compared with T. parva.";
RL Science 309:131-133(2005).
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CC -----
DR EMBL; CR940353; CAI76274.1; -; Genomic_DNA.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 1684 AA; 194143 MW; B15B653F0A7AFDDF CRC64;

Query Match 55.7%; Score 44; DB 2; Length 1684;
Best Local Similarity 75.0%; Pred. No. 3.5e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EYLNLLASLYL 14
Db 534 EYLNLLASLYL 545

RESULT 11
Q8IBR8 PLAF7 PRELIMINARY; PRT; 2543 AA.
ID Q8IBR8 PLAF7
AC Q8IBR8;

DR EMBL; AL844506; CAD50930.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR011641; GCC2_GCC3.
DR Pfam; PF07699; GCC2_GCC3; 3.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS01186; EGF 2; 3.
SQ SEQUENCE 2543 AA; 296919 MW; 4353B37FF076D572 CRC64;

Query Match 55.7%; Score 44; DB 2; Length 2543;
Best Local Similarity 57.1%; Pred. No. 5.5e+02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 EYLNLLASLYLDF 16
Db 657 DDYLELLLSYLDY 670

RESULT 12
Q5HUA7 CAMJR PRELIMINARY; PRT; 248 AA.
ID Q5HUA7;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Hypothetical protein.
GN OrderedLocusNames=CJEL1136;
OS Campylobacter jejuni (strain RM1221).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OC NCBI_TaxID=195099;
RN [1];
RC NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15660156; DOI=10.1371/journal.pbio.0030015;
RA Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Rasko D.A.,
RA Ravel J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,
RA Dodson R.J., Durkin A.S., Madupu R., Sullivan S.A., Shetty J.U.,
RA Ayodeji M.A., Shvartsbeyn A., Schatz M.C., Badger J.H., Fraser C.M.,
RA Nelson K.E.;
RA "Major structural differences and novel potential virulence mechanisms
RT from the genomes of multiple Campylobacter species.";
RL PLoS Biol. 3:72-85(2005).
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CC -----
DR EMBL; CP000025; AAW35463.1; -; Genomic_DNA.
DR TIGR; CJEL1136; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 248 AA; 29753 MW; D530FF310BC05233 CRC64;

Query Match 54.4%; Score 43; DB 2; Length 248;
Best Local Similarity 47.4%; Pred. No. 69;
Matches 9; Conservative 4; Mismatches 2; Indels 4; Gaps 1;
```

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QY 2 IEQYNLL----LASYLDF 16
Db 104 ISEYNVLQGLFAGYIDF 122

RESULT 13
Q5280 ASF
ID Q5280_CABEL PRELIMINARY; PRT; 309 AA.
AC Q5280;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE Hypothetical protein Y39F10A.3.
GN ORFNames=Y39F10A.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998)
CC -----
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CC -----
DR EMBL; AF125450; AAD12817.1; -; Genomic_DNA.
DR PIR; T33888; T33888.
DR Ensembl; Y39F10A.3; Caenorhabditis elegans.
DR WormPep; Y39F10A.3; CE21727.
DR InterPro; IPR007744; DUF672.
DR Pfam; PF05050; DUF672; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 309 AA; 34939 MW; 0325BFDE32A09183 CRC64;

Query Match 54.4%; Score 43; DB 2; Length 309;
Best Local Similarity 53.3%; Pred. No. 87;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IEQYNLLLASYLDF 16
Db 293 VEKYGGLKVANYLDF 307

RESULT 14
Q5280 ASF
ID Q5280_ASF PRELIMINARY; PRT; 375 AA.
AC Q5280;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE T-lymphocyte surface antigen CD2 homologue.
GN Name=LW8DR;
OS African swine fever virus (ASFV).
OC Viruses; dsDNA viruses, no RNA stage; Asfarviridae; Asfivirus.
OX NCBI_TaxID=10497;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Malawi Lil-20/1;
RX MEDLINE=94167882; PubMed=7907198;
RA Borca M.V., Kutish G.F., Afonso C.L., Irueta P., Carrillo C., Brun A.,
RA Sussman M.D., Rock D.L.;
RT "An African swine fever virus gene with similarity to the T-lymphocyte
RT surface antigen CD2 mediates hemadsorption.";
RL Virology 199:463-468(1994).
CC -----
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CC -----
CC EMBL; L15337; AAA42720.1; -; Genomic_DNA.
SQ SEQUENCE 375 AA; 42430 MW; 61A38A8DABDA132F CRC64;

Query Match 54.4%; Score 43; DB 2; Length 375;
Best Local Similarity 72.7%; Pred. No. 1.1e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 LNLILLASYLDF 16
Db 191 INTLLSSYLDF 201

RESULT 15
Q5KYT5 PICTO
ID Q6KYT5_PICTO PRELIMINARY; PRT; 493 AA.
AC Q6KYT5;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Phytoene dehydrogenase (EC 1.3.-.-).
GN OrderedLocustNames=PTO1532;
OS Picrophilus torridus.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Picrophilaceae; Picrophilus.
OX NCBI_TaxID=82076;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=DSM 9790 / ATCC 700027;
RX PubMed=15184574; DOI=10.1073/pnas.0401356101;
RA Fuetterer O., Angelov A., Liesegang H., Gottschalk G., Schleper C.,
RA Schepers B., Dock C., Antranikian G., Liebl W.;
RT "Genome sequence of Picrophilus torridus and its implications for life
RT around pH 0.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096(2004).
CC -----
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CC -----
EMBL; AE017261; AAT44117.1; -; Genomic_DNA.
DR GO; GO:0050660; FAD binding; IEA.
DR GO; GO:0016705; P:oxidoreductase activity, acting on paired d. . .; IEA.
DR GO; GO:0016117; P:carotenoid biosynthesis; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006076; FAD oxred.
DR InterPro; IPR008151; Phytoene_DH_rel.
DR Pfam; PF01593; Amino_oxidase; 1.
DR Pfam; PF01266; DAO; 1.
DR ProDom; PD139017; Phytol dehydro; 1.
KW Complete proteome; Oxidoreductase.
SQ SEQUENCE 493 AA; 56625 MW; 4136BFF4D3588E16 CRC64;

Query Match 54.4%; Score 43; DB 2; Length 493;
Best Local Similarity 43.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIEQYNLLASYLDF 16
Db 393 KLEEYLNENIIDYIDF 408

Search completed: July 5, 2006, 19:18:20
Job time : 189 secs
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 18:44:12 ; Search time 147.667 Seconds
(without alignments)
49.540 Million cell updates/sec

Title: US-10-774-928a-13
Perfect score: 79
Sequence: 1 ETEQYLNLLASVLDLF 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 8.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*
10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	16	AAO26393	Aao26393 Psoriasis
2	79	100.0	16	ADVO4418	Adv04418 Leishmania
3	44	55.7	385	ABG27716	Abg27716 Novel hum
4	44	55.7	417	AAE33677	Aae33677 Human str
5	43	54.4	127	AAE72685	Aag72685 Murine OR
6	42	53.2	471	ADN72161	Adn72161 Thale cre
7	42	53.2	496	ABG99094	Abg99094 Methanoco
8	42	53.2	496	ADL23828	Adl23828 Methanoco
9	42	53.2	496	AEF76704	Aef76704 Methanoco
10	42	53.2	1711	ADN46550	Adn46550 Thermococ
11	42	53.2	3583	ABB64814	Abb64814 Drosophil
12	41	51.9	170	AAE06786	Aae06786 Human dua
13	41	51.9	220	ABR52601	Abr52601 Protein s
14	41	51.9	220	ADK63900	Adk63900 Disease t
15	41	51.9	241	AAE06776	Aae06776 Human, dua
16	41	51.9	498	AAE04835	Aae04835 Human-SGP
17	41	51.9	509	AAE06775	Aae06775 Human dua
18	41	51.9	509	AAE07045	Aae07045 Human dua
19	41	51.9	509	AAE07044	Aae07044 Human dua
20	41	51.9	509	ADN76018	Adn76018 Human DSP
21	41	51.9	509	ADN75960	Adn75960 Human sig
22	41	51.9	509	ADY37105	Ady37105 Protein t
23	41	51.9	590	ABG34140	Abg34140 Antibody

24	41	51.9	590	7	ADC66319	Adc66319 Chinese h
25	41	51.9	590	7	ADL18099	Adl18099 Anti-lect
26	41	51.9	590	7	ADL35263	Adl35263 Chinese h
27	41	51.9	597	6	ADA33416	Ada33416 Acinetoba
28	40	50.6	128	3	AAG11666	Aag11666 Arabidops
29	40	50.6	128	3	AAG53339	Aag53339 Arabidops
30	40	50.6	128	8	ADT55865	Adt55865 Plant pol
31	40	50.6	128	10	AEF29162	Aef29162 Lead_Cere
32	40	50.6	128	10	AEF29160	Aef29160 Protein e
33	40	50.6	180	9	AEC77038	Aec77038 Protein e
34	40	50.6	180	9	AEC77041	Aec77041 Protein e
35	40	50.6	239	6	ABM68652	Abm68652 Photorhab
36	40	50.6	301	6	ABM68681	Abm68681 Photorhab
37	40	50.6	336	6	ABM68968	Abm68968 Photorhab
38	40	50.6	500	6	ABU39986	Abu39986 Protein e
39	40	50.6	594	2	AAW36811	Aaw36811 Human GDP
40	40	50.6	594	8	ADO57047	Ado57047 Human fuc
41	40	50.6	594	9	ADX80743	Adx80743 Human fuc
42	40	50.6	748	5	ABP73773	Abp73773 Candida a
43	40	50.6	804	4	AAU34800	Aau34800 E. coli c
44	40	50.6	804	6	ABU28825	Abu28825 Protein e
45	40	50.6	966	4	ABB61168	Abb61168 Drosophil

ALIGNMENTS

RESULT 1
AAO26393
ID AAO26393 standard; peptide; 16 AA.
XX
AC AAO26393;
XX
DT 30-JAN-2003 (first entry)
XX
DE Psoriasis treating immunotherapeutic peptide, SEQ ID No 13.
XX
KW Antipsoriatic; immunostimulant; gene therapy; pharmaceutical composition;
KW vaccine; immunogenic variant; immunotherapeutic agent; psoriasis;
KW gene therapy.
XX
OS Leishmania sp.
XX
PN WO200274239-A2.
XX
PD 26-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006496.
XX
PR 16-MAR-2001; 2001US-00809003.
XX
(AKIV-) AKIVA LLC.
XX
O'daly JA;
XX
WPI; 2003-018763/01.
XX
New polypeptide and immunogenic variants comprising amino acid sequences of particulate antigens, useful for the treatment and clinical remission of psoriasis.
XX
Claim 1; Page 43; 56pp; English.
XX
The invention relates to a polypeptide comprising an isolated amino acid sequence or immunogenic variants selected from any of 14 fully defined sequences of 7-16 amino acids, given in the specification. The immunotherapeutic agents and a pharmaceutical compositions comprising polynucleotides and vectors of the invention are useful for the treatment and clinical remission of psoriasis. The isolated nucleic acids are useful as probes. The sequences of the invention can be used in the treatment of disorders by gene therapy. This sequence represents one of the 14 immunotherapeutic peptides of the invention

SQ Sequence 16 AA;

Query Match 100.0%; Score 79; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EIEQYLNLLASYLDF 16
|||||
DB 1 EIEQYLNLLASYLDF 16

RESULT 2
ADV04418
ID ADV04418 standard; peptide; 16 AA.
XX
AC ADV04418;
XX
DT 24-FEB-2005 (first entry)
XX
DE Leishmania immunotherapeutic peptide SEQ ID NO:13.
XX
KW T-lymphocyte; immunogenicity; antigen; antipsoriatic; immunostimulant;
KW psoriasis.
XX
OS Leishmania sp.
XX
PN US2004241168-A1.
XX
PD 02-DEC-2004.
XX
PF 09-FEB-2004; 2004US-00774928.
XX
PR 16-MAR-2001; 2001US-00809003.
PR 17-OCT-2003; 2003US-00687892.
XX
PA (ODAL/) ODALY J A.
PI Odaly JA;
XX
WPI; 2005-011563/01.
XX
Inhibiting selectively T-cell rolling in human, by administering compound
PT interfering with cutaneous lymphocyte antigen-E selectin interaction and
PT leukocyte function associated antigen-1 interaction.
XX
Claim 18; SEQ ID NO 13; 21pp; English.
XX
The invention relates to a novel method for selectively inhibiting T-cell
CC rolling in a human host, comprising administering a compound that
CC selectively interferes with the cutaneous lymphocyte antigen (CLA)-E
CC selectin interaction and leukocyte function associated antigen (LFA)-
CC 1/intercellular adhesion molecule (ICAM) and very late antigen
CC (VLA)/vascular cell adhesion molecule (VCAM) interactions. The compound
CC includes an immunotherapeutic agent, which comprises a purified protein
CC extract that is isolated by diethylaminoethyl Sephadex chromatography of
CC a Nonidet P-40 insoluble particulate antigen fraction derived from
CC isolated killed cells of anastigotes from one or more species of the
CC Leishmania genus, where the particulate antigen fraction is solubilized
CC with 8M urea and 0.025 M Tris(hydroxymethyl)aminomethane pH 8.3 applied
CC to diethylaminoethyl Sephadex and is eluted with a solution comprising
CC 0.1 M sodium chloride, 8 M urea and 0.025 M
CC Tris(hydroxymethyl)aminomethane pH 8.3, and the purified protein extract
CC includes polypeptides having apparent molecular weights of 73, 80 and 82
CC kDa, after total reduction and alkylation. The species is L. amazonensis,
CC L. venezuelensis, L. brasiliensis and/or L. chagasi. A compound of the
CC invention has antipsoriatic and immunostimulant activity, and inhibits T-
CC cell rolling by interfering with CLA-E selectin interaction and LFA-
CC 1/ICAM and VLA/VCAM interactions. The method is useful for selectively
CC inhibiting T-cell rolling in a human host, and for treating psoriasis.
CC The present sequence represents a Leishmania peptide used in the
XX invention.

SQ Sequence 16 AA;

Query Match 100.0%; Score 79; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EIEQYLNLLASYLDF 16
|||||
DB 1 EIEQYLNLLASYLDF 16

RESULT 3
ABG27716
ID ABG27716 standard; protein; 385 AA.
XX
AC ABG27716;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #27707.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
WPI; 2001-639362/73.
DR N-PSDB; AAS91903.
XX
New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
Claim 20; SEQ ID NO 58075; 103pp; English.
XX
The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 385 AA;

Query Match 55.7%; Score 44; DB 4; Length 385;

Best Local Similarity 73.3%; Pred. No. 1.1e+02; Mismatches 4; Indels 0; Gaps 0;
Matches 11; Conservative 0;

QY 1 EIEQYLNLLASYLD 15
| | | | |
Db 172 ETMQSLNDLLASYLD 186

RESULT 4

AAE33677
ID AAE33677 standard; protein; 417 AA.

XX AC AAE33677;

XX DT 16-APR-2003 (first entry)

XX DE Human structural and cytoskeleton-associated protein (SCAP) #11.

XX Human; structural and cytoskeleton-associated protein; SCAP; leukaemia;
KW cell proliferative disorder; actinic keratosis; cancer; gastroenteritis;
KW cirrhosis; psoriasis; adenocarcinoma; Creutzfeldt-Jakob disease; stroke;
KW sarcoma; neurological disorder; epilepsy; seasonal affective disorder;
KW Huntington's disease; Alzheimer's disease; lymphoma; melanoma; myeloma;
KW anxiety; schizophrenia; amnesia; viral infection; pneumonia; influenza;
KW arteriosclerosis; smallpox; Colorado tick fever; rabies; gene therapy;
KW neuroprotective; nootropic; neuroleptic; cytostatic; virucide.

XX OS Homo sapiens.

XX PN WO2002101009-A2.

XX PD 19-DEC-2002.

XX PF 06-JUN-2002; 2002WO-US017956.

XX PR 07-JUN-2001; 2001US-0296865P.

XX PR 08-JUN-2001; 2001US-0296878P.

XX PR 15-JUN-2001; 2001US-0298664P.

XX PR 21-JUN-2001; 2001US-0300149P.

XX PR 29-JUN-2001; 2001US-0302340P.

XX PR 06-JUL-2001; 2001US-0303481P.

XX PR 12-JUL-2001; 2001US-0305059P.

XX PR 21-DEC-2001; 2001US-0343557P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Tang TY, Warren BA, Honchell CD, Richardson TW, Elliott VS;

XX PI Wallia NK, Yue H, Batra S, Griffin JA, Baughn MR, Forsythe IU;

XX PI Burford N, Emerling BM, Sanjanwala MM, Khan FA, Lu DAM, Hafalia AJA;

XX PI Nguyen DB, Yang J, Li JX, Becha SD, Yao MG, Gietzen KJ, Luo W;

XX PI Lee EA, Ison CH, Lasek AKW;

XX WPI; 2003-148791/14.

XX DR N-PSDB; AAD51574.

XX PS Claim 1; Col 181-182; 121pp; English.

XX The invention relates to human structural and cytoskeleton-associated
CC proteins (SCAP) and genes. SCAP sequence and agonist are useful for
CC treating a disease or condition associated with decreased expression of
CC functional SCAP. The antagonist is useful for treating a disease or
CC condition associated with over expression of functional SCAP. The
CC antibody that specifically binds to the polypeptide is useful for
CC diagnosing a condition or disease associated with the expression of SCAP.
CC SCAP sequence, agonists and antagonists are particularly useful for
CC diagnosing, treating or preventing cell proliferative disorders (e.g.
CC actinic keratosis, arteriosclerosis, cirrhosis, psoriasis, or cancers
CC including adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma or

CC sarcoma), neurological disorders (e.g. epilepsy, seasonal affective
CC disorder, Huntington's disease, stroke, Alzheimer's disease, anxiety,
CC Creutzfeldt-Jakob disease, schizophrenia or amnesia) or viral infections
CC (e.g. pneumonia, herpes, influenza, Colorado tick fever, smallpox, rabies
CC or gastroenteritis). SCAP DNA is also used in gene therapy. The present
CC sequence is human SCAP protein

XX Sequence 417 AA;

Query Match 55.7%; Score 44; DB 6; Length 417;

Best Local Similarity 73.3%; Pred. NO. 1.2e+02;

Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIEQYLNLLASYLD 15

Db 80 ETMQSLNDLLASYLD 94

RESULT 5

AAAG72685

ID AAG72685 standard; protein; 127 AA.

XX AC AAG72685;

XX DT 31-JUL-2001 (first entry)

XX DE Murine OR-like polypeptide query sequence, SEQ ID NO: 2367.

XX KW Mouse; olfactory receptor; OR; primary scent determination;

XX KW secondary scent determination; polypeptide library; odour receptor;

XX KW scent profile; scent fingerprint; scent representation.

XX OS Mus musculus.

XX PN WO200127158-A2.

XX PD 19-APR-2001.

XX PF 06-OCT-2000; 2000WO-US027582.

XX PR 08-OCT-1999; 99US-0158615P.

XX PR 24-FEB-2000; 2000US-0184809P.

XX PA (DIGI-) DIGISCENTS.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

XX WPI; 2001-290713/30.

XX New polynucleotides which encode polypeptides involved in olfactory

XX sensation for identifying olfactory agonists and antagonists.

XX Example 6; Page 1603; 1857pp; English.

XX The present sequence is a polypeptide encoded by one of 105 newly mined

XX mouse genes. It was used as a query sequence in a database search of

XX olfactory receptor (OR)-like sequences. The invention relates to isolated

XX polynucleotides encoding polypeptides involved in olfactory sensation.

XX The polynucleotides can be used in screening for olfactory agonists and

XX antagonists. The methods allow for the determination of primary scents

XX and the identification of the odour receptors used to detect these

XX primary scents. The methods also enable determination of secondary scents

XX and the identification of combinations of odour receptors that are

XX involved in detecting such secondary scents. This enables the

XX construction of a scent representation (also called a scent fingerprint

XX or scent profile), which may be used to re-create and edit scents.

XX Libraries of olfactory receptors are useful for determining the

XX interaction pattern of a composition with the receptors, and can be used

XX for determining differences in the olfactory faculties of different

XX individuals

XX Sequence 127 AA;

Query Match 54.4%; Score 43; DB 4; Length 127;
 Best Local Similarity 66.7%; Pred. No. 46;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 QYLNLLASYLD 15
 |||||: |||
 Db 4 QYLNLLINLSYID 15

RESULT 6
 ADN72161
 ID ADN72161 standard; protein; 471 AA.
 XX
 AC ADN72161;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 56.
 KW plant; transgenic; E2Fa/Dpa transcription factor; growth regulator;
 KW animal feed product; thale cress; cell wall biosynthesis;
 KW nitrogen metabolism; carbon metabolism.
 XX
 OS Arabidopsis thaliana.
 XX
 PN WO2004035798-A2.
 XX
 PD 29-APR-2004.
 XX
 PF 20-OCT-2003; 2003WO-EP011659.
 XX
 PR 18-OCT-2002; 2002EP-00079408.
 XX
 PA (CROP-) CROPDESIGN NV.
 XX
 PI Inze D, De Veylder L, Vlieghe K;
 XX
 DR WPI; 2004-348466/32.
 DR N-PSDB; ADN72160.
 XX
 PT Altering plant characteristics, useful for producing plants for enzyme or
 PT pharmaceutical production comprises modifying in a plant, expression of
 PT one or more nucleic acids and/or modifying level or activity of one or
 PT more proteins.
 XX
 PS Claim 1; SEQ ID NO 56; 134pp; English.
 XX
 CC This invention relates to a novel method for altering one or more plant
 CC characteristics. Specifically, it refers to identifying genes that are up
 CC - or down-regulated in transgenic plants overexpressing the heterodimeric
 CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to
 CC alter plant characteristics accordingly. The present invention describes
 CC generating transgenic plants for the production of growth regulators,
 CC enzymes, therapeutic, pharmaceuticals and animal feed products, where
 CC the altered plant characteristics are selected from increased yield or
 CC biomass, enhanced survival capacity, stress tolerance, plant architecture
 CC or physiology, altered endoreplication, biochemistry, signal
 CC transduction, storage lipid mobilisation and/or altered photosynthesis,
 CC each relative to the corresponding wild type plants. Accordingly, these
 CC sequences can also be useful as positive or negative selectable markers
 CC during transformation of cells or tissues. The identified genes play a
 CC role in a variety of biological processes such as DNA replication, cell
 CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as
 CC transcription factors. This polypeptide sequence is thale cress protein
 CC expressed by a gene upregulated 1.3 fold or more in plants overexpressing
 CC the E2Fa/Dpa transcription factor, given in an exemplification of the
 CC invention.
 XX
 SQ Sequence 471 AA;

Query Match 53.2%; Score 42; DB 8; Length 471;
 Best Local Similarity 62.5%; Pred. No. 2.9e+02;

Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIEOYLNLLASYLDF 16
 |||:|||||
 Db 107 EITRYGNLLSASYKGF 122

RESULT 7
 ABG99094
 ID ABG99094 standard; protein; 496 AA.
 XX
 AC ABG99094;
 XX
 DT 11-SEP-2003 (revised)
 DT 14-JAN-2003 (first entry)
 XX
 DE Methanococcus jannaschii intein Mja r-Gyr.
 XX
 KW Intein; intein-catalysed cyclic peptide library; cancer; tumour cell;
 KW cardiovascular disease; obesity; neurological disorder; apoptosis;
 KW cell death; cell division; cell growth; arrhythmia potential;
 KW cardiomyocyte; heart failure; sarcotomal calcium cycling; stroke;
 KW cell proliferation; atherosclerosis; metabolism; skin disorder;
 KW bone morphogenetic protein; endocrinology; infectious disease;
 KW viral infection; bacterial infection; diabetic ulcer; wound healing;
 KW keloid formation; skin connective tissue cell; antibiotic transport;
 KW drug resistance; cytostatic; anorectic; neuroprotective; cardiant;
 KW haemostatic.
 XX
 OS Methanocaldococcus jannaschii.
 XX
 PN WO200166565-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 06-MAR-2001; 2001WO-US007162.
 XX
 PR 06-MAR-2000; 2000US-0187130P.
 XX
 PA (RIGE-) RIGEL PHARM INC.
 XX
 PI Kinsella TM;
 XX
 DR WPI; 2001-589926/66.
 XX
 PT Fusion polypeptide for generating libraries of cyclic peptides in vivo,
 PT comprises terminal intein motifs and a random peptide.
 XX
 PS Disclosure; Fig 3T; 115pp; English.
 XX
 CC The present invention relates to methods and compositions utilising
 CC inteins to generate libraries of cyclic peptides in vivo. The
 CC compositions of the invention are useful for making cyclic peptides in
 CC vivo. Libraries of cells can be transformed with libraries of fusion for
 CC nucleic acids. Intein-catalysed cyclic peptide libraries are useful for
 CC screening for an altered phenotype and identifying target molecules. The
 CC library is introduced into a cell, screened for an altered phenotype and
 CC target molecules that bind to the cyclic peptide are isolated. The method
 CC is useful for making cyclic peptides which retain biological activity,
 CC and for screening for cyclic peptides capable of altering the phenotype
 CC of a cell. The cyclic peptides are useful for altering cellular
 CC phenotypes and/or physiology, in screening assays to identify target
 CC molecules associated with changes in cellular phenotype or physiology and
 CC as drugs to treat a number of disease state, such as cancer,
 CC cardiovascular diseases, obesity and neurological disorders. The
 CC bioactive cyclic peptide is useful as the starting point for
 CC designing/synthesising derivative molecules with similar or more
 CC favourable properties for use as a drug and to pull out target molecules.
 CC By introducing random libraries into any tumour cell, peptides which
 CC induce apoptosis, cell death, loss of cell division or decreased cell
 CC growth can be identified and this method is useful in cancer
 CC applications. The methods are also useful in cardiovascular applications,
 CC to screen for diminished arrhythmia potential in cardiomyocytes, for

CC enhanced contractile properties of cardiomyocytes and diminish heart
 CC failure potential and to identify agents that regulate the intracellular
 CC and sarcolemmal calcium cycling in cardiomyocytes to prevent arrhythmias
 CC and agents that diminish embolic phenomena in arteries and arterioles
 CC leading to stroke. Candidate bioactive peptide libraries are inserted
 CC into these cell types and their proliferation in response to specific
 CC stimuli is monitored. Furthermore, the methods are also useful in
 CC screening for decreases in atherosclerosis, in screens to regulate
 CC obesity by controlling food intake mechanisms or reducing the responses
 CC of the receptor signalling pathways that regulate metabolism, in
 CC neurobiology applications, to screen for agonists of bone morphogenetic
 CC proteins, in skin biology applications, endocrinology applications,
 CC infectious disease applications including viral and bacterial infection,
 CC to screen for cyclic peptides which block HIV-1 infection, regulation or
 CC inhibition of keloid formation and wound healing for diabetic ulcers.
 CC Candidate libraries are inserted into skin connective tissue cells and
 CC bioactive peptides which promote the growth of these cells are isolated.
 CC Further applications include screening for bioactive peptides that block
 CC antibiotic transport mechanisms, drug toxicities and drug resistance,
 CC improving the performance of existing or developmental drugs, and in
 CC biotechnology. ABG99075-ABG99098 represent inteins from different
 CC organisms. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 496 AA;

Query Match 53.2%; Score 42; DB 4; Length 496;
 Best Local Similarity 53.8%; Pred. No. 3e+02;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 EOYNLLASYLD 15
 DB 280 ESYNALIAGYFD 292

RESULT 8

ADL23828
 ID ADL23828 standard; protein; 496 AA.

XX AC ADL23828;

XX DT 03-JUN-2004 (first entry)

DE Methanococcus jannaschii intein Mja r-Gyr amino acid sequence.

XX cyclic peptide; interacting protein inhibition; fusion nucleic acid;
 KW intein motif; intein; intein-catalysed cyclic peptide library;
 KW cancer cell line; cardiovascular; neurobiology; bone biology;
 KW biotechnology; skin biology; endocrinology; drug toxicity;
 KW drug resistance; drug development.

XX OS Methanocaldococcus jannaschii.

XX PN WO2004019890-A2.

XX PD 11-MAR-2004.

XX PF 30-AUG-2003; 2003WO-US027371.

XX PR 30-AUG-2002; 2002US-00232758.

XX PR 23-APR-2003; 2003US-00422536.

XX PA (RIGE-) RIGEL PHARM INC.

XX PI Lorens JB, Pray T, Kinsella TM, Bennett MK;

XX DR WPI; 2004-239115/22.

XX Generating intracellular cyclic peptide libraries, useful in identifying
 PT interaction of interacting proteins by providing cells comprising first
 PT and second interacting protein, and contacting cells with library of
 PT fusion nucleic acids.

XX Disclosure; Fig 3T; 156pp; English.

XX The present invention describes a method (M1) for identifying a cell
 CC comprising cyclic peptides which prevent interaction of interacting
 CC proteins. M1 comprises providing cells with first and second interacting
 CC proteins and contacting cells with a library of fusion nucleic acids
 CC comprising (from 5' to 3'): a nucleic acid encoding a C-terminal intein
 CC motif, a peptide, and an N-terminal intein motif, under conditions such
 CC that cyclic peptide is formed. Also described is a method (M2) for
 CC isolating the nucleic acid that encodes the cyclic peptide which when
 CC introduced into cell caused the change in ubiquitination of the molecule,
 CC comprising contacting a cell culture with an intein-catalysed cyclic
 CC peptide library such that cells in the culture receive not more than one
 CC member of the library, and monitoring the cells for a change in
 CC ubiquitination of a molecule. M1 is useful for identifying a cell
 CC comprising a cyclic peptide which is capable of preventing interaction of
 CC interacting proteins. M1 is useful in creating cell lines from cancer
 CC patients and in cardiovascular, neurobiology, drug toxicities and drug
 CC resistance applications. M1 is useful for identifying agents that
 CC regulates intracellular and sarcolemmal calcium cycling in
 CC cardiomyocytes, agents that diminish embolic phenomena in arteries and
 CC arterioles, and for screening peptides that block transport mechanisms.
 CC M1 is useful for screening enhanced contractile properties of
 CC cardiomyocytes. M1 enables screening of a large number of cell types
 CC under a wide variety of conditions. M1 enables improvement in the
 CC performance of existing or developmental drugs. The present sequence is
 CC used in the exemplification of the present invention.

XX Sequence 496 AA;

Query Match 53.2%; Score 42; DB 8; Length 496;
 Best Local Similarity 53.8%; Pred. No. 3e+02;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 EOYNLLASYLD 15
 DB 280 ESYNALIAGYFD 292

RESULT 9

AEF76704

ID AEF76704 standard; protein; 496 AA.

XX AC AEF76704;

XX DT 06-APR-2006 (first entry)

DE Methanococcus jannaschii intein Mja r-Gyr amino acid sequence.

XX screening; protein interaction; protein production; intein; cytostatic;
 KW cardiovascular-gen.; neuroprotective; cancer; cardiovascular disease;
 KW neurodegenerative disease.

XX OS Methanocaldococcus jannaschii.

XX PN US2005260626-A1.

XX PD 24-NOV-2005.

XX PF 28-FEB-2005; 2005US-00069642.

XX PR 06-MAR-2000; 2000US-0187130P.

XX PR 06-MAR-2001; 2001US-00800770.

XX PR 30-AUG-2003; 2003WO-US027371.

XX PA (RIGE-) RIGEL PHARM INC.

XX PI Lorens JB, Pray TR, Kinsella TM, Bennett MK;

XX DR WPI; 2006-190833/20.

XX Identifying a cyclic peptide capable of modulating the ubiquitination of
 PT a molecule, comprises contacting a cell culture with a nucleic acid

PT library encoding an intein-catalyzed cyclic peptide library.
XX Disclosure; SEQ ID NO 20; 205pp; English.
PS
XX The invention relates to a screening method comprising contacting a
culture of cells with a nucleic acid library encoding an intein-catalyzed
cyclic peptide library, monitoring the cells for a change in
ubiquitination of a molecule within a cell, and isolating the nucleic
acid that encodes the cyclic peptide that when introduced into the cell
caused the change in ubiquitination of the molecule. The method is useful
for identifying a cyclic peptide capable of modulating ubiquitination of
a molecule. The screening method (not necessarily limited to identifying
only cyclic peptides that affect ubiquitination) can be used for
identifying cyclic peptides for treating a wide variety of conditions
e.g. cancer, cardiovascular disease, or neurodegenerative disease. The
present sequence represents an intein amino acid sequence, which is used
in the exemplification of the present invention.
XX
SQ Sequence 496 AA;
Query Match 53.2%; Score 42; DB 10; Length 496;
Best Local Similarity 53.8%; Pred. No. 3e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 3 EOYLNLLASYLD 15
| | | | |
Db 280 ESYINALIAGYFD 292
| | | | |
RESULT 10
ADN46550
ID ADN46550 standard; protein; 1711 AA.
AC ADN46550;
XX
XX 01-JUL-2004 (first entry)
XX Thermococcus kodakaraensis KOD1 protein sequence SeqID428.
XX gene disruption; gene targeting; marker gene; transformation;
KW homologous recombination; hyperthermostable archaeobacterium; KOD1;
KW gene structure; gene function; enzyme activity; medicine;
KW forensic science; food; drug inspection; molecular biology; immunology.
XX
XX Thermococcus kodakaraensis.
OS
XX WO2004022736-A1.
FN
XX 18-MAR-2004.
PD
XX 29-AUG-2003; 2003WO-IB003597.
PF
XX 30-AUG-2002; 2002JP-00319011.
PR
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA
XX Imanaka T, Atomi H;
PI
XX WPI; 2004-257583/24.
DR
XX
XX Method for disrupting targeted gene in genome of organism particularly
thermostable bacterium and with genome chips for analysis, applicable in
PT studying gene structure and functions.
PT
XX Claim 9; SEQ ID NO 428; 598pp; Japanese.
PS
XX This invention relates to a novel method for targeting disruption of an
arbitrary gene in a genome of an organism which comprises providing the
whole sequential data of the genome of such organism, selecting at least
1 arbitrary region in the sequence, providing a vector that contains a
sequence homologous with the selected region and a marker gene.
CC transformation, and homologous recombination. The genome is preferably
the genome of a hyperthermostable archaeobacterium, particularly

CC Thermococcus kodakaraensis KOD1. The method is for targeting the
disruption of a gene in the genome of an organism, which is applicable in
studying gene structure and functions as well as enzyme activities of
encoded proteins and useful in medicine, forensic science, food or drug
inspection, molecular biology and immunology. With this method, the
disruption of a gene at an arbitrary position in a genome can be achieved
efficiently and reliably. The present sequence is that of a protein
encoded by the genome of Thermococcus kodakaraensis which was derived
using the method of the invention. Note: The sequence data for this
patent did not form part of the printed specification, but was obtained
in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1711 AA;
Query Match 53.2%; Score 42; DB 8; Length 1711;
Best Local Similarity 46.2%; Pred. No. 1.2e+03;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 3 EOYLNLLASYLD 15
| | | | |
Db 1235 BEYNAMIAGYFD 1247
| | | | |
RESULT 11
ABB64814
ID ABB64814 standard; protein; 3583 AA.
AC ABB64814;
XX
XX 26-MAR-2002 (first entry)
XX Drosophila melanogaster polypeptide SEQ ID NO 21234.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
KW
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
FN
XX 27-SEP-2001.
PD
XX 23-MAR-2001; 2001WO-US009231.
PF
XX 23-MAR-2000; 2000US-0191637P.
PR
XX 11-JUL-2000; 2000US-00614150.
PR
XX (PEKE) PE CORP NY.
PA
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI; 2001-656860/75.
DR
XX N-PSDB; ABL08917.
DR
XX New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signalling and cell-cell
interactions.
PT
XX Disclosure; SEQ ID NO 21234; 21pp + Sequence Listing; English.
PS
XX The invention relates to an isolated nucleic acid detection reagent
capable of detecting 1000 or more genes from Drosophila. The invention is
useful in developmental biology and in elucidating cell signalling and
cell-cell interactions in higher eukaryotes for the development of
insecticides, therapeutics and pharmaceutical drugs. The invention
discloses genomic DNA sequences (ABU16176-ABL30511), expressed DNA
sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
ABB72072). The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3583 AA;

Query Match 53.2%; Score 42; DB 4; Length 3583;
Best Local Similarity 53.8%; Pred. No. 2.7e+03;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY	4 QYLNLLASYLDF	16
	: : : : : :	
Db	2360 RYLNFLIADHLEF	2372

RESULT 12
AAE06786
ID AAE06786 standard; protein: 170 AA.

AC AAE06786;

DT 16-OCT-2001 (first entry)

DE Human dual-specificity phosphatase (DSP)-13 partial protein.

Human; dual-specificity phosphatase; DSP-13; dual phosphorylation motif; mitogen-activated protein kinase; MAP-kinase; graft-versus-host disease; GVHD; Duchenne muscular dystrophy; therapy; cancer; autoimmune disease; allergy; metabolic disease; cell growth; cell proliferation; cytostatic; cell cycle abnormality; cell differentiation; antiallergic; muscular; immunosuppressive.

OS Homo sapiens.

XX
PN
WO200157221-A2.

09-AUG-2001.

01-FEB-2001; 2001WO-US003429.

AA
PR 02-FEB-2000; 2000US-0179886P.

PA (CEPT-) CEPTYR INC.

XX Luche RM, Wei B;

WPI; 2001-488887/53.

PT New isolated dual-specificity phosphatase polypeptide for treating
PT cancer, graft-versus-host disease, autoimmune diseases, allergies,
PT metabolic diseases, abnormal cell growth and abnormal cell proliferation.
PT

PS Example 1; Fig 6: 81pp; English.

The present sequence is human dual-specificity phosphatase (DSP)-13 partial protein. Inactivation of mitogen-activated protein kinase (MAP-kinase) is mediated by dephosphorylation at a dual phosphorylation motif by DSP which is referred to as MAP-kinase phosphatase. An agent that modulates DSP is useful for treating a disorder selected from Duchenne muscular dystrophy, cancer, graft-versus-host disease (GVHD), autoimmune diseases, allergies, metabolic diseases, abnormal cell growth, abnormal cell proliferation and cell cycle abnormalities. DSP is useful for identifying antibodies and other agents that inhibit DSP-12 and/or DSP-13 activity. DSP and the agents identified are useful for modulating cell proliferation, differentiation and survival. DSP is useful in screening assays for modulators of enzyme activity and substrate binding and for dephosphorylating a substrate of DSP-12 or DSP-13.

Sequence 170 AA;

```
Query Match      51.9%; Score 41; DB 4; Length 170;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

QY 1 EIEQYLNLLASYL 14
DB 157 QLEEQGILLASFL 17

RESULT 13
ABR52601
ID ABR52601 standard; protein: 220 AA.

AC ABR52601;

DT 20-JUN-2003 (first entry)

Protein sequence #SEQ ID 67.

XX Multiprotein complex; eukaryote; drug target; diagnosis.

OS *Saccharomyces cerevisiae*.

XX
PN
EP1258494-A1.

20-NOV-2002.

XX
PF 20-DEC-2001: 2001EP-00130253XX
PR 15-MAY-2001: 2001EP-001111774XX
PA
(CELL.-) CELL.ZONE AG.XX
PT
Bauer A. Gavin A. Grandi P. Krause R. Krause IM. Kuester RD.

FI Marzioch M, schultz JU, superti-furga GU, XX

DR WPI; 2003-250078/25.
DR N-PSDB: ACC60643.

XX New isolated prot
PT

PT preferably a drug target in the treatment or prevention of disease or disorder.
PT disorder.

PS Disclosure: SEQ ID NO 67: 17pp + Sequence Listing: English: [XX](#)

CC The invention relates to multiprotein complexes from eukaryotes. Proteins
CC of the invention and DNA sequences encoding them are given in records
CC ABRS2568-ABRS3903 and ACCG06310-ACCG19344 respectively. The complexes are
CC obtainable by using a protein as a bait and isolating the set of proteins
CC which is attached thereto from cells. Such protein complexes may comprise
CC up to 30 distinct proteins. Protein complexes of the invention are useful
CC for diagnosing a disease or disorder, or as a target for an active agent
CC of a pharmaceutical, preferably a drug target in the treatment or
CC prevention of a disease or disorder. Note: The sequence data for this
CC patent is not represented in the printed specification, but is based on
CC sequence information supplied by the European Patent Office. The complete
CC document is available on CD-ROM

Sequence 220 AA;

Query Match	51.9%	Score 41;	DB 6;	Length 220;
Best Local Similarity	61.5%;	Pred. No. 1.8e+03;		
Matches	8;	Conservative	2;	Mismatches 3;
				Indels 0;
				Gaps 0;

QY 3 EQYLNLLASYLD 15
|:|:|:|:|:|
Db 162 EYLNLLFENYGD 174

RESULT 14
ADK63900
ID ADK63900 standard; protein; 220 AA.

AC ADK63900;

06-MAY-2004 (first entry)

XX Disease treating protein complex-derived protein #1425.
DE
XX protein complex; drug target; diagnosis.
KW

```
XX OS Unidentified.
XX PN EP1338608-A2.
XX FT 27-AUG-2003.
XX PD 20-DEC-2002; 2002EP-00102902.
XX PF 20-DEC-2001; 2001EP-00130253.
XX PR (CELL-) CELLZOME AG.
XX PA
XX PI Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;
XX PI Marzioch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;
XX PI Michon A, Leutwein C, Rick J;
XX DR WPI; 2003-638460/61.
XX DR N-PSDB; ADK63901.
XX PT New proteins and protein complexes from eukaryotes, useful as targets in
XX PT drug screening, or in diagnosing or screening for the presence of a
XX PT disease or disorder, or a predisposition for developing a disease or
XX PT disorder in a subject.
XX PS Disclosure; SEQ ID NO 2849; 13pp; English.
XX CC The invention relates to novel protein complexes comprising a first and a
XX CC second protein, or its derivative, fragment, homologue or variant. The
XX CC proteins are selected from given protein complexes, which are not defined
XX CC in the specification. The variants are encoded by nucleic acids that
XX CC hybridize to the nucleic acids encoding the proteins under low stringency
XX CC conditions. The protein complexes are useful as targets for an active
XX CC agent of a pharmaceutical. These protein complexes are particularly
XX CC useful as drugs targets for the treatment or preventing of a disease or
XX CC disorder. The complexes and methods above are useful in diagnosing or
XX CC screening for the presence of a disease or disorder or a predisposition
XX CC for developing a disease or disorder in a subject. These are also useful
XX CC in screening for a drug for treatment or prevention of a disease or
XX CC disorder. The molecule that modulates the amount, activity or protein
XX CC components of the complex is useful for the manufacture of a medicament
XX CC for the treatment or prevention of a disease or disorder. This sequence
XX CC corresponds to a protein of the invention. (Note: the sequence data for
XX CC this patent did not form part of the printed specification but was
XX CC obtained from the EPO in electronic format).
XX SQ Sequence 220 AA;
    Query Match 51.9%; Score 41; DB 7; Length 220;
    Best Local Similarity 61.5%; Pred. No. 1.8e+02;
    Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 3 EQYNLLASYLD 15
Db 162 ERYNLLFENYGD 174
    :|||||:|
RESULT 15
AAE06776
ID AAE06776 standard; protein; 241 AA.
XX AC
XX AC AAE06776;
XX DT
XX DT 16-OCT-2001 (first entry)
XX DE Human dual-specificity phosphatase (DSP)-13 splice variant protein.
XX KW Human; dual-specificity phosphatase; DSP-13; dual phosphorylation motif;
XX KW mitogen-activated protein kinase; MAP-kinase; graft-versus-host disease;
XX KW GVHD; Duchenne muscular dystrophy; therapy; cancer; autoimmune disease;
XX KW allergy; metabolic disease; cell growth; cell proliferation; cytostatic;
XX KW cell cycle abnormality; cell differentiation; antiallergic; muscular;
XX KW immunosuppressive; splice variant.
```

```
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT 127..147
XX FT Domain /note= "Active site domain"
XX PN WO200157221-A2.
XX PD 09-AUG-2001.
XX PF 01-FEB-2001; 2001WO-US003429.
XX PR 02-FEB-2000; 2000US-0179886P.
XX PA (CEPT-) CEPTYR INC.
XX PI Luche RM, Wei B;
XX DR WPI; 2001-488887/53.
XX DR N-PSDB; AAD12967.
XX PT New isolated dual-specificity phosphatase polypeptide for treating
XX PT cancer, graft-versus-host disease, autoimmune diseases, allergies,
XX PT metabolic diseases, abnormal cell growth and abnormal cell proliferation.
XX PS Example 1; Fig 5B; 8pp; English.
XX CC The present sequence is human dual-specificity phosphatase (DSP)-13
XX CC alternate splice variant protein. Inactivation of mitogen-activated
XX CC protein kinase (MAP-kinase) is mediated by dephosphorylation at a dual
XX CC phosphorylation motif by DSP which is referred to as MAP-kinase
XX CC phosphatase. An agent that modulates DSP is useful for treating a
XX CC disorder selected from Duchenne muscular dystrophy, cancer, graft-versus-
XX CC host disease (GVHD), autoimmune diseases, allergies, metabolic diseases,
XX CC abnormal cell growth, abnormal cell proliferation and cell cycle
XX CC abnormalities. DSP is useful for identifying antibodies and other agents
XX CC that inhibit DSP-12 and/or DSP-13 activity. DSP and the agents identified
XX CC are useful for modulating cell proliferation, differentiation and
XX CC survival. DSP is useful in screening assays for modulators of enzyme
XX CC activity and substrate binding and for dephosphorylating a substrate of
XX CC DSP-12 or DSP-13
XX SQ Sequence 241 AA;
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Query Match 51.9%; Score 41; DB 4; Length 241;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 1 BIEQVNLNLLASYL 14
    :|:|:|:|:|:|
Db 177 QLEFYQGILLASFL 190
    :|:|:|:|:|:|
Search completed: July 5, 2006, 19:08:54
Job time : 149.667 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: July 5, 2006, 20:52:16 ; Search time 84.6667 seconds
(without alignments)
87.537 Million cell updates/sec

Title: US-10-774-928A-13
Perfect score: 79
Sequence: 1 EIEQYLNLLASVLDLF 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2077797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2077797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

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- 3: /EMC_Celerra_SID33/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SID33/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	16	5	US-10-774-928-13
2	44	55.7	385	5	US-10-450-763-58075
3	44	55.7	417	5	US-10-479-764-11
4	42	53.2	496	3	US-09-800-770-20
5	42	53.2	496	4	US-10-422-536-20
6	42	53.2	496	6	US-11-011-880-20
7	42	53.2	496	6	US-11-069-642-20
8	42	53.2	3583	6	US-11-097-143-21234
9	41	51.9	57	4	US-10-437-963-178257
10	41	51.9	111	4	US-10-425-115-222175
11	41	51.9	170	3	US-09-775-925-32
12	41	51.9	170	5	US-10-962-126-32
13	41	51.9	220	4	US-10-477-369-87
14	41	51.9	241	3	US-09-775-925-8
15	41	51.9	241	5	US-10-962-126-8
16	41	51.9	254	4	US-10-425-115-266235
17	41	51.9	355	6	US-11-188-298-15448
18	41	51.9	357	6	US-11-087-099-3020
19	41	51.9	498	4	US-10-168-506-15
20	41	51.9	498	5	US-10-838-181-15
21	41	51.9	509	3	US-09-775-925-6
22	41	51.9	509	3	US-09-555-732-14
23	41	51.9	509	4	US-10-444-795B-785
24	41	51.9	509	5	US-10-962-126-6
25	41	51.9	590	3	US-09-971-773-73
26	41	51.9	590	4	US-10-327-663-63
27	41	51.9	590	4	US-10-409-616-90

28	41	51.9	590	5	US-10-409-611-20	Sequence 20, Appl
29	41	51.9	590	6	US-11-131-212-73	Sequence 73, Appl
30	41	51.9	590	6	US-11-218-473-73	Sequence 73, Appl
31	41	51.9	590	6	US-11-240-579-73	Sequence 73, Appl
32	41	51.9	590	6	US-11-287-324-73	Sequence 73, Appl
33	41	51.9	590	6	US-11-287-359-73	Sequence 73, Appl
34	41	51.9	784	6	US-11-188-298-8237	Sequence 8237, Ap
35	40	50.6	98	4	US-10-425-115-310606	Sequence 310606,
36	40	50.6	105	4	US-10-767-701-58372	Sequence 58372, A
37	40	50.6	108	4	US-10-424-599-249754	Sequence 249754,
38	40	50.6	128	5	US-10-739-930-5942	Sequence 5942, Ap
39	40	50.6	128	6	US-11-172-740-1360	Sequence 1360, Ap
40	40	50.6	128	6	US-11-172-740-1362	Sequence 1362, Ap
41	40	50.6	335	6	US-11-188-298-21671	Sequence 21671, A
42	40	50.6	341	6	US-11-188-298-20692	Sequence 20692, A
43	40	50.6	357	6	US-11-188-298-13772	Sequence 13772, A
44	40	50.6	357	6	US-11-188-298-14546	Sequence 14546, A
45	40	50.6	358	6	US-11-188-298-9968	Sequence 9968, Ap

ALIGNMENTS

RESULT 1
US-10-774-928-13
; Sequence 13, Application US/10774928
; Publication No. US20040341168A1
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; FILE OF INVENTION: Psoriasis
; FILE REFERENCE: 302178
; CURRENT APPLICATION NUMBER: US/10/774,928
; CURRENT FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 13
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Leishmania
US-10-774-928-13

Query Match 100.0%; Score 79; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIEQYLNLLASVLDLF 16
Db 1 EIEQYLNLLASVLDLF 16

RESULT 2
US-10-450-763-58075
; Sequence 58075, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT FILING DATE: 2003-06-11
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 58075
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Homo sapiens

RESULT 6

US-11-011-880-20
; Sequence 20, Application US/11011880
; Publication No. US20050158820A1
; GENERAL INFORMATION:

; APPLICANT: Kinsella, Todd
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES
; FILE REFERENCE: A-68614-1/DJB/RMS/RMK
; CURRENT APPLICATION NUMBER: US/11/011,880
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US/09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: US 60/187,130
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Methanococcus jannaschii
US-11-011-880-20

Query Match 53.2%; Score 42; DB 6; Length 496;
Best Local Similarity 53.8%; Pred. No. 3.6e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 EOYLNLLASYLD 15

Db 280 ESYNALIAGYFD 292

RESULT 7

US-11-069-642-20
; Sequence 20, Application US/11069642
; Publication No. US2005026026A1
; GENERAL INFORMATION:

; APPLICANT: LORENS, JAMES B.
; APPLICANT: PRAY, TODD R.
; APPLICANT: KINSELLA, TODD M.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; TITLE OF INVENTION: INHIBITING PROTEIN-PROTEIN INTERACTION
; FILE REFERENCE: RIGL-022CIP3

; CURRENT APPLICATION NUMBER: US/11/069,642
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Methanococcus jannaschii

US-11-069-642-20

Query Match 53.2%; Score 42; DB 6; Length 496;
Best Local Similarity 53.8%; Pred. No. 3.6e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 EOYLNLLASYLD 15

Db 280 ESYNALIAGYFD 292

RESULT 8

US-11-069-642-20
; Sequence 20, Application US/11069642
; Publication No. US2005026026A1
; GENERAL INFORMATION:

; APPLICANT: LORENS, JAMES B.
; APPLICANT: PRAY, TODD R.
; APPLICANT: KINSELLA, TODD M.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; TITLE OF INVENTION: INHIBITING PROTEIN-PROTEIN INTERACTION
; FILE REFERENCE: RIGL-022CIP3

US-11-097-143-21234

; Sequence 21234, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21234
; LENGTH: 3583
; TYPE: PRT
; ORGANISM: DROSOPHILA

US-11-097-143-21234

Query Match 53.2%; Score 42; DB 6; Length 3583;
Best Local Similarity 53.8%; Pred. No. 2.8e+03;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4 OYLNLLASYLDF 16

Db 2360 RYLNFLIADHLEF 2372

RESULT 9

US-10-437-963-178257
; Sequence 178257, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 178257
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MET4530_75830C.1.pap
US-10-437-963-178257

Query Match

51.9%; Score 41; DB 4; Length 57;

Best Local Similarity 53.8%; Pred. No. 55;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 EIQYNLLLSYL 14
Db 25 VEIYMNILHSYL 37

RESULT 10
US-10-425-115-222175
; Sequence 222175, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 222175
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(111)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_134213C.1.pep
US-10-425-115-222175

Query Match 51.9%; Score 41; DB 4; Length 111;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 EIQYNLLLSYLD 16
Db 17 QHYNLLLSYHSF 30

RESULT 11
US-09-775-925-32
; Sequence 32, Application US/09775925
; Patent No. US20010049358A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY
; FILE REFERENCE: 200125.420
; CURRENT APPLICATION NUMBER: US/09/775,925
; CURRENT FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-925-32

Query Match 51.9%; Score 41; DB 3; Length 170;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIEQYNLLLSYL 14
Db 157 QLEEQGILLASFL 170

RESULT 12
US-10-962-126-32
; Sequence 32, Application US/10962126
; Publication No. US20050058650A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY
; TITLE OF INVENTION: PHOSPHATASES
; FILE REFERENCE: 200125.420C1
; CURRENT APPLICATION NUMBER: US/10/962,126
; CURRENT FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: US 09/775,925
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: US 60/179,886
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-962-126-32

Query Match 51.9%; Score 41; DB 5; Length 170;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIEQYNLLLSYL 14
Db 157 QLEEQGILLASFL 170

RESULT 13
US-10-477-369-87
; Sequence 87, Application US/10477369
; Publication No. US20040167066A1
; GENERAL INFORMATION:
; APPLICANT: Marzloch et al.
; TITLE OF INVENTION: CLEAVAGE AND POLYADENYLATION COMPLEX OF PRECURSOR MRNA
; FILE REFERENCE: 224967
; CURRENT APPLICATION NUMBER: US/10/477,369
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/EP02/05359
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: EP 01111774.4
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: EP 01130253.6
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-477-369-87

Query Match 51.9%; Score 41; DB 4; Length 220;
Best Local Similarity 61.5%; Pred. No. 2.2e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EIQYNLLLSYLD 15
Db 162 BEYNLLSFENYGD 174

RESULT 14
US-09-775-925-8
; Sequence 8, Application US/09775925
; Patent No. US20010049358A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo

;; TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY
;; TITLE OF INVENTION: PHOSPHATASES
;; FILE REFERENCE: 200125.420
;; CURRENT APPLICATION NUMBER: US/09/775,925
;; CURRENT FILING DATE: 2001-02-01
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 8
;; LENGTH: 241
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-775-925-8

Query Match 51.9%; Score 41; DB 3; Length 241;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIEQYLNLLASFL 14
Db 177 QLEEQGILLASFL 190

RESULT 15
US-10-962-126-8
;; Sequence 8, Application US/10962126
;; Publication No. US20050058650A1
;; GENERAL INFORMATION:
;; APPLICANT: Luche, Ralf M.
;; APPLICANT: Wei, Bo
;; TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY
;; TITLE OF INVENTION: PHOSPHATASES
;; FILE REFERENCE: 200125.420C1
;; CURRENT APPLICATION NUMBER: US/10/962,126
;; CURRENT FILING DATE: 2004-10-08
;; PRIOR APPLICATION NUMBER: US 09/775,925
;; PRIOR FILING DATE: 2001-02-01
;; PRIOR APPLICATION NUMBER: US 60/179,886
;; PRIOR FILING DATE: 2000-02-02
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 8
;; LENGTH: 241
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-962-126-8

Query Match 51.9%; Score 41; DB 5; Length 241;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIEQYLNLLASFL 14
Db 177 QLEEQGILLASFL 190

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Job time : 85.6667 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 20:53:13 ; Search time 7.33333 Seconds
(without alignments)
58.543 Million cell updates/sec

Title: US-10-774-928A-13
Perfect score: 79
Sequence: 1 EIEQYINLLASVLD 16

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Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 112942

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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3: /EMC_Celerra_SID33/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
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5: /EMC_Celerra_SID33/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
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8: /EMC_Celerra_SID33/ptodata/1/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	40	50.6	402	6	US-10-449-902-48763
2	39	49.4	152	6	US-10-449-902-42014
3	39	49.4	185	6	US-10-471-571A-3746
4	39	49.4	648	6	US-10-449-902-39990
5	38	48.1	363	6	US-10-953-349-8457
6	38	48.1	372	6	US-10-449-902-54430
7	38	48.1	381	6	US-10-953-349-8456
8	38	48.1	387	6	US-10-953-349-8455
9	38	48.1	430	6	US-11-105-233-181
10	38	48.1	481	6	US-10-953-349-942
11	38	48.1	486	6	US-10-449-902-32091
12	38	48.1	487	6	US-10-953-349-941
13	38	48.1	487	6	US-10-449-902-53883
14	38	48.1	506	6	US-10-953-349-940
15	38	48.1	838	6	US-10-449-902-45252
16	37	46.8	259	7	US-11-293-697-4615
17	37	46.8	599	7	US-11-293-697-2635
18	37	46.8	788	6	US-10-449-902-45161
19	37	46.8	788	6	US-10-449-902-50822
20	37	46.8	862	6	US-10-199-229-14
21	37	46.8	875	6	US-10-199-229-10
22	36	45.6	148	7	US-11-251-208-282
23	36	45.6	400	7	US-11-105-233-182
24	36	45.6	438	6	US-10-449-902-30884
25	36	45.6	605	7	US-11-174-307B-4484

26	36	45.6	783	6	US-10-449-902-48641	Sequence 48641, A
27	35	44.3	180	6	US-10-953-349-27478	Sequence 27478, A
28	35	44.3	192	6	US-10-449-902-38683	Sequence 38683, A
29	35	44.3	300	6	US-10-449-902-54706	Sequence 54706, A
30	35	44.3	304	6	US-10-449-902-44655	Sequence 44655, A
31	35	44.3	344	6	US-10-471-571A-2622	Sequence 2622, A
32	35	44.3	413	6	US-10-449-902-37744	Sequence 37744, A
33	35	44.3	964	6	US-10-449-902-47345	Sequence 47345, A
34	34.5	43.7	86	6	US-10-449-902-34003	Sequence 34003, A
35	34.5	43.7	86	6	US-10-449-902-34042	Sequence 34042, A
36	34.5	43.7	428	6	US-10-953-349-6430	Sequence 6430, A
37	34.5	43.7	920	6	US-10-471-571A-1018	Sequence 1018, A
38	34	43.0	82	6	US-10-449-902-29815	Sequence 29815, A
39	34	43.0	212	6	US-10-449-902-32024	Sequence 32024, A
40	34	43.0	212	6	US-10-449-902-36956	Sequence 36956, A
41	34	43.0	212	6	US-10-449-902-48220	Sequence 48220, A
42	34	43.0	258	6	US-10-449-902-36848	Sequence 36848, A
43	34	43.0	289	6	US-10-505-928-365	Sequence 365, App
44	34	43.0	290	6	US-10-471-571A-498	Sequence 498, App
45	34	43.0	299	6	US-10-449-902-30294	Sequence 30294, A

ALIGNMENTS

RESULT 1
US-10-449-902-48763
; Sequence 48763, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 48763
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-48763

Query Match 50.6%; Score 40; DB 6; Length 402;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 QYINLLASVLD 15
: : : : :
Db 133 EYINLVDSYLD 144

RESULT 2
US-10-449-902-42014
; Sequence 42014, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269

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; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42014
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-42014

Query Match      49.4%; Score 39; DB 6; Length 152;
Best Local Similarity 53.3%; Pred. No. 9.6;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EIEQYNLLLSYLD 15
Db 97 EIEQYISSQLAEQVD 111

RESULT 3
US-10-471-571A-3746
; Sequence 3746, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWinn99, version 1.03
; SEQ ID NO 3746
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(185)
; OTHER INFORMATION: hypothetical protein
US-10-471-571A-3746

Query Match      49.4%; Score 39; DB 6; Length 185;
Best Local Similarity 64.3%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IEQYNLLLSYLD 15
Db 166 IEAYRNYLLNIYLD 179

RESULT 4
US-10-449-902-39990
; Sequence 3990, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39990
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-42014

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; LENGTH: 648
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-39990

Query Match      49.4%; Score 39; DB 6; Length 648;
Best Local Similarity 57.1%; Pred. No. 46;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIEQYNLLLSYLD 14
Db 255 EIQYLLHLLVIYL 268

RESULT 5
US-10-953-349-8457
; Sequence 8457, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: ENCODED THERBY
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8457
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-8457

Query Match      48.1%; Score 38; DB 6; Length 363;
Best Local Similarity 57.1%; Pred. No. 36;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 EQYNLLLSYLD 16
Db 178 ETLNLLLRNYLHY 191

RESULT 6
US-10-449-902-54430
; Sequence 54430, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54430
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-54430

Query Match      48.1%; Score 38; DB 6; Length 372;
Best Local Similarity 57.1%; Pred. No. 37;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 EQYNLLLSYLD 16

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Db 201 ETLNLLRLNYLHY 214

RESULT 7

US-10-953-349-8456
; Sequence 8456, Application US/10953349
; Publication No. US20060107345A1

GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8456
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-8456

Query Match 48.1%; Score 38; DB 6; Length 381;
Best Local Similarity 57.1%; Pred. No. 38;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 EQYNLLLASLYDF 16
| | | | | : | | :
Db 196 ETLNLLRLNYLHY 209

RESULT 8

US-10-953-349-8455
; Sequence 8455, Application US/10953349
; Publication No. US20060107345A1

GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8455
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-8455

Query Match 48.1%; Score 38; DB 6; Length 387;
Best Local Similarity 57.1%; Pred. No. 39;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 EQYNLLLASLYDF 16
| | | | | : | | :
Db 202 ETLNLLRLNYLHY 215

RESULT 9

US-11-105-233-181
; Sequence 181, Application US/11105233
; Publication No. US20060134653A1

GENERAL INFORMATION:

; APPLICANT: Thiagalagam et al
; TITLE OF INVENTION: Differential Expression of Genes in MSI Tumors
; FILE REFERENCE: 1657/2001
; CURRENT APPLICATION NUMBER: US/11/105,233
; CURRENT FILING DATE: 2005-04-13
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 181

; LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-233-181

Query Match 48.1%; Score 38; DB 7; Length 430;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIEQVNLNLLASLYD 15
| | | | | : | | :
Db 82 ETMQSLNDRLASLYD 96

RESULT 10

US-10-953-349-942
; Sequence 942, Application US/10953349
; Publication No. US20060107345A1

GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 942
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-942

Query Match 48.1%; Score 38; DB 6; Length 481;
Best Local Similarity 57.1%; Pred. No. 49;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 EOYNLLLASLYDF 16
| | | | | : | | :
Db 195 ETLNLLRLNYLHY 208

RESULT 11

US-10-449-902-32091
; Sequence 32091, Application US/10449902
; Publication No. US20060123505A1

GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32091
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-32091

Query Match 48.1%; Score 38; DB 6; Length 486;
Best Local Similarity 57.1%; Pred. No. 50;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 EOYNLLLASLYDF 16
| | | | | : | | :
Db 195 ETLNLLRLNYLHY 208

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Db      200 ETLNLLRLNYLHY 213

RESULT 12
US-10-953-349-941
; Sequence 941, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 941
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-941

Query Match      48.1%; Score 38; DB 6; Length 487;
Best Local Similarity 57.1%; Pred. No. 50;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      3 EQYNLLLSYLDLF 16
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Db      201 ETLNLLRLNYLHY 214

RESULT 13
US-10-449-902-53883
; Sequence 53883, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53883
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-53883

Query Match      48.1%; Score 38; DB 6; Length 487;
Best Local Similarity 57.1%; Pred. No. 50;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      3 EQYNLLLSYLDLF 16
      | | | | | : | | :
Db      201 ETLNLLRLNYLHY 214

RESULT 14
US-10-953-349-940
; Sequence 940, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
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; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 940
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-940

Query Match      48.1%; Score 38; DB 6; Length 506;
Best Local Similarity 57.1%; Pred. No. 52;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      3 EQYNLLLSYLDLF 16
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Db      220 ETLNLLRLNYLHY 233

RESULT 15
US-10-449-902-45252
; Sequence 45252, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45252
; LENGTH: 838
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-45252

Query Match      48.1%; Score 38; DB 6; Length 838;
Best Local Similarity 56.2%; Pred. No. 90;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      1 BIEQVNLNLLSYLDLF 16
      | | | | | : | | :
Db      710 EANQCLNVLAKYDFF 725

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OM protein - protein search, using sw model

Run on: July 5, 2006, 19:24:38 ; Search time 28.3333 Seconds
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Title: US-10-774-928A-13
Perfect score: 79
Sequence: 1 ETEQYLNLLASVLDLF 16

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Listing first 45 summaries

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4: /EMC_Celerra_SID33/ptodata/2/iaa/H COMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	16	2	US-09-809-003A-13
2	42	53.2	117	2	US-09-248-796A-22931
3	42	53.2	496	2	US-09-800-170-20
4	41	51.9	170	2	US-09-775-925-32
5	41	51.9	241	2	US-09-775-925-8
6	41	51.9	509	2	US-09-955-732A-14
7	41	51.9	509	2	US-09-775-925-6
8	41	51.9	590	2	US-09-971-773-73
9	41	51.9	597	2	US-09-328-352-4703
10	41	51.9	1092	2	US-09-538-092-122
11	40	50.6	318	2	US-09-248-796A-18266
12	40	50.6	453	2	US-09-248-796A-14922
13	40	50.6	594	2	US-08-826-964-2
14	40	50.6	606	2	US-09-949-016-7691
15	39.5	50.0	192	2	US-09-248-796A-28177
16	39	49.4	253	2	US-09-248-796A-21157
17	39	49.4	328	2	US-09-270-767-58019
18	39	49.4	339	2	US-09-198-452A-1013
19	39	49.4	376	2	US-09-949-016-8106
20	39	49.4	377	2	US-09-949-016-8141
21	39	49.4	389	2	US-09-248-796A-15248
22	39	49.4	404	2	US-09-949-016-6202
23	39	49.4	416	2	US-09-949-016-6201
24	39	49.4	429	2	US-09-248-796A-19384
25	39	49.4	433	2	US-09-949-016-10900
26	39	49.4	436	2	US-09-949-016-6983

ALIGNMENTS

RESULT 1

US-09-809-003A-13
; Sequence 13, Application US/09809003A
; Patent No. 6673351

; GENERAL INFORMATION:

; APPLICANT: O'Daly, Jose

; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission

; FILE OF INVENTION: Psoriasis

; FILE REFERENCE: 302178

; CURRENT APPLICATION NUMBER: US/09/809, 003A

; CURRENT FILING DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 13

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Leishmania

US-09-809-003A-13

Query Match 100.0%; Score 79; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ETEQYLNLLASVLDLF	16
Db	1	ETEQYLNLLASVLDLF	16

RESULT 2

US-09-248-796A-22931
; Sequence 22931, Application US/09248796A
; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstein et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

; FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196 132

; CURRENT APPLICATION NUMBER: US/09/248, 796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074, 725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096, 409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 22931

; LENGTH: 117

; TYPE: PRT

; ORGANISM: Candida albicans

; FEATURE:

Sequence 42699, A
Sequence 943, App
Sequence 14, Appli
Sequence 7, Appli
Sequence 21952, A
Sequence 34402, A
Sequence 49619, A
Sequence 22814, A
Sequence 42787, A
Sequence 11, Appli
Sequence 9, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 105, App
Sequence 11032, A
Sequence 346, App
Sequence 6595, Ap
Sequence 10716, A

564 2 US-09-270-767-42699
829 2 US-09-438-185A-943
16 2 US-09-809-003A-14
22 1 US-07-934-656A-7
160 2 US-09-248-796A-21952
189 2 US-09-270-767-34402
189 2 US-09-270-767-49619
191 2 US-09-248-796A-22814
322 2 US-09-270-767-42787
335 2 US-09-700-397-11
357 2 US-09-947-027-9
422 1 US-08-758-621-12
422 2 US-09-107-858-12
422 2 US-09-579-174-12
430 2 US-09-919-039-105
447 2 US-09-949-016-11032
476 2 US-09-538-092-346
179 2 US-09-107-532A-6595
313 2 US-09-902-540-10716

ALIGNMENTS

RESULT 1

US-09-809-003A-13
; Sequence 13, Application US/09809003A
; Patent No. 6673351

; GENERAL INFORMATION:

; APPLICANT: O'Daly, Jose

; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission

; FILE OF INVENTION: Psoriasis

; FILE REFERENCE: 302178

; CURRENT APPLICATION NUMBER: US/09/809, 003A

; CURRENT FILING DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 13

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Leishmania

US-09-809-003A-13

Query Match 100.0%; Score 79; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ETEQYLNLLASVLDLF	16
Db	1	ETEQYLNLLASVLDLF	16

RESULT 2

US-09-248-796A-22931
; Sequence 22931, Application US/09248796A
; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstein et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

; FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196 132

; CURRENT APPLICATION NUMBER: US/09/248, 796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074, 725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096, 409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 22931

; LENGTH: 117

; TYPE: PRT

; ORGANISM: Candida albicans

; FEATURE:

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 5, 2006, 19:24:38 ; Search time 28.3333 Seconds
(without alignments)
49.429 Million cell updates/sec

Title: US-10-774-928A-13
Perfect score: 79
Sequence: 1 ETEQYLNLLASVLDLF 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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4: /EMC_Celerra_SID33/ptodata/2/iaa/H COMB.pcp.*
5: /EMC_Celerra_SID33/ptodata/2/iaa/PCTUS COMB.pcp.*
6: /EMC_Celerra_SID33/ptodata/2/iaa/RE COMB.pcp.*
7: /EMC_Celerra_SID33/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	16	2	US-09-809-003A-13
2	42	53.2	117	2	US-09-248-796A-22931
3	42	53.2	496	2	US-09-800-170-20
4	41	51.9	170	2	US-09-775-925-32
5	41	51.9	241	2	US-09-775-925-8
6	41	51.9	509	2	US-09-955-732A-14
7	41	51.9	509	2	US-09-775-925-6
8	41	51.9	590	2	US-09-971-773-73
9	41	51.9	597	2	US-09-328-352-4703
10	41	51.9	1092	2	US-09-538-092-122
11	40	50.6	318	2	US-09-248-796A-18266
12	40	50.6	453	2	US-09-248-796A-14922
13	40	50.6	594	2	US-08-826-964-2
14	40	50.6	606	2	US-09-949-016-7691
15	39.5	50.0	192	2	US-09-248-796A-28177
16	39	49.4	253	2	US-09-248-796A-21157
17	39	49.4	328	2	US-09-270-767-58019
18	39	49.4	339	2	US-09-198-452A-1013
19	39	49.4	376	2	US-09-949-016-8106
20	39	49.4	377	2	US-09-949-016-8141
21	39	49.4	389	2	US-09-248-796A-15248
22	39	49.4	404	2	US-09-949-016-6202
23	39	49.4	416	2	US-09-949-016-6201
24	39	49.4	429	2	US-09-248-796A-19384
25	39	49.4	433	2	US-09-949-016-10900
26	39	49.4	436	2	US-09-949-016-6983

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; NAME/KEY: UNSURE
; LOCATION: (8),(66),(73),(75),(79)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-22931

Query Match      53.2%; Score 42; DB 2; Length 117;
Best Local Similarity 31.2%; Pred. No. 11;
Matches 5; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIEQYNLLLSYLDF 16
   ::|::|::|::|::|
Db 89 KLRNYINIILSPYIEF 104

RESULT 3
US-09-800-170-20
; Sequence 20, Application US/09800170
; Patent No. 6481667
; GENERAL INFORMATION:
; APPLICANT: Kinsella, Todd
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES
; FILE REFERENCE: A-66614-1/DJB/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/800,170
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/187,130
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Methanococcus jannaschii
US-09-800-170-20

Query Match      53.2%; Score 42; DB 2; Length 496;
Best Local Similarity 53.8%; Pred. No. 56;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 EQLNLLLSYLD 15
   ||::|::|::|::|
Db 280 ESYNALIAGYVD 292

RESULT 4
US-09-775-925-32
; Sequence 32, Application US/09775925
; Patent No. 6902919
; GENERAL INFORMATION:
; APPLICANT: Lucche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY PHOSPHATASES
; FILE REFERENCE: 200125.420
; CURRENT APPLICATION NUMBER: US/09/775,925
; CURRENT FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-925-32

Query Match      51.9%; Score 41; DB 2; Length 170;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIEQYNLLLSYL 14
   ::|::|::|::|::|
Db 157 QLEEQGILLASFL 170

RESULT 5
US-09-775-925-6
; Sequence 6, Application US/09775925
; Patent No. 6902919
; GENERAL INFORMATION:
; APPLICANT: Lucche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY PHOSPHATASES
; FILE REFERENCE: 200125.420
; CURRENT APPLICATION NUMBER: US/09/775,925
; CURRENT FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-925-6

Query Match      51.9%; Score 41; DB 2; Length 509;
Best Local Similarity 50.0%; Pred. No. 86;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIEQYNLLLSYL 14
   ::|::|::|::|::|
Db 445 QLEEQGILLASFL 458

RESULT 6
US-09-775-925-8
; Sequence 8, Application US/09775925
; Patent No. 6902919
; GENERAL INFORMATION:
; APPLICANT: Lucche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY PHOSPHATASES
; FILE REFERENCE: 200125.420
; CURRENT APPLICATION NUMBER: US/09/775,925
; CURRENT FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-925-8

Query Match      51.9%; Score 41; DB 2; Length 241;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIEQYNLLLSYL 14
   ::|::|::|::|::|
Db 177 QLEEQGILLASFL 190

RESULT 7
US-09-955-732A-14
; Sequence 14, Application US/09955732A
; Patent No. 6825021
; GENERAL INFORMATION:
; APPLICANT: Lucche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.433
; CURRENT APPLICATION NUMBER: US/09/955,732A
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-732A-14

Query Match      51.9%; Score 41; DB 2; Length 509;
Best Local Similarity 50.0%; Pred. No. 86;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIEQYNLLLSYL 14
   ::|::|::|::|::|
Db 445 QLEEQGILLASFL 458

RESULT 7
US-09-775-925-6
; Sequence 6, Application US/09775925
; Patent No. 6902919
; GENERAL INFORMATION:
; APPLICANT: Lucche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY PHOSPHATASES
; FILE REFERENCE: 200125.420
; CURRENT APPLICATION NUMBER: US/09/775,925
; CURRENT FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-925-6

Query Match      51.9%; Score 41; DB 2; Length 170;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIEQYNLLLSYL 14
   ::|::|::|::|::|
Db 157 QLEEQGILLASFL 170
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; Sequence 14922, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14922
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14922

Query Match 50.6%; Score 40; DB 2; Length 453;
Best Local Similarity 58.3%; Pred. No. 1.1e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3 IEQYLNLLASYL 14
Db 232 EQYLSLLISKFL 243

RESULT 13
US-08-826-964-2
; Sequence 2, Application US/08826964
; Patent No. 6033663
; GENERAL INFORMATION:
; APPLICANT: Ketcham, Catherine M.
; TITLE OF INVENTION: Nucleic Acids Encoding GDP-Fucose
; TITLE OF INVENTION: Pyrophosphorylase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,964
; FILING DATE: 09-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/015,241
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 014137-009910US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 594 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-826-964-2

Query Match 50.6%; Score 40; DB 2; Length 594;

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Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IEQYLNLLASYLDF 16
Db 140 IQOMLEKLAMYIDF 154

RESULT 14
US-09-949-016-7691
; Sequence 7691, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7691
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7691

Query Match 50.6%; Score 40; DB 2; Length 606;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IEQYLNLLASYLDF 16
Db 152 IQOMLEKLAMYIDF 166

RESULT 15
US-09-248-796A-28177
; Sequence 28177, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 28177
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-28177

Query Match 50.0%; Score 39.5; DB 2; Length 192;
Best Local Similarity 64.3%; Pred. No. 51;
Matches 9; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 1 EIEQYLNLLASYL 14
Db 68 EIEYVNLVI-SYL 80

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Job time : 29.3333 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 5, 2006, 19:09:18 ; Search time 19.4175 Seconds
(without alignments)
79.283 Million cell updates/sec

Title: US-10-774-928a-14
Perfect score: 77
Sequence: 1 STMQELNSRLASYLDK 16

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Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	622	I37984	keratin 9, type I,
2	66	85.7	423	I59463	keratin, type I, c
3	65	84.4	432	S30433	keratin 17, type I
4	64	83.1	327	S04511	keratin 3, type I,
5	64	83.1	400	KRHU9	keratin 19, type I
6	64	83.1	401	S57657	keratin 19 - potoz
7	64	83.1	403	JQ0028	cytokeratin 19 - m
8	64	83.1	411	S45318	keratin 12 - rabbi
9	64	83.1	437	A55682	keratin 13, type I
10	64	83.1	452	I49595	cytokeratin 15 - m
11	64	83.1	456	KRHU5	keratin 15, type I
12	64	83.1	472	KRHU6	keratin 14, type I
13	64	83.1	473	JC4313	keratin 16, type I
14	64	83.1	486	KRXL	keratin 3, type I,
15	64	83.1	526	KRBOVI	keratin, 54K type
16	64	83.1	561	A31994	keratin 10, type I
17	64	83.1	593	KRHU0	keratin 10, type I
18	62	80.5	599	KRMSE1	keratin, 59K type
19	61	79.2	430	S05481	keratin 18, type I
20	60	77.9	339	A25470	cytokeratin 19 - b
21	60	77.9	419	A25438	keratin, type I cy
22	60	77.9	420	A37343	keratin 13, type I
23	60	77.9	458	KRHU3	keratin 13, type-I
24	59	76.6	368	A28825	keratin, type I no
25	59	76.6	473	A33652	probable keratin 1
26	58	75.3	433	S01631	keratin, type I, e
27	58	75.3	467	I50476	keratin type I - g
28	58	75.3	570	S07330	keratin, epidermal
29	57	74.0	362	I37459	keratin Ha3-II, ty

ALIGNMENTS

RESULT 1

I37984
N:Alternate names: cytokeatrin 9; scatter protein 60K chain, placental
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text change 09-Jul-2004
C:Accession: I37984; S40307; S7921; S41161; B35494; I37943
R:Reis, A.; Hennies, H.C.; Langbein, L.; Digweed, M.; Mischke, D.; Drechsler, M.; Schroet Nature Genet. 6, 174-179, 1994
A:Title: Keratin 9 gene mutations in epidermolytic palmoplantar keratoderma (EPPK).
A:Reference number: I37984; MUID:94214498; PMID:7512862
A:Accession: I37984
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-622 <RES>
A:Cross-references: UNIPROT:P35527; UNIPARC:UPI000012DAE1; EMBL:X75015; NID:9453154; PIDN R:Langbein, L.; Heid, H.W.; Moll, I.; Franke, W.W.
Differentiation 55, 57-71, 1993
A:Title: Molecular characterization of the body site-specific human epidermal cytokeatrin A:Reference number: I37943; MUID:94131202; PMID:7507869
A:Accession: S40307
A:Molecule type: mRNA
A:Residues: 1-622 <LAN>
A:Cross-references: UNIPARC:UPI000012DAE1; EMBL:Z29074; NID:9435475; PIDN:CAA82315.1; PII A:Accession: S77921
A:Molecule type: protein
A:Residues: 29-53;62-104;167-188;199-233;241-249;295-362;374-430;450-480;579-604 <LAF>
A:Cross-references: UNIPARC:UPI00001774A9; UNIPARC:UPI00001774AA; UNIPARC:UPI00001774AB; 4B0; UNIPARC:UPI00001774B1
R:Langbein, L.
submitted to the EMBL Data Library, December 1993
A:Reference number: S41161
A:Accession: S41161
A:Molecule type: mRNA
A:Residues: 1-11, 'SR', 13-622 <LAW>
A:Cross-references: UNIPARC:UPI000016ABA2; EMBL:Z29074; NID:9435475; PIDN:CAA82315.1; PII R:Rosen, E.M.; Meromsky, L.; Romero, R.; Setter, E.; Goldberg, I.
Biochem. Biophys. Res. Commun. 168, 1082-1088, 1990
A:Title: Human placenta contains an epithelial scatter protein.
A:Reference number: A35494; MUID:90267446; PMID:2140676
A:Accession: B35494
A:Molecule type: protein
A:Residues: 'X', 450-465 <ROS>
A:Cross-references: UNIPARC:UPI00001774B2
C:Genetics:
A:Gene: GDB:KRT9; EPPK
A:Cross-references: GDB:303970; OMIM:144200
A:Map position: 17q12-17q21
A:Introns: 213/3; 241/2; 293/3; 347/3; 389/3; 464/2
A>Note: defects in this gene may cause epidermolytic palmoplantar keratoderma
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament

keratin, 47.6K typ
keratin, 48K type
keratin Ha1, type
keratin 12 - mouse
keratin 2, type I,
MH2(keratin acidi
keratin A, type I
keratin, type I, h
keratin 20, type I
keratin, 47K type I
keratin 21, type I
vimentin - common
hypothetical prote
intermediate filam
intermediate filam
intermediate filam

30 57 74.0 404 2 JS0073
31 57 74.0 412 1 KRSHL1
32 57 74.0 416 2 S60034
33 57 74.0 483 2 A55033
34 55 71.4 392 2 A60777
35 55 71.4 407 2 I48739
36 55 71.4 416 2 A61404
37 55 71.4 416 2 A45559
38 55 71.4 424 2 S37780
39 55 71.4 429 2 A25145
40 55 71.4 429 2 A40452
41 53 68.8 455 2 A43950
42 53 68.8 560 2 T16562
43 53 68.8 575 2 S48329
44 53 68.8 576 2 S12277
45 53 68.8 582 2 S24545

F:1-153/Domain: head #status predicted <HEA>
 F:154-459/Domain: helical rod #status predicted <ROD>
 F:460-622/Domain: tail #status predicted <TAIL>

Query Match 100.0%; Score 77; DB 2; Length 622;
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STMQELNSRLASYLDK 16
 |||||
 DB 154 STMQELNSRLASYLDK 169

RESULT 2

I59463
 N:Alternate names: endo B cytoskeletal - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text_change 09-Jul-2004
 C:Accession: I59463; A25621; A28428; JT0406
 R:Alonso, A.; Weber, T.; Jorcano, J.L.
 Roux's Arch. Biol. 196, 16-21, 1987
 A:Title: Cloning and characterization of keratin D, a murine endodermal cytoskeletal protein
 A:Reference number: I59463
 A:Accession: I59463
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-423 <RES>
 A:Cross-references: UNIPROT:P05784; UNIPARC:UPI000016CE78; GB:M36376; NID:g198587; PIDN:
 R:Singer, P.A.; Trevor, K.; Oshima, R.G.
 J. Biol. Chem. 261, 538-547, 1986
 A:Title: Molecular cloning and characterization of the endo B cytoskeleton expressed in P
 A:Reference number: A25621; MUID:86085876; PMID:2416755
 A:Accession: A25621
 A:Molecule type: mRNA
 A:Residues: 1-243, 'D', 245-252, 'A', 254-423 <SIN>
 A:Cross-references: UNIPARC:UPI0000164A33; GB:M11686; NID:g198620; PIDN:AAA39390.1; PID:
 R:Oshima, R.G.; Trevor, K.; Shevinsky, L.H.; Ryder, O.A.; Cecena, G.
 Genes Dev. 2, 505-516, 1988
 A:Title: Identification of the gene coding for the endo B murine cytoskeleton and its med
 A:Reference number: A28428; MUID:88255838; PMID:2454868
 A:Accession: A28428
 A:Molecule type: DNA
 A:Residues: 1-132 <OSH>
 A:Cross-references: UNIPARC:UPI000011E072; GB:Y00217; NID:g50842; PIDN:CAA68365.1; PID:g
 R:Ichinose, Y.; Morita, T.; Zhang, F.; Srimahasonggram, S.; Tondella, M.L.C.; Matsumoto,
 Gene 70, 85-95, 1988
 A:Title: Nucleotide sequence and structure of the mouse cytoskeleton endoB gene.
 A:Reference number: JT0406; MUID:89196920; PMID:2467843
 A:Accession: JT0406
 A:Molecule type: DNA
 A:Residues: 1-133, 'F', 135-243, 'D', 245-252, 'A', 254-423 <ICH>
 A:Cross-references: UNIPARC:UPI000016CD33; GB:M22832; NID:g340757; PIDN:AAA37552.1; PID:
 C:Genetics:
 A:Gene: endoB; KERG
 A:Introns: 132/3; 160/2; 212/3; 267/3; 309/3; 384/2
 C:Superfamily: cytoskeletal keratin
 C:Keywords: coiled coil; intermediate filament

Query Match 85.7%; Score 66; DB 2; Length 423;
 Best Local Similarity 86.7%; Pred. No. 0.001;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TMOQLNSRLASYLDK 16
 |||||
 DB 75 TMOQLNSRLASYLDK 89

RESULT 3

S30433
 N:Alternate names: cytoskeletal - human
 C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S30433; S23648; I78538; B29139
 R:Troyanovsky, S.W.; Leube, R.E.; Franke, W.W.
 Eur. J. Cell Biol. 59, 127-137, 1992
 A:Title: Characterization of the human gene encoding cyto keratin 17 and its expression p
 A:Reference number: S30433; MUID:93105967; PMID:1281771
 A:Accession: S30433
 A:Molecule type: DNA
 A:Residues: 1-432 <TRO>
 A:Cross-references: UNIPROT:Q04695; UNIPARC:UPI0000148FD6; EMBL:X62571; NID:g30378; PIDN:
 R:Flohr, T.; Buwitt, U.; Bonnekoh, B.; Decker, T.; Boettger, E.C.
 Eur. J. Immunol. 22, 975-979, 1992
 A:Title: Interferon-gamma regulates expression of a novel keratin class I gene.
 A:Reference number: S23648; MUID:92201318; PMID:1372562
 A:Accession: S23648
 A:Molecule type: mRNA
 A:Residues: 1-432 <FLO>
 A:Cross-references: UNIPARC:UPI0000148FD6; EMBL:X62571; NID:g34074; PIDN:CAA44451.1; PID:
 R:McLean, W.H.I.; Rugg, E.L.; Lunny, D.P.; Morley, S.M.; Lane, E.B.; Swensson, O.; Doppir
 Kunkeler, L.; Munro, C.S.
 Nature Genet. 9, 273-278, 1995
 A:Title: Keratin 16 and keratin 17 mutations cause pachyonychia congenita.
 A:Reference number: I58129; MUID:95291318; PMID:7539673
 A:Accession: I78538
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 85-91, 'D', 93-101 <MCL>
 A:Cross-references: UNIPARC:UPI000016B490; GB:S78515; NID:g1000378; PIDN:AAB34565.1; PID:
 R:Kartasova, T.; Cornelissen, B.J.C.; Belt, P.; van de Putte, P.
 Nucleic Acids Res. 15, 5945-5962, 1987
 A:Title: Effects of UV, 4-NOO and TPA on gene expression in cultured human epidermal ker
 A:Reference number: A29139; MUID:87316861; PMID:2442723
 A:Accession: B29139
 A:Molecule type: mRNA
 A:Residues: 167, 'E', 169-175, 'D', 177-432 <KAR>
 A:Cross-references: UNIPARC:UPI0000072C1D; GB:X05803; NID:g34080; PIDN:CAA29248.1; PID:g
 C:Genetics:
 A:Gene: GDB:KRT17
 A:Cross-references: GDB:I36211; OMIM:148069
 A:Map position: 17q12-17q21
 A:Introns: 144/3; 172/2; 224/3; 278/3; 320/3; 394/2; 402/1
 A:Note: defects in this gene may result in Jackson-Lawler pachyonychia congenita
 C:Superfamily: cytoskeletal keratin
 C:Keywords: coiled coil

Query Match 84.4%; Score 65; DB 2; Length 432;
 Best Local Similarity 81.2%; Pred. No. 0.0016;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STMQELNSRLASYLDK 16
 |||||
 DB 86 ATMQLNDRSLASYLDK 101

RESULT 4

S04511
 N:Alternate names: cyto keratin 3, type I, cytoskeletal (clone pUF451) - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 10-Dec-1999
 C:Accession: S04511
 R:Hoffmann, W.; Sterrer, S.; Koenigstorfer, A.
 FEBS Lett. 237, 178-182, 1988
 A:Title: Amino acid sequence microheterogeneities of a type I cyto keratin of M(r) 51000
 A:Reference number: S01327; MUID:89005622; PMID:2458965
 A:Accession: S04511
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-327 <HOF>
 A:Cross-references: UNIPARC:UPI00001774BA
 C:Superfamily: cytoskeletal keratin
 C:Keywords: coiled coil; intermediate filament
 F:1-310/Domain: helical rod #status predicted <ROD>

C:Superfamily: cytoskeletal keratin

C:Keywords: coiled coil

F:1-75/Domain: head <HED>

F:76-118/Domain: coil 1a, alpha-helical rod <ClA>

F:133-228/Domain: coil 1b, alpha-helical rod <ClB>

F:249-390/Domain: coil 2, alpha-helical rod <HC2>

Query Match 83.1%; Score 64; DB 2; Length 403;

Best Local Similarity 86.7%; Pred. No. 0.0022;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TMOELNSRLASYLDK 16

|||||

Db 86 TMOQLNDRLASYLDK 100

RESULT 8

S45318

keratin 12 - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 06-Jan-1995 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C:Accession: S45318

R:Wu, R.L.; Zhu, G.; Galvin, S.; Xu, C.; Haseba, T.; Chaloin-Dufau, C.; Dhovally, D.; W

A:Title: Lineage-specific and differentiation-dependent expression of K12 keratin in rab

A:Reference number: S45319; MUID:94192891; PMID:7511548

A:Accession: S45318

A:Molecule type: mRNA

A:Residues: 1-411 <WUR>

A:Cross-references: UNIPROT:Q28706; UNIPARC:UPI000012DAE5; EMBL:X77665; NID:g495260; PID

C:Superfamily: cytoskeletal keratin

C:Keywords: coiled coil; intermediate filament

Query Match

Best Local Similarity 83.1%; Score 64; DB 2; Length 411;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TMOELNSRLASYLDK 16

|||||

Db 46 TMOQLNDRLASYLDK 60

RESULT 9

A55682

keratin 13, type I cytoskeletal - mouse

C:Species: Mus musculus (house mouse)

C>Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004

C:Accession: A55682; B23518; A60493

R:Fillon, M.; Sarafian, V.; Lussier, M.; Belanger, C.; Lapointe, L.; Royal, A.

Genomics 24, 303-310, 1994

A:Title: Arrangement of a cluster of three mouse type I keratin genes expressed sequenti

A:Reference number: A55682; MUID:95213021; PMID:753287

A:Accession: A55682

A:Molecule type: DNA

A:Residues: 1-437 <FIL>

A:Cross-references: UNIPROT:P08730; UNIPARC:UPI000020FPB; GB:U13921; NID:G541610; PIDN:

R:Knapp, B.; Rentrop, M.; Schweizer, J.; Winter, H.

Nucleic Acids Res. 14, 751-763, 1986

A:Title: Nonepidermal members of the keratin multigene family: cDNA sequences and in sit

A:Reference number: A93640; MUID:86120369; PMID:2418416

A:Accession: B23518

A:Molecule type: mRNA

A:Residues: 126-437 <KNA>

A:Cross-references: UNIPARC:UPI000016CE75; GB:X03492; NID:G52782; PIDN:CAA27208.1; PID:G

R:Winter, H.; Rentrop, M.; Nischt, R.; Schweizer, J.

Differentiation 43, 105-114, 1990

A:Title: Tissue-specific expression of murine keratin K13 in internal stratified squamou

lation state of a distinct CpG site in the remote 5'-flanking region of the gene.

A:Reference number: A60493; MUID:90323435; PMID:1695590

A:Accession: A60493

A:Molecule type: DNA

A:Residues: 1-157 <WIN>

A:Cross-references: UNIPARC:UPI000016CB63; GB:X53320; NID:G288245; PIDN:CAA37407.1; PID:

C:Genetics:

A:Gene: K13

A:introns: 157/3; 185/2; 237/3; 291/3; 333/3; 407/2; 415/1

C:Superfamily: cytoskeletal keratin

C:Keywords: coiled coil; intermediate filament

Query Match 83.1%; Score 64; DB 2; Length 437;

Best Local Similarity 86.7%; Pred. No. 0.0024;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TMOELNSRLASYLDK 16

|||||

Db 99 TMOQLNDRLASYLDK 113

RESULT 10

I49595

cytokeratin 15 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I49595

R:Nozaki, M.; Mori, M.; Matsushiro, A.

Gene 138, 197-200, 1994

A:Title: The complete sequence of the gene encoding mouse cytokeratin 15.

A:Reference number: I49595; MUID:94171037; PMID:7510260

A:Accession: I49595

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-452 <RES>

A:Cross-references: UNIPROT:Q61414; UNIPARC:UPI000002862A; GB:D16313; NID:G487914; PIDN:

C:Genetics:

A:introns: 159/3; 187/2; 239/3; 293/3; 335/3; 409/2; 418/1

C:Superfamily: Cytoskeletal keratin

Query Match

Best Local Similarity 83.1%; Score 64; DB 2; Length 452;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TMOELNSRLASYLDK 16

|||||

Db 101 TMOQLNDRLASYLDK 115

RESULT 11

KRHUS

keratin 15, type I, cytoskeletal - human

N:Alternate names: acidic cytokeratin; cytokeratin 15

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C:Accession: S01069; B61556; A33211; B30186

R:Leube, R.E.; Bader, B.L.; Bosch, F.X.; Zimbelmann, R.; Achtstaetter, T.; Franke, W.W.

J. Cell Biol. 106, 1249-1261, 1988

A:Title: Molecular characterization and expression of the stratification-related cytokerat

A:Reference number: S01068; MUID:88198369; PMID:2452170

A:Accession: S01069

A:Molecule type: mRNA

A:Residues: 1-456 <LEU>

A:Cross-references: UNIPROT:P19012; UNIPARC:UPI0000049C51; EMBL:X07696; NID:G34070; PIDN:

R:Bader, B.L.; Jahn, L.; Franke, W.W.

Eur. J. Cell Biol. 47, 300-319, 1988

A:Title: Low level expression of cytokeratins 8, 18 and 19 in vascular smooth muscle cell

ontaining the cytokeratin 19 gene.

A:Reference number: A61556; MUID:89210901; PMID:2468493

A:Accession: B61556

A:Molecule type: DNA

A:Residues: 1-166,195-456 <BAD>

A:Cross-references: UNIPARC:UPI0000173D4F

A>Note: authors translated the codon GTC for residue 259 as Gly

A>Note: translation of this genomic sequence omits, between regions shown as exon 1 and

is paper appears to correspond to the missing coding region

C:Genetics:

A:Gene: GDB:KRT15

A:Cross-references: GDB:120124; OMIM:148030

A>Note: defects in this gene may result in epidermolysis bullosa simplex, Dowling-Meara C;Complex: heterotetramer of two type I and two type II proteins, usually keratin 5 (see C;Keywords: coiled coil; heterotetramer; intermediate filament F;2-472/Product: keratin, 50K type 1 cytoskeletal #status predicted <MAT> F;2-115/Domain: head <HD> F;2-115/Region: E1 and V1 subdomains F;116-426/Domain: rod <RD> F;116-150/Region: coil 1A F;151-161/Region: linker 1 F;162-262/Region: coil 1B F;263-278/Region: linker 12 F;279-297/Region: coil 2A F;298-305/Region: linker 2 F;306-426/Region: coil 2B F;364/Region: stutter F;427-472/Domain: tail <END> F;427-472/Region: V2 and E2 subdomains

Query Match 83.1%; Score 64; DB 1; Length 472;
Best Local Similarity 86.7%; Pred. No. 0.0026;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TMOELNSRLASYLDK 16
|||||
DB 118 TMOQLNRLASYLDK 132

RESULT 13
JC4313
keratin 16, type I, cytoskeletal - human
N;Alternate names: 46K keratin type I; cytokeratin 16
C;Species: Homo sapiens (man)
C;Date: 06-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4313; A24843; I58129
R;Paladini, R.D.; Takahashi, K.; Gant, T.M.; Coulombe, P.A.
Biochem. Biophys. Res. Commun. 215, 517-523, 1995
A;Title: cDNA cloning and bacterial expression of the human type I keratin 16.
A;Reference number: JC4313; MUID:96011809; PMID:7487986
A;Accession: JC4313
A;Molecule type: mRNA
A;Residues: 1-473 <PAL>
A;Cross-references: UNIPROT:P08779; UNIPARC:UPI000016B4A5; GB:S79867; NID:g1195530; PIDN:gl195530;
A;Experimental source: epidermal keratinocytes
R;Raychaudhury, A.; Marchuk, D.; Lindhurst, M.; Fuchs, E.
Mol. Cell. Biol. 6, 539-548, 1986
A;Title: Three tightly linked genes encoding human type I keratins: conservation of sequence
A;Reference number: A24843; MUID:87064338; PMID:2431270
A;Accession: A24843
A;Molecule type: DNA
A;Residues: 1,'T',3-25,'A',27-37,'A',39-40,43,'ASTY',48-49,'A',51-186,'HAL',190-207,'ARPC
A;Cross-references: UNIPARC:UPI00001774B6; GB:M28439; NID:g186683; PIDN:AAAS9460.1; PID:5944
R;McLean, W.H.I.; Rugg, E.L.; Lunny, D.P.; Morley, S.M.; Lane, E.B.; Swensson, O.; Doppir
Kunkeler, L.; Munro, C.S.
Nature Genet. 9, 273-278, 1995
A;Title: Keratin 16 and keratin 17 mutations cause pachyonychia congenita.
A;Reference number: I58129; MUID:95291318; PMID:7535673
A;Accession: I58129
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 118-131,'P',133-134 <MCL>
A;Cross-references: UNIPARC:UPI000016B48F; GB:S78514; NID:g1000376; PIDN:AAB34564.1; PID
A;Note: this is a mutant sequence
C;Comment: This protein is an intermediate filament protein and expressed in epithelial t
ound healing, psoriasis and cancer.
C;Genetics:
A;Gene: GDB:KRT16
A;Cross-references: GDB:136207; OMIM:148067
A;Map position: 17pter-17qter
A;Note: defects in this gene may result in Jadassohn-Lewandowsky pachyonychia congenita
C;Superfamily: cytoskeletal keratin
C;Keywords: coiled coil

```

Query Match      83.1%; Score 64; DB 2; Length 473;
Best Local Similarity 86.7%; Pred. No. 0.0027;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TMQELNSRLASYLDK 16
Db 120 TMQNLDRLASYLDK 134

RESULT 14
KRXL
keratin 3, type I, cytoskeletal (clone pUF1001) - African clawed frog
N:Alternate names: cytokekeratin, 51K
C:Species: Xenopus laevis (African clawed frog)
C:Date: 28-Aug-1985 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S01327; A02943
R:Hoffmann, W.; Sterrer, S.; Koenigstorfer, A.
FEBS Lett. 237, 178-182, 1988
A:Title: Amino acid sequence microheterogeneities of a type I cytokekeratin of M(r) 51000
A:Reference number: S01327; PMID:89005622; PMID:2458965
A:Accession: S01327
A:Molecule type: mRNA
A:Residues: 1-486 <HOF>
A:CROSS-references: UNIPROT:P02537; UNIPARC:UPI000012DADB; EMBL:X00968; NID:g64490; PIDN:
R:Hoffmann, W.; Franz, J.K.
EMBO J. 3, 1301-1306, 1984
A:Title: Amino acid sequence of the carboxy-terminal part of an acidic type I cytokekerati
A:Reference number: A02943; PMID:84261417; PMID:6204859
A:Accession: A02943
A:Molecule type: mRNA
A:Residues: 339-351, 'T', 353-486 <HOF2>
A:CROSS-references: UNIPARC:UPI00000FC7EB; GB:X00629; NID:g64868; PIDN:CAA25263.1; PID:9
A:Note: this sequence has been revised in paper S01327
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament
F:1-120/Domain: head <HEA>
F:121-438/Domain: helical rod #status predicted <ROD>
F:439-486/Domain: tail <TAI>

Query Match      83.1%; Score 64; DB 1; Length 486;
Best Local Similarity 86.7%; Pred. No. 0.0027;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TMQELNSRLASYLDK 16
Db 129 TMQNLDRLASYLDK 143

RESULT 15
KRB0V1
keratin, 54K type I cytoskeletal - bovine
N:Alternate names: 54-kDa type I keratin; cytokekeratin V1b
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A02941; S07262
R:Rieger, M.; Jorcano, J.L.; Franke, W.W.
EMBO J. 4, 2261-2267, 1985
A:Title: Complete sequence of a bovine type I cytokekeratin gene: conserved and variable i
A:Reference number: A02941; PMID:86081734; PMID:2416562
A:Accession: A02941
A:Molecule type: DNA
A:Residues: 1-526 <RIE>
A:CROSS-references: UNIPROT:P06394; UNIPARC:UPI000012DAB2; GB:X02870; NID:g478; PIDN:CAA
R:Jorcano, J.L.; Rieger, M.; Franz, J.K.; Schiller, D.L.; Moll, R.; Franke, W.W.
J. Mol. Biol. 179, 257-281, 1984
A:Title: Identification of two types of keratin polypeptides within the acidic cytokekerat
A:Reference number: S07262; PMID:85058191; PMID:6209405
A:Accession: S07262
A:Molecule type: mRNA
A:Residues: 281-466, 'PAAATAAEVORRRPRFRROVG', 490-491, 494, 'PVAVARRRK', 504-526 <JOR>
A:CROSS-references: UNIPARC:UPI0000173D56; EMBL:X01460
A:Note: this sequence has been revised in reference A02941
C:Genetics:

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A:Gene: cytokekeratin V1b
A:introns: 190/3; 218/2; 270/3; 324/3; 366/3; 439/2; 525/2
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament
F:1-127/Domain: head <HED>
F:1-127/Region: E1 and V1 subdomains
F:128-441/Domain: rod <ROD>
F:128-162/Region: coil 1A
F:163-176/Region: linker 1
F:177-277/Region: coil 1B
F:278-293/Region: linker 12
F:294-312/Region: coil 2A
F:313-320/Region: linker 2
F:321-441/Region: coil 2B
F:379/Region: stutter
F:442-526/Domain: tail <END>
F:442-526/Region: V2 and E2 subdomains

Query Match      83.1%; Score 64; DB 1; Length 526;
Best Local Similarity 86.7%; Pred. No. 0.003;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TMQELNSRLASYLDK 16
Db 130 TMQNLDRLASYLDK 144

Search completed: July 5, 2006, 19:20:25
Job time : 19.4175 secs

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GenCore version 5.1.1.9

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OM protein - protein search, using sw model

Run on: July 5, 2006, 18:28:56 ; Search time 163.728 Seconds
(without alignments)
90.395 Million cell updates/sec

Title: US-10-774-928A-14

Perfect score: 77
Sequence: 1 STMQELNRLASYLDK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_prot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	623	1 K1C9 HUMAN	P35527 homo sapien
2	71	92.2	786	2 O18740 CANFA	O18740 canis faml
3	66	85.7	422	1 K1C18 MOUSE	P05784 mus musculu
4	66	85.7	422	1 K1C18 RAT	Q5bjy9 rattus norv
5	66	85.7	423	2 Q3TIX1 MOUSE	Q3tix1 mus musculu
6	66	85.7	423	2 Q3TJH6 MOUSE	Q3tjh6 m 15 days p
7	66	85.7	423	2 Q3TJW7 MOUSE	Q3tjw7 m blastocys
8	65	84.4	280	2 O97624 CANFA	O97624 canis faml
9	65	84.4	423	1 K1C19 CHICK	O93256 gallus gall
10	65	84.4	424	2 Q5K2N8 PROAT	Q5k2n8 protopteris
11	65	84.4	426	2 Q8N1P6 HUMAN	O8nlp6 homo sapien
12	65	84.4	431	1 K1C17 HUMAN	O04695 homo sapien
13	65	84.4	432	1 K1C17 MOUSE	Q9qwl7 mus musculu
14	65	84.4	433	2 Q6IFU8 RAT	Q6ifu8 rattus norv
15	64	83.1	123	2 Q9Z253 RAT	Q9z253 rattus norv
16	64	83.1	338	2 Q5K2P3 PROAT	Q5k2p3 protopteris
17	64	83.1	400	1 K1C19 HUMAN	P08727 homo sapien
18	64	83.1	400	1 K1C19_PONPY	Q5r8s9 pongo pygma
19	64	83.1	401	1 K1C19_POTTR	P51856 potorous tr
20	64	83.1	403	1 K1C19_MOUSE	P19001 mus musculu
21	64	83.1	403	1 K1C19 RAT	Q63279 rattus norv
22	64	83.1	411	1 K1C12 RABIT	Q28706 oryctolagus
23	64	83.1	412	2 Q6IRP5 XENLA	Q6irp5 xenopus lae
24	64	83.1	437	1 K1C13 MOUSE	P08730 mus musculu
25	64	83.1	447	1 K1C15 RAT	Q6ifv3 rattus norv
26	64	83.1	452	1 K1C15_MOUSE	Q61414 mus musculu
27	64	83.1	456	1 K1C15 HUMAN	P19012 homo sapien
28	64	83.1	467	2 Q642P1 XENLA	Q642p1 xenopus lae
29	64	83.1	471	1 K1C14 HUMAN	P02533 homo sapien
30	64	83.1	472	1 K1C16 HUMAN	P08779 homo sapien
31	64	83.1	483	2 Q505L4 XENLA	Q505l4 xenopus lae

32	64	83.1	486	1 K1C0 XENLA	P02537 xenopus lae
33	64	83.1	491	2 Q8AV12 XENLA	Q8av12 xenopus lae
34	64	83.1	494	1 K1C12 HUMAN	Q99456 homo sapien
35	64	83.1	526	1 K1C10_BOVIN	P06394 bos taurus
36	64	83.1	561	2 O14664 HUMAN	Q14664 homo sapien
37	64	83.1	568	2 Q6RIZO_CANFA	Q6eiz0 canis faml
38	64	83.1	584	2 Q8N175 HUMAN	Q8n175 homo sapien
39	64	83.1	593	1 K1C10_HUMAN	P13645 homo sapien
40	63	81.8	437	2 Q8BKC6 MOUSE	Q8bkc6 mus musculu
41	62	80.5	334	2 Q9JKB4 MOUSE	Q9jkb4 mus musculu
42	62	80.5	414	2 Q98UJ2 XENLA	Q98uj2 xenopus lae
43	62	80.5	431	2 Q566F9_XENLA	Q566f9 xenopus lae
44	62	80.5	431	2 Q6GLQ7_XENLA	Q6glq7 xenopus lae
45	62	80.5	456	2 Q5KZP1_PROAT	Q5kzp1 protoceris

ALIGNMENTS

RESULT 1

K1C9 HUMAN
ID K1C9 HUMAN STANDARD; PRT; 623 AA.
AC P35527; O00109; Q14665;
DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
DT 08-NOV-2005, sequence version 2.
DT 07-FEB-2006, entry version 50.
DE Keratin, type I cytoskeletal 9 (Cytokeratin-9) (CK-9) (Keratin-9) (K9).
GN Name=KRT9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND PARTIAL PROTEIN SEQUENCE.
RC TISSUE=Foot sole tissue;
RX MEDLINE=94131202; PubMed=7507869;
RA Langbein L., Heid H.W., Moll I., Franke W.W.;
RT "Molecular characterization of the body site-specific human epidermal cyokeratin 9: cDNA cloning, amino acid sequence, and tissue specificity of gene expression."
RT Differentiation 55:57-72(1993).
RL [2]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS EPPK LYS-161; GLN-163 AND TRP-163.
RX MEDLINE=94214498; PubMed=7512862;
RA Reis A., Hennies H.-C., Langbein L., Digweed M., Mischke D.,
RA Dreschler M., Schroek E., Royer-Pokora B., Franke W.W., Sperling K.,
RA Kuester W.;
RT "Keratin 9 gene mutations in epidermolytic palmoplantar keratoderma (EPPK).";
RN [3]
RP PROTEIN SEQUENCE OF 14-29, AND MASS SPECTROMETRY.
RC TISSUE=cervix carcinoma;
RA Bienvenut W.V.;
RN [4]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 147-372, AND VARIANT EPPK GLN-163.
RX MEDLINE=96228052; PubMed=8647270; DOI=10.1016/0014-5793(96)00393-6;
RA Kobayashi S., Tanaka T., Matsuyoshi N., Imamura S.;
RT "Keratin 9 point mutation in the pedigree of epidermolytic hereditary palmoplantar keratoderma perturbs keratin intermediate filament network formation."
RN [5]
RP FEBS Lett. 386:149-155(1996).
RN [6]
RP PROTEIN SEQUENCE OF 450-466.
RX MEDLINE=90267446; PubMed=2140676;
RA Rosen E.M., Meromsky L., Romero R., Setter E., Goldberg I.;
RT "Human placenta contains an epithelial scatter protein."
RL Biochem. Biophys. Res. Commun. 168:1082-1088(1990).

RP VARIANTS EPPK VAL-157 AND PRO-172
RX MEDLINE=94274199; PubMed=7516304; DOI=10.1007/BF00201564;
RA Hennies H.-C., Zehender D., Kunze J., Kuester W., Reis A.;
RT "Keratin 9 gene mutational heterogeneity in patients with
epidermolytic palmoplantar keratoderma.";
RL Hum. Genet. 93:649-654(1994).
RN [7]
RP VARIANT EPPK SER-161.
RX MEDLINE=95015968; PubMed=7523529; DOI=10.1111/1523-1747.ep12395570;
RA Bonifas J.M., Macumura K., Chen M.A., Berth-Jones J.,
RX Hutchinson P.B., Zloczower M., Fritsch P.O., Epstein E.H. Jr.;
RT "Mutations of keratin 9 in two families with palmoplantar
epidermolytic hyperkeratosis.";
RL J. Invest. Dermatol. 103:474-477(1994).
RN [8]
RP VARIANT EPPK TYR-161.
RX MEDLINE=94184355; PubMed=7511021;
RA Torchard D., Blanchet-Bardon C., Serova O., Langbein L., Narod S.,
RA Janin N., Goguel A.F., Bernheim A., Franke W.M., Lenoir G.M.,
RA Feunteun J.;
RT "Epidermolytic palmoplantar keratoderma cosegregates with a keratin 9
mutation in a pedigree with breast and ovarian cancer.";
RL Nat. Genet. 6:108-110(1994).
RN [9]
RP VARIANTS EPPK TRP-163 AND SER-168.
RX MEDLINE=95164983; PubMed=7532199; DOI=10.1111/1523-1747.ep12666018;
RA Roehnael J.A., Wojcik S., Lisefer K.M., Dominey A.M., Huber M.,
RA Hohl D., Koop D.R.;
RT "Mutations in the 1A domain of keratin 9 in patients with
epidermolytic palmoplantar keratoderma.";
RL J. Invest. Dermatol. 104:430-433(1995).
RN [10]
RP VARIANT EPPK VAL-160.
RX MEDLINE=97348961; PubMed=9204965; DOI=10.1111/1523-1747.ep12276751;
RA Endo H., Hatamochi A., Shinkai H.;
RT "A novel mutation of a leucine residue in coil 1A of keratin 9 in
epidermolytic palmoplantar keratoderma.";
RL J. Invest. Dermatol. 109:113-115(1997).
RN [11]
RP VARIANTS EPPK THR-157; VAL-157 AND GLN-163.
RX MEDLINE=99072662; PubMed=9856842;
RA DOI=10.1046/j.1523-1747.1998.00445.x;
RA Covello S.P., Irvine A.D., McKenna K.E., Munro C.S., Nevin N.C.,
RA Smith F.J.D., Uitto J., McLean W.H.I.;
RT "Mutations in keratin 9 in kindreds with epidermolytic palmoplantar
keratoderma and epidemiology in Northern Ireland.";
RL J. Invest. Dermatol. 111:1207-1209(1998).
CC -!- FUNCTION: May serve an important special function either in the
mature palmar and plantar skin tissue or in the morphogenic
program of the formation of these tissues.
CC -!- SUBUNIT: Heterotetramer of two type I and two type II keratins.
CC -!- TISSUE SPECIFICITY: Expressed in the terminally differentiated
epidermis of palms and soles.
CC -!- DISEASE: Defects in KRT9 are a cause of epidermolytic palmoplantar
keratoderma (EPPK) [MIM:142001]; also abbreviated EHPK. EPPK is
an autosomal dominant disease characterized by diffuse thickening
of the epidermis on the entire surface of palms and soles sharply
bordered with erythematous margins.
CC -!- MISCELLANEOUS: There are two types of cytoskeletal and
microfibrillar keratin, I (acidic) and II (neutral to basic) (40-
55 and 56-70 kDa, respectively).
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -!- CAUTION: Was originally (Ref.4) thought to be a 60 kDa chain of
placental scatter protein.
CC -!- DATABASE: NAME=Human Intermediate Filament Mutation Database;
WWW="http://www.interfil.org".
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC -----
CC EMBL; Z29074; CAA82315.1; -; mRNA.
CC EMBL; S69510; AAC60619.1; -; mRNA.
CC EMBL; X75015; CAA52924.1; -; Genomic_DNA.

DR EMBL; AB001594; BAAL9418.1; -; mRNA.
DR PIR; I37984; I37984.
DR HSSP; P08670; 1GK7.
DR IntAct; P35527; -.
DR Ensembl; ENSG00000171403; Homo sapiens.
DR HGNC; HGNC:6447; KRT9.
DR MIN; 144200; phenotype.
DR MIN; 607606; gene.
DR GO; GO:0005200; P:structural constituent of cytoskeleton; TAS.
DR GO; GO:0008544; P:epidermis development; TAS.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PROSITE; PS00226; IF; 1.
DR Coiled coil; Direct protein sequencing; Disease mutation;
KW Intermediate filament; Keratin.
FT CHAIN 1 623 Keratin, type I cytoskeletal 9.
FT /FTid=PRO_0000063640.
FT REGION 1 152 Head.
FT REGION 153 461 Rod.
FT REGION 153 188 Coil 1A.
FT REGION 189 207 Linker 1.
FT REGION 208 299 Coil 1B.
FT REGION 300 322 Linker 12.
FT REGION 323 461 Coil 2.
FT REGION 462 623 Tail.
FT COMBIAS 15 26 Poly-Gly.
FT VARIANT 157 157 M -> T (in EPPK).
FT /FTid=VAR_010499.
FT VARIANT 157 157 M -> V (in EPPK).
FT /FTid=VAR_010500.
FT VARIANT 160 160 L -> V (in EPPK).
FT /FTid=VAR_010501.
FT VARIANT 161 161 N -> K (in EPPK).
FT /FTid=VAR_003822.
FT VARIANT 161 161 N -> S (in EPPK).
FT /FTid=VAR_010502.
FT VARIANT 161 161 N -> Y (in EPPK).
FT /FTid=VAR_010503.
FT VARIANT 163 163 R -> Q (in EPPK).
FT /FTid=VAR_003823.
FT VARIANT 163 163 R -> W (in EPPK).
FT /FTid=VAR_003824.
FT VARIANT 168 168 L -> S (in EPPK).
FT /FTid=VAR_003825.
FT VARIANT 172 172 Q -> P (in EPPK).
FT /FTid=VAR_010504.
FT CONFLICT 12 13 SR -> T (in Ref. 1; AAC60619 and 2).
SQ SEQUENCE 623 AA; 62129 MW; DE1DSA462FF96D10 CRC64;
Query Match 100.0%; Score 77; DB 1; Length 623;
Best Local Similarity 100.0%; Pred. No. 0.00028; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;
Qy 1 STMQELNSRLASYLDK 16
Db 155 STMQELNSRLASYLDK 170
RESULT 2
O18740 CANFA PRELIMINARY; PRT; 786 AA.
ID O18740 CANFA
AC O18740
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-FEB-1998, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Keratin.
GN Name=KRT9;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.

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OX NCB1_TaxID=9615;
RN NUCLEOTIDE SEQUENCE.
RA Lacharme P., Hite C., Jouquand S., Priat C., Galibert F.;
RT "Identification and analysis of the dog keratin 9 (KRT9) gene.";
RL Anim. Genet. 9:173-178(1998).
CC -----
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CC -----
DR ENBL; AF000949; AAC26971.1; -; Genomic_DNA.
DR HSP; P08670; ICK7.
DR Ensembl; ENSCAFG0000015952; Canis familiaris.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR002952; Eggshell.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01228; EGGSHLL.
DR PRINTS; PR01248; TYPE1KERATIN.
SQ SEQUENCE 786 AA; 76354 MW; 272AB5425DD09535 CRC64;

Query Match 92.2%; Score 71; DB 2; Length 786;
Best Local Similarity 87.5%; Pred. No. 0.004;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STWQELNSRLASYLDK 16
Db 139 TTQDLNLSRLASYLDK 154

RESULT 3
KIC18_MOUSE
ID KIC18_MOUSE STANDARD; PRT; 422 AA.
AC P05784; Q61766;
DT 01-NOV-1988, integrated into UniProtKB/Swiss-Prot.
DT 15-JUL-1998, sequence version 51.
DT 07-FEB-2006, entry version 51.
DE Keratin, type I cytoskeletal 18 (Cytokeratin-18) (CK-18) (Keratin-18)
DE (K18) (Cytokeratin endo B) (Keratin D).
GN Name=Krt18; Synonyms=Kerd, Krt1-18;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=89196920; PubMed=2467843; DOI=10.1016/0378-1119(88)90107-2;
RA Ichinose Y., Morita T., Zhang F., Srinahasongram S., Tondella M.L.C.,
RA Matsumoto M., Nozaki M., Matsushiro A.;
RT "Nucleotide sequence and structure of the mouse cytoke-
RT ratin endo B
RL Gene 70:85-95(1988).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=86085876; PubMed=2416755;
RA Alonso A., Weber T., Jorcano J.L.;
RT "Cloning and characterization of keratin D, a murine endodermal
RT cytoskeletal protein induced during in vitro differentiation of F9
RT teratocarcinoma cells";
RL Roux's Arch. Dev. Biol. 196:16-21(1987).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=86085876; PubMed=2416755;
RA Singer P.A., Trevor K., Oshima R.G.;
RT "Molecular cloning and characterization of the Endo B cytoke-
RT ratin expressed in preimplantation mouse embryos.";
RL J. Biol. Chem. 261:538-547(1986).
RN [4]
RN NUCLEOTIDE SEQUENCE OF 1-131.
RX MEDLINE=88255838; PubMed=2454868;
RA Oshima R.G., Trevor K., Shevinsky L.H., Ryder O.A., Cecena G.;
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RT "Identification of the gene coding for the Endo B murine cytoke-
RT ratin and its methylated, stable inactive state in mouse non-epithelial
RL cells.";
RL Genes Dev. 2:505-516(1988).
CC -I- SUBUNIT: Heterotrimer of two type I and two type II keratins.
CC Keratin 18 associates with keratin 8. Interacts with PNN (By
CC similarity).
CC -I- MISCELLANEOUS: There are two types of cytoskeletal and
CC microfibrillar keratin, I (acidic) and II (neutral to basic) (40-
CC 55 and 56-70 kDa, respectively).
CC -I- SIMILARITY: Belongs to the intermediate filament family.
CC -----
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CC -----
DR ENBL; M22832; AAA37552.1; -; Genomic_DNA.
DR ENBL; M36376; AAA39373.1; -; mRNA.
DR ENBL; M11686; AAA39390.1; -; mRNA.
DR ENBL; Y00217; CAA68365.1; -; Genomic_DNA.
DR PIR; I59463; I59463.
DR HSP; P08670; ICK7.
DR SWISS-2DPAGE; P05784; MOUSE.
DR Ensembl; ENSMUSG00000023043; Mus musculus.
DR MGI; MGI:96692; Krt1-18.
DR GO; GO:0005739; C: mitochondrion; IDA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Acetylation; Coiled coil; Glycoprotein; Intermediate filament;
KW Keratin.
FT INIT MET 0 0 By similarity.
FT CHAIN 1 422 Keratin, type I cytoskeletal 18.
FT /FTID=PRO_0000063667.
FT REGION 1 70 Head.
FT REGION 61 365 Necessary for interaction with PNN (By
FT similarity).
FT REGION 71 379 Rod.
FT REGION 71 106 Coiled 1A.
FT REGION 107 124 Linker 1.
FT REGION 125 216 Coiled 1B.
FT REGION 217 240 Linker 12.
FT REGION 241 379 Coiled 2.
FT REGION 380 422 Tail.
FT SITE 263 263 Stutter.
FT SITE 323 323 Stutter.
FT MOD RES 1 1 N-acetyls erine (By similarity).
FT CARBOHYD 30 30 O-linked (GlcNAc) (By similarity).
FT CARBOHYD 31 31 O-linked (GlcNAc) (By similarity).
FT CARBOHYD 49 49 O-linked (GlcNAc) (By similarity).
FT CONFLICT 133 133 L -> F (in Ref. 1).
FT CONFLICT 243 243 D -> N (in Ref. 2).
FT CONFLICT 252 252 A -> G (in Ref. 2).
SQ SEQUENCE 422 AA; 47373 MW; 4D5B0E9C7732F2F3 CRC64;

Query Match 85.7%; Score 66; DB 1; Length 422;
Best Local Similarity 86.7%; Pred. No. 0.015;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TWQELNSRLASYLDK 16
Db 74 TTQDLNLSRLASYLDK 88

RESULT 4
KIC18_RAT
ID KIC18_RAT STANDARD; PRT; 422 AA.
AC Q5BJY9; Q63278;
DT 16-AUG-2005, integrated into UniProtKB/Swiss-Prot.
DT 16-AUG-2005, sequence version 2.
DT 07-MAR-2006, entry version 13.
DE Keratin, type I cytoskeletal 18 (Cytokeratin-18) (CK-18) (Keratin-18)
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RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 RX PubMed=16141073; DOI=10.1126/science.11112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome";
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusci V., Clothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Caasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedziński R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Mulcais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashina T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyszynski B., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sakai D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fletschmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Yashaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [6]
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RC STRAIN=C57BL/6J; TISSUE=Placenta;
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 RA Carninci P., Shibata Y., Sugahara N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN [7]
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 RC STRAIN=C57BL/6J; TISSUE=Placenta;
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 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-394-format
 sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]
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 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
 RA Horii F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
 RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the intermediate filament family.
 CC Copyrighted under the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL: AK167676; BAE39725.1; -; mRNA.
 DR MGI: MGI:96692; Krt1-18.
 DR GO: GO:0005739; C:mitochondrion; IDA.
 DR InterPro: IPR001664; IF.
 DR InterPro: IPR002957; Keratin_I.
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 DR PRINTS: PR01248; TYPE1KERATIN.
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 DB 75 TWQDLNRLASYLDK 89
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 AC Q3TJH6;
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 DT 11-OCT-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE 15 days pregnant adult female placenta cDNA, RIKEN full-length
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 DE gene 18, full insert sequence (1530014C23 product:keratin complex 1, acidic,
 DE cDNA, RIKEN full-length enriched library, clone:1530016C20
 DE product:keratin complex 1, acidic, gene 18, full insert sequence)
 DE (Blastocyst blastocyst cDNA, RIKEN full-length enriched library,
 DE clone:1530029J15 product:keratin complex 1, acidic, gene 18, full
 DE insert sequence).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

- OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
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RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
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RC STRAIN=C57BL/6J; TISSUE=Placenta;
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RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
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RA Di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Iwano N.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
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RA Mortagui-Tabar S., Mulder N., Nakano N., Nakaguchi H., Ng P.,
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RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanihi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Bruce V., Quackenbush J.,
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RA Matick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
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RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
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RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
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RX PubMed=16141073; DOI=10.1126/science.11112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RT (Genome Network Core Team) and the FANTOM Consortium;
RL "Antisense transcription in the Mammalian Transcriptome.";
RN Science 309:1564-1566(2005).
RN [4]
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RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
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RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RT Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RN NUCLEOTIDE SEQUENCE.
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RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber F., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Bonfelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
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RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
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RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
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RC STRAIN=C57BL/6J; TISSUE=Placenta;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Iwama K., Ohara E., Watahiki M.,
RA Yoneda Y., Iehikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Horii F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,


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RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: AK167432; BAE39519.1; -; mRNA.
DR EMBL: AK167469; BAE39553.1; -; mRNA.
DR EMBL: AK167072; BAE39232.1; -; mRNA.
DR GO: GO:0005739; C-mitochondrion; IDA.
DR InterPro: IPR001664; IPI.
DR InterPro: IPR02957; Keratin I.
DR Pfam: PF00038; Filament; 1.
DR PRINTS: PR01248; TYPE1KERATIN.
DR PROSITE: PS00226; IF; 1.
KW Intermediate filament; Keratin.
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Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 75 TMQDLNDRLASLYLDK 89

RESULT 7
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AC Q3TJW7;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 5.
DE Blastocyst blastocyst cDNA, RIKEN full-length enriched library,
DE clone:11C0047008 product:keratin complex 1, acidic, gene 18, full
DE insert sequence (4 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:10C0039P11 product:keratin complex 1, acidic,
DE gene 18, full insert sequence).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
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RA Davis M.J., Wilming L.G., Adkins J., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
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RA Jakt M., Kanapin A., Katch M., Kawasawa Y., Kelso J., Kitamura H.,

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RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
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RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
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RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
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RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
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RC STRAIN=C57BL/6J; TISSUE=Whole body;
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RA Hirozane-Kishikawa T., Konno H., Nakamura K., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Miyazaki A., Sakai K., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=1217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

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RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Kasavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guscinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynchaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[6]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body; DOI=10.1101/gr.145100;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[7]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body; DOI=10.1101/gr.152600;
RX MEDLINE=20530913; PubMed=11076961;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[8]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
[9]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AK167265; BAE39378.1; -; mRNA.
DR EMBL; AK145413; BAE26424.1; -; mRNA.
DR GO; GO:0005739; C:mitochondrion; IDA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
SQ SEQUENCE 423 AA; 47510 MW; C70574E694E89898 CRC64;
Query Match 85.7%; Score 66; DB 2; Length 423;
Best Local Similarity 86.7%; Pred. No. 0.015;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 TMQELNSRLASYLDK 16
:|||||
DB 75 TMQDLNDRLASLYDK 89
RESULT 8
O97624 CANFA PRELIMINARY; PRT; 280 AA.
ID O97624 CANFA PRELIMINARY; PRT; 280 AA.
AC O97624;
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Keratin 17 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99189141; PubMed=10087295; DOI=10.1007/s003359901004;
RA Miller A.B., Breen M., Murphy K.E.;
RT "Chromosomal localization of acidic and basic keratin genes of the
domestic dog.";
RL Mamm. Genome 10:371-375(1999).
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF084571; AAD11416.1; -; Genomic_DNA.
DR HSP; P08670; 1GK7.
DR Ensembl; ENSCAFG0000015944; Canis familiaris.
DR LinkHub; O97624;
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
KW Keratin.
FT NON TER 280
SQ SEQUENCE 280 AA; 30557 MW; 2758FBE80E31B04D CRC64;
Query Match 84.4%; Score 65; DB 2; Length 280;
Best Local Similarity 81.2%; Pred. No. 0.015;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 STMQELNSRLASYLDK 16
:|||||
DB 86 ATMQNLNDRLASLYDK 101
RESULT 9
K1C19 CHICK STANDARD; PRT; 423 AA.
ID K1C19 CHICK STANDARD; PRT; 423 AA.
AC O93256;
DT 07-MAR-2006, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1998, sequence version 1.
DE Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19)
DE (K19) (GK-19).
GN Name=KRT19;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
```

OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND DEVELOPMENTAL STAGE.
RC TISSUE=Embryo;
RX MEDLINE=98152854; PubMed=9493835;
RX DOI=10.1046/j.1440-169X.1997.t01-5-00011.x;
RA Sato K., Yasugi S.;
RT "Chicken keratin-19: cloning of cDNA and analysis of expression in the
Dev. Growth Differ. 39:751-761(1997).
CC -!- FUNCTION: Involved in the organization of myofibers. Together with
CC KRT8, helps to link the contractile apparatus to dystrophin at the
CC costameres of striated muscle (By similarity).
CC -!- SUBUNIT: Heterotrimer of two type I and two type II keratins.
CC Interacts with PNN and the actin-binding domain of DMD (By
CC similarity).
CC -!- DEVELOPMENTAL STAGE: Expressed in the digestive tract throughout
CC development in the epithelia of proventriculus and glandular
CC structures. In 13 day embryo, strongly expressed in esophagus with
CC moderate expression in proventriculus and lung. Weak expression in
CC gizzard, small intestine, lung and dorsal skin. In embryos over 13
CC days old, observed in ectodermal, endodermal epithelium and also
CC in neural and mesodermal tissues (i.e. notochord), floorplate in
CC the neural tube, somatic mesoderm, splanchnic mesoderm and
CC dermatome. In more developed embryos, expression was localized in
CC the anterior lobe of the pituitary gland, notochord and
CC hypothalamus of the diencephalon (derived from the floor plate of
CC the neural tube). Also localized in the mesonephric mesoderm and
CC lateral plate mesoderm.
CC -!- DOMAIN: This keratin differs from all other IF proteins in lacking
CC the C-terminal tail domain.
CC -!- MISCELLANEOUS: There are two types of cytoskeletal and
CC microfibrillar keratin, I (acidic; 40-55 kDa) [K9 to K20] and II
CC (neutral to basic; 56-70 kDa) [K1 to K8].
CC -!- SIMILARITY: Belongs to the intermediate filament family.
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CC -----
CC EMBL: AB016281; BAA31952.1; -; mRNA.
CC HSP: P08670; IGK7.
CC Ensembl: ENSGALG0000003843; Gallus gallus.
CC InterPro: IPR001664; IF.
CC InterPro: IPR002957; Keratin_I.
CC Pfam: PF00038; Filament; 1.
CC PRINTS: PR01248; TYPEIKERATIN.
CC PROSITE: PS00226; IF; 1.
KW Coiled coil; Intermediate filament; Keratin; Phosphorylation.
FT CHAIN 1 423 Keratin, type I cytoskeletal 19.
FT /FTrd=PRO_0000227527.
FT REGION 1 93 Head.
FT REGION 94 401 Rod.
FT REGION 94 401 Coiled coil 1A.
FT REGION 130 147 Linker 1.
FT REGION 148 239 Coiled coil 1B.
FT REGION 240 262 Linker 12.
FT REGION 258 415 Necessary for interaction with PNN (By
FT similarity).
FT REGION 263 401 Coiled coil 2.
FT REGION 402 414 Rod-like helical tail.
FT COMPIAS 15 92 Gly-rich.
FT SITE 281 281 Stutter.
FT SITE 341 341 Stutter.
FT MOD RES 33 33 Phosphoserine (By similarity).
FT MOD RES 33 33 Phosphoserine (By similarity).
SQ SEQUENCE 423 AA; 46082 MW; E03390A9558AD2D0 CRC64;
Query Match 84.4%; Score 65; DB 1; Length 423;
Best Local Similarity 81.2%; Pred. No. 0.023;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 STWQELNSRLASVLDK 16
DB 96 TTQNLNDRSLASVLDK 111

RESULT 10
Q5K2N8 PROAT PRELIMINARY; PRT; 424 AA.
AC Q5K2N8;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Type I keratin 19.
GN Name=krt19;
OS Procterus aethiopicus (Marbled lungfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Dipnoi; Lepidosireniiformes; Protopteridae; Propterus.
OX NCBI_TaxID=7886;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Schaffeld M., Bremer M., Hunzinger C., Markl J.;
RT "Evolution of tissue-specific keratins as deduced from novel cDNA
RT sequences of the lungfish Propterus aethiopicus";
RL Eur. J. Cell Biol. 84:363-377(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Bremer M.;
RT "Primary structure and evolution of intermediate filament proteins
RT from the lungfish Propterus aethiopicus";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: AU785793; CAH05049.1; -; mRNA.
CC GO: GO:0005882; C:intermediate filament; IEA.
CC GO: GO:0005198; F:structural molecule activity; IEA.
CC InterPro: IPR001664; IF.
CC InterPro: IPR002957; Keratin_I.
CC InterPro: IPR002155; Thiolase.
CC Pfam: PF00038; Filament; 1.
CC PRINTS: PR01248; TYPEIKERATIN.
CC PROSITE: PS00099; THIOLASE_3; UNKNOWN_1.
KW Keratin.
SQ SEQUENCE 424 AA; 46548 MW; C811F1B9E67E3419 CRC64;
Query Match 84.4%; Score 65; DB 2; Length 424;
Best Local Similarity 81.2%; Pred. No. 0.023;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 STWQELNSRLASVLDK 16
DB 106 ATMQLNDRSLASVLDK 121

RESULT 11
Q8NIP6 HUMAN PRELIMINARY; PRT; 426 AA.
AC Q8NIP6;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-MAR-2006, entry version 19.
DE CDNA FLJ38023 fis, clone CTONG2012901, highly similar to KERATIN, TYPE
DE I CYTOSKELETAL 17.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OX Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Tongue;
RX PubMed=14702039; DOI=10.1038/ng1285;
RX Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RX Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RX Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RL J. Invest. Dermatol. 113:848-850(1999).
 RN [9]
 RP VARIANTS PC2 93-PRO--TYR-97 DEL; PRO-93 AND GLN-94.
 RX MEDLINE=21246897; PubMed=11348474;
 RA DOI=10.1046/j.1522-202x.2001.01335.x;
 RA Smith F.J.D., Coleman C.M., Bayoumy N.M., Tenconi R., Nelson J.,
 RA David A., McLean W.H.I.;
 RA "Novel keratin 17 mutations in pachyonychia congenita type 2.";
 RT J. Invest. Dermatol. 116:806-808(2001).
 RN [10]
 RP VARIANTS PC2 PRO-94; SER-96 DEL AND PRO-98.
 RX MEDLINE=21864371; PubMed=11874497;
 RA DOI=10.1046/j.0022-202x.2001.01701.x;
 RA Hashiguchi T., Yocumoto S., Shimada H., Terasaki K., Setoyama M.,
 RA Kobayashi K., Saheki T., Kanzaki T.;
 RA "A novel point mutation in the keratin 17 gene in a Japanese case of
 pachyonychia congenita type 2.";
 RT J. Invest. Dermatol. 118:545-547(2002).
 RN [11]
 RP "Novel and recurrent mutations in the genes encoding keratins K6a, K16
 and K17 in 13 cases of pachyonychia congenita.";
 RT J. Invest. Dermatol. 117:1391-1396(2001).
 RN [12]
 RP VARIANTS PC2 MET-101.
 RX MEDLINE=21864371; PubMed=11874497;
 RA DOI=10.1046/j.0022-202x.2001.01701.x;
 RA Hashiguchi T., Yocumoto S., Shimada H., Terasaki K., Setoyama M.,
 RA Kobayashi K., Saheki T., Kanzaki T.;
 RA "A novel point mutation in the keratin 17 gene in a Japanese case of
 pachyonychia congenita type 2.";
 RT J. Invest. Dermatol. 118:545-547(2002).
 RN [13]
 RP FUNCTION: May be a marker of basal cell differentiation in complex
 epithelia and therefore indicative of a certain type of epithelial
 "stem cells".
 RT J. Invest. Dermatol. 118:545-547(2002).
 RN [14]
 RP SUBUNIT: Heterodimer of a type I and a type II keratin. KRT17
 associates with KRT6 isomers.
 RT J. Invest. Dermatol. 118:545-547(2002).
 RN [15]
 RP INTERACTION:
 RT J. Invest. Dermatol. 118:545-547(2002).
 RN [16]
 RP TISSUE SPECIFICITY: Expressed in the hair follicle, nail bed,
 mucosal stratified squamous epithelia and in basal cells of oral
 epithelium, palmo-plantar epidermis and sweat and mammary glands.
 RT J. Invest. Dermatol. 118:545-547(2002).
 RN [17]
 RP INDUCTION: Induced in damaged or stressed epidermis.
 RT J. Invest. Dermatol. 118:545-547(2002).
 RN [18]
 RP DISEASE: Defects in KRT17 are a cause of pachyonychia congenita
 type 2 (PC2) [MIM:167210]; also known as Jadassohn-Lewandowsky (J-
 L) syndrome. PC2 is characterized by onychogryphosis, limited
 plantar hyperkeratosis, multiple epidermal cysts, abnormal eyebrow
 and body hair and by the presence of natal teeth.
 RT J. Invest. Dermatol. 118:545-547(2002).
 RN [19]
 RP DISEASE: Defects in KRT17 are a cause of steatocystoma multiplex
 (SM) [MIM:184500]. SM is a disease characterized by round or oval
 cystic tumors widely distributed on the back, anterior trunk,
 arms, scrotum, and thighs.
 RT J. Invest. Dermatol. 118:545-547(2002).
 RN [20]
 RP DISEASE: KRT16 and KRT17 are coexpressed only in pathological
 situations such as metaplasias and carcinomas of the uterine
 cervix and in psoriasis vulgaris.
 RT J. Invest. Dermatol. 118:545-547(2002).
 RN [21]
 RP MISCELLANEOUS: There are two types of cytoskeletal and
 microfibrillar keratin, I (acidic) and II (neutral to basic) (40-
 55 and 56-70 kDa, respectively).
 RT J. Invest. Dermatol. 118:545-547(2002).
 RN [22]
 RP SIMILARITY: Belongs to the intermediate filament family.
 RT J. Invest. Dermatol. 118:545-547(2002).
 RN [23]
 RP DATABASE: NAME=Human Intermediate Filament Mutation Database;
 WWW="http://www.interfil.org".
 RT J. Invest. Dermatol. 118:545-547(2002).
 RN [24]
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 DR EMBL: Z19574; CAA79626.1; -; Genomic_DNA.
 DR EMBL: X62571; CAA44451.1; -; mRNA.
 DR EMBL: S78515; AAB34565.1; -; Genomic_DNA.
 DR EMBL: BC000159; AAH00159.2; -; mRNA.
 DR EMBL: BC011901; AAH11901.1; -; mRNA.
 DR EMBL: BC056421; AAH56421.1; -; mRNA.
 DR EMBL: BC072019; AAH72019.1; -; mRNA.
 DR PIR: S30433; S30433.
 DR HSSP: P08670; 1GK7.
 DR IntAct: Q04695; -.
 DR SWISS-2DPAGE: Q04695; HUMAN.
 DR PHCI-2DPAGE: Q04695; -.

DR Ensembl; ENSG00000186831; Homo sapiens.
 DR H-InvDB; HIX0013814; -.
 DR HGNC; HGNC:6427; KRT17.
 DR MIM; 148069; gene.
 DR MIM; 167210; phenotype.
 DR MIM; 184500; phenotype.
 DR LinkHub; Q04695; -.
 DR GO; GO:0005882; C:intermediate filament; TAS.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; TAS.
 DR GO; GO:0008544; P:epidermis development; TAS.
 DR InterPro; IPR001664; IF.
 DR Pfam; PF00038; Filament; 1.
 DR PRINTS; PR01248; TYPEKERATIN.
 DR PROSITE; PS00226; IF; 1.
 KW Coiled coil; Disease mutation; Intermediate filament; Keratin.
 FT INIT MET 0 0 By similarity.
 FT CHAIN 1 431 Keratin, type I cytoskeletal 17.
 FT /FTID=PRO_0000063664.
 FT REGION 1 82 Head.
 FT REGION 83 391 Rod.
 FT REGION 83 119 Coil 1A.
 FT REGION 120 137 Linker 1.
 FT REGION 138 229 Coil 1B.
 FT REGION 230 249 Linker 12.
 FT REGION 250 391 Coil 2.
 FT REGION 392 431 Tail.
 FT VARIANT 87 87 M -> T (in PC2).
 FT VARIANT 91 91 /FTID=VAR_010512.
 FT VARIANT 91 91 N -> D (in PC2).
 FT VARIANT 91 91 /FTID=VAR_003847.
 FT VARIANT 91 91 N -> H (in SM).
 FT VARIANT 91 91 /FTID=VAR_003848.
 FT VARIANT 91 91 N -> S (in PC2).
 FT VARIANT 93 97 /FTID=VAR_003849.
 FT VARIANT 93 97 Missing (in PC2).
 FT VARIANT 93 97 /FTID=VAR_017069.
 FT VARIANT 93 93 R -> C (in PC2 and SM).
 Query Match 84.4%; Score 65; DB 1; Length 431;
 Best Local Similarity 81.2%; Pred. No. 0.023;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 STMQELNSRLASVLDK 16
 DB 85 ATMQNLNRLASVLDK 100
 RESULT 13
 KLC17_MOUSE
 ID KLC17_MOUSE STANDARD; PRT; 432 AA.
 AC Q9QWL7; Q61783;
 DT 19-SEP-2002, integrated into UniProtKB/Swiss-Prot.
 DT 19-SEP-2002, sequence version 2.
 DT 07-FEB-2006, entry version 37.
 DE Keratin, type I cytoskeletal 17 (Cytokeratin-17) (CK-17) (Keratin-17)
 DE {K17}.
 GN Name=Krt17; Synonyms=Krt1-17;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [mRNA].
 RC STRAIN=C57BL/10J; TISSUE=Skin;
 RX MEDLINE=99189238; PubMed=10087197; DOI=10.1006/geno.1998.5721;
 RA Sato H., Koide T., Sagai T., Ishiguro S.I., Tamai M., Saitou N.,
 RA Shiroishi T.;
 RT "The genomic organization of type I keratin genes in mice.";
 RL Genomics 56:303-309(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [mRNA] OF 228-432.

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RX MEDLINE=87109202; PubMed=2433272;
RA Knapp B., Rentrop M., Schweizer J., Winter H.;
RT "Three cDNA sequences of mouse type I keratins: cellular localization
of the mRNAs in normal and hyperproliferative tissues.";
RL J. Biol. Chem. 262:938-945(1987).
RN [3]
RP DEVELOPMENTAL STAGE.
RX MEDLINE=99003303; PubMed=9786956; DOI=10.1083/jcb.143.2.469;
RA McGowan K.M., Coulombe P.A.;
RT "Onset of keratin 17 expression coincides with the definition of major
epithelial lineages during skin development.";
RL J. Cell Biol. 143:469-486(1998).
CC -!- SUBUNIT: Heterodimer of a type I and a type II keratin. KRT17
associates with KRT6 isomers (by similarity).
CC -!- DEVELOPMENTAL STAGE: Expression first occurs in a subset of
epithelial cells within the single-layered, undifferentiated
ectoderm of embryonic day 10.5 mouse fetuses. In the ensuing 48
hours, K17-expressing cells give rise to placodes, the precursors
of ectoderm-derived appendages (hair, glands, and tooth), and to
periderm.
CC -!- MISCELLANEOUS: There are two types of cytoskeletal and
microfibrillar keratin, I (acidic) and II (neutral to basic) (40-
55 and 56-70 kDa, respectively).
CC -!- SIMILARITY: Belongs to the intermediate filament family.
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CC -----
DR EMBL; AB013608; BAA34229.1; -; mRNA.
DR EMBL; M13805; AAA39394.1; -; mRNA.
DR PIR; C26135; C26135.
DR HSSP; P08670; 1GK7.
DR Ensembl; ENSMUSG00000035557; Mus musculus.
DR MGI; MGI:96691; Krt11-17.
DR LinkHub; Q9QLW7; -.
DR InterPro; IPR001664; Keratin_I.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PROSITE; PS00226; IF, 1.
KW Coiled coil; Intermediate filament; Keratin.
FT INIT MET 0
FT CHAIN 1 432
FT REGION 1 82
FT REGION 83 391
FT REGION 83 119
FT REGION 120 137
FT REGION 138 229
FT REGION 230 249
FT REGION 250 391
FT REGION 332 432
SQ REGION 432 AA; 48031 MW; 58703AD00A230042 CRC64;

Query Match 84.4%; Score 65; DB 1; Length 432;
Best Local Similarity 81.2%; Pred. No. 0.023;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STMQELNSRLASYLDK 16
Db 85 ATMQNLDRLASYLDK 100
:|||||

RESULT 14
Q6IFU8 RAT PRELIMINARY; PRT; 433 AA.
AC Q6IFU8;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE 07-MAR-2006, entry version 13.
DE Type I keratin K17.
GN Name=K17;
OS Rattus norvegicus (Rat).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BN;
RX MEDLINE=23257644; PubMed=15085952; DOI=10.1078/0171-9335-00354;
RA Heese M., Zimek A., Weber K., Magin T.M.;
RT "Comprehensive analysis of keratin gene clusters in humans and
rodents.";
RL Eur. J. Cell Biol. 83:19-26(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heltan E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RG NIH MGC Project;
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
EMBL/GenBank/DBJ third party annotation (TPA) entry.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BK004050; DAA04484.1; -; mRNA.
DR EMBL; BC100058; AAI00059.1; -; Rattus norvegicus.
DR Ensembl; ENSRNOG0000026371; Rattus norvegicus.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PROSITE; PS00226; IF, 1.
KW Intermediate filament; Keratin.
SQ SEQUENCE 433 AA; 48123 MW; 7CB5C921841382D2 CRC64;

Query Match 84.4%; Score 65; DB 2; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.023;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STMQELNSRLASYLDK 16
Db 86 ATMQNLDRLASYLDK 101
:|||||

RESULT 15
Q52253 RAT PRELIMINARY; PRT; 123 AA.
ID Q52253_RAT

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Search completed: July 5, 2006, 19:01:24
Job time : 165.828 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 18:28:26 ; Search time 139.029 Seconds
(without alignments)
52.618 Million cell updates/sec

Title: US-10-774-928A-14
Perfect score: 77
Sequence: 1 STMQELNRLASYLDK 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 8: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *
10: geneseqp2006s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	77	100.0	16	AAO26394	Aao26394 Psoriasis
2	77	100.0	16	ADV04419	Adv04419 Leishmani
3	77	100.0	622	ADS88365	Ads88365 Human pro
4	77	100.0	622	AEAL5476	Aeal5476 Human pol
5	77	100.0	622	AEAL3340	Aeal3340 Mutant ke
6	66	85.7	423	ADF91430	Adf91430 Mouse cyt
7	65	84.4	167	AAB43930	Aab43930 Human can
8	65	84.4	218	ADT50990	Adt50990 Cancer re
9	65	84.4	247	ADT50969	Adt50969 Cancer re
10	65	84.4	249	ADT50968	Adt50968 Cancer re
11	65	84.4	262	ADT50985	Adt50985 Cancer re
12	65	84.4	303	ADT50991	Adt50991 Cancer re
13	65	84.4	332	ADT50984	Adt50984 Cancer re
14	65	84.4	432	AAW54233	Aaw54233 Human cyt
15	65	84.4	432	ABG77168	Abg77168 Prostate
16	65	84.4	432	ADNO4112	Adno4112 Antipsori-
17	65	84.4	432	ADN99874	Adn99874 Novel hum
18	65	84.4	432	ABM81869	Abm81869 Tumour-as
19	65	84.4	432	ADV85758	Adv85758 Human pro
20	65	84.4	432	AEAL15479	Aeal15479 Human pol
21	65	84.4	432	AED74635	Aed74635 Human pla
22	65	84.4	433	ABM81838	Abm81838 Tumour-as
23	65	84.4	459	3 AAB58761	Aab58761 Breast an

24	65	84.4	757	4	ABG06703	Abg06703 Novel hum
25	65	84.4	887	4	ABG23684	Abg23684 Novel hum
26	65	84.4	1113	4	ABG06702	Abg06702 Novel hum
27	64	83.1	128	3	AAB57152	Aab57152 Human pro
28	64	83.1	142	2	AAY29566	Aay29566 Human lun
29	64	83.1	142	3	AAB44489	Aab44489 Human lun
30	64	83.1	142	4	AAEL13831	Aael13831 Human lun
31	64	83.1	142	7	ADD66521	Add66521 Human lun
32	64	83.1	142	7	ADE87775	Ade87775 Human lun
33	64	83.1	166	4	ABG05346	Abg05346 Novel hum
34	64	83.1	189	8	ABO60480	Abo60480 Human gen
35	64	83.1	200	8	ADR98843	Adr98843 Lung spec
36	64	83.1	221	4	ABG23687	Abg23687 Novel hum
37	64	83.1	265	8	ADF56617	Adf56617 Human bre
38	64	83.1	281	8	ADT51001	Adt51001 Cancer re
39	64	83.1	315	8	ADP56622	Adp56622 Human bre
40	64	83.1	338	8	ADP56623	Adp56623 Human bre
41	64	83.1	388	8	ADR98903	Adr98903 Lung spec
42	64	83.1	393	8	ADT50998	Adt50998 Cancer re
43	64	83.1	400	6	ABF55382	Abp55382 Human col
44	64	83.1	400	7	ADI62966	Adi62966 Human apo
45	64	83.1	400	7	ADI62989	Adi62989 Human apo

ALIGNMENTS

RESULT 1
AAO26394
ID AAO26394 standard; peptide; 16 AA.
XX
AC AAO26394;
XX
DT 30-JAN-2003 (first entry)
XX
DE Psoriasis treating immunotherapeutic peptide, SEQ ID No 14.
XX
KW Antipsoriatic; immunostimulant; gene therapy; pharmaceutical composition;
KW vaccine; immunogenic variant; immunotherapeutic agent; psoriasis;
KW gene therapy.
XX
OS Leishmania sp.
XX
PN WO200274239-A2.
XX
PD 26-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006496.
XX
PR 16-MAR-2001; 2001US-00809003.
XX
PA (AKIV-) AKIVA LLC.
XX
PI O'daly JA;
XX
DR WPI; 2003-018763/01.
XX
PT New polypeptide and immunogenic variants comprising amino acid sequences of particulate antigens, useful for the treatment and clinical remission of psoriasis.
XX
PS Claim 1; Page 43; 56pp; English.
XX
CC The invention relates to a polypeptide comprising an isolated amino acid sequence or immunogenic variants selected from any of 14 fully defined sequences of 7-16 amino acids, given in the specification. The
CC immunotherapeutic agents and a pharmaceutical compositions comprising polynucleotides and vectors of the invention are useful for the treatment and clinical remission of psoriasis. The isolated nucleic acids are
CC useful as probes. The sequences of the invention can be used in the treatment of disorders by gene therapy. This sequence represents one of the 14 immunotherapeutic peptides of the invention
XX

```
SQ      Sequence 16 AA;
Query Match      100.0%; Score 77; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 STMQELNSRLASYLDK 16
      |||||
DB      1 STMQELNSRLASYLDK 16
      |||||

RESULT 2
ADV04419
ID      ADV04419 standard; peptide; 16 AA.
XX
AC      ADV04419;
XX
DT      24-FEB-2005 (first entry)
XX
DE      Leishmania immunotherapeutic peptide SEQ ID NO.14.
XX
KW      T-lymphocyte; immunogenicity; antigen; antipsoriatic; immunostimulant;
KW      psoriasis.
XX
OS      Leishmania sp.
XX
PN      US2004241168-A1.
XX
PD      02-DEC-2004.
XX
PF      09-FEB-2004; 2004US-00774928.
XX
PR      16-MAR-2001; 2001US-00809003.
XX
PR      17-OCT-2003; 2003US-00687892.
XX
PA      (ODAL/) ODALY J A.
PI      Odaly JA;
PI      WPI; 2005-011563/01.
XX
DR      Inhibiting selectively T-cell rolling in human, by administering compound
PT      interfering with cutaneous lymphocyte antigen-E selectin interaction and
PT      leukocyte function associated antigen-1 interaction.
XX
PS      Claim 18; SEQ ID NO 14; 21pp; English.
XX
CC      The invention relates to a novel method for selectively inhibiting T-cell
CC      rolling in a human host, comprising administering a compound that
CC      selectively interferes with the cutaneous lymphocyte antigen (CLA)-E
CC      selectin interaction and leukocyte function associated antigen (LFA)-
CC      1/intercellular adhesion molecule (ICAM) and very late antigen
CC      (VLA)/vascular cell adhesion molecule (VCAM) interactions. The compound
CC      includes an immunotherapeutic agent, which comprises a purified protein
CC      extract that is isolated by diethylaminoethyl Sephadex chromatography of
CC      a Nonidet P-40 insoluble particulate antigen fraction derived from
CC      isolated killed cells of amastigotes from one or more species of the
CC      Leishmania genus, where the particulate antigen fraction is solubilized
CC      with 8M urea and 0.025 M Tris(hydroxymethyl)aminomethane pH 8.3 applied
CC      to diethylaminoethyl Sephadex and is eluted with a solution comprising
CC      0.1 M sodium chloride, 8 M urea and 0.025 M
CC      Tris(hydroxymethyl)aminomethane pH 8.3, and the purified protein extract
CC      includes polypeptides having apparent molecular weights of 73, 80 and 82
CC      kDa, after total reduction and alkylation. The species is L. amazonensis,
CC      L. venezuelensis, L. brasiliensis and/or L. chagasi. A compound of the
CC      invention has antipsoriatic and immunostimulant activity, and inhibits T-
CC      cell rolling by interfering with CLA-E selectin interaction and LFA-
CC      1/ICAM and VLA/VCAM interactions. The method is useful for selectively
CC      inhibiting T-cell rolling in a human host, and for treating psoriasis.
CC      The present sequence represents a Leishmania peptide used in the
CC      invention.
XX
SQ      Sequence 16 AA;
Query Match      100.0%; Score 77; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 STMQELNSRLASYLDK 16
      |||||
DB      1 STMQELNSRLASYLDK 16
      |||||

RESULT 3
ADS88365
ID      ADS88365 standard; protein; 622 AA.
XX
AC      ADS88365;
XX
DT      18-NOV-2004 (first entry)
XX
DE      Human protein of a TNF-alpha signalling pathway protein complex Seq 220.
XX
KW      protein complex; tumour necrosis factor-alpha signalling pathway;
KW      TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
KW      inflammatory bowel disease; infectious disease; septic shock;
KW      bacterial infection; neurological disease; stroke-induced inflammation;
KW      neurodegenerative disease; cancer; antiinflammatory; antiarthritic;
KW      antirheumatic; cytostatic; antibacterial; gene therapy; human.
XX
OS      Homo sapiens.
XX
PN      WO2004035783-A2.
XX
PD      29-APR-2004.
XX
PF      24-SEP-2003; 2003WO-EP050655.
XX
PR      26-SEP-2002; 2002EP-00021809.
XX
PR      10-FEB-2003; 2003EP-00100274.
XX
PA      (CELL-) CELLZOME AG.
PI      Bouwmeester T, Huhse B, Bauch A, Ruffner H, Bauer A, Kuester B;
PI      Superti-Furga G, Kruse U;
XX
DR      WPI; 2004-348460/32.
XX
PT      New protein complex comprising at least one first and second protein of
PT      the Tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful for
PT      diagnosing or treating inflammation, neurological diseases, infectious
XX
PS      diseases or cancer.
XX
CC      Example; SEQ ID NO 220; 1980pp; English.
XX
CC      This invention relates to novel protein complexes of the tumour necrosis
CC      factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to
CC      methods for preparing these complexes comprising at least two component
CC      proteins, as well as screening methods to identify modulators of the
CC      pathway, which include antibodies, agonists and antagonists thereof. The
CC      present invention describes a protein complex and kit that are useful for
CC      diagnosing, prognosing or treating chronic inflammatory diseases such as
CC      rheumatoid arthritis and inflammatory bowel disease; infectious diseases
CC      such as septic shock and bacterial infections; neurological diseases such
CC      as stroke-induced inflammation in neurons; neurodegenerative diseases and
CC      cancer. Accordingly, these complexes can be used for the development of
CC      pharmaceutical compositions that exhibit antiinflammatory, antiarthritic,
CC      antirheumatic, cytostatic and antibacterial activities and can be used
CC      for gene therapy purposes. In particular, the invention further provides
CC      siRNA-oligonucleotides useful for inhibiting protein expression for in
CC      vitro or cell culture assays. This polypeptide is a human protein that
CC      can be used in combination with other proteins provided in the
CC      specification to form novel complexes of the TNF-alpha signalling pathway
XX
SQ      Sequence 622 AA;
```

Query Match 100.0%; Score 77; DB 8; Length 622;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STMQELNSRLASYLDK 16
 |||||
DB 154 STMQELNSRLASYLDK 169

RESULT 4
AEAL5476
ID AEAL5476 standard; protein; 622 AA.
XX AC AEAL5476;
AC XX
DT DT 28-JUL-2005 (first entry)
XX XX Human polypeptide #95.
DE DE
XX XX
KW KW Diagnosis; prognosis; cancer; breast tumor; ovary tumor; stomach tumor;
KW colon tumor; esophagus tumor; bladder tumor; non-small-cell lung cancer;
KW cytostatic; neoplasm.
XX XX
OS OS Homo sapiens.
XX OS
PN PN W02005047534-A2.
XX XX
PD PD 26-MAY-2005.
XX XX
PF PF 15-OCT-2004; 2004WO-EP011599.
XX XX
PT PT 28-OCT-2003; 2003EP-00024565.
XX XX
PA PA (FARB) BAYER HEALTHCARE AG.
XX XX
PI PI Wirtz R, Munnes M;
XX PI
DR DR MPI; 2005-372393/38.
DR N-PSDB; AEA15398.
XX XX
PT PT Predicting a response to cancer treatment by detecting at least 2
PT markers, which are genes or genomic nucleic acid sequences that are
PT located on one chromosomal region, which is altered in malignant
PT neoplasia.
XX XX
PS PS Claim 7; SEQ ID NO 438; 464pp; English.

The invention relates to a method of predicting response to cancer treatment comprising detection of at least 2 markers, where the markers are genes and fragments or genomic nucleic acid sequences that are located on one chromosomal region, which is altered in malignant neoplasia. The invention also relates to a method for the prediction, diagnosis or prognosis of malignant neoplasia, methods for detecting deregulations in malignant neoplasia and breast cancer, a method of determining the phenotype of a cell or tissue, a method for identifying genomic regions which are altered on the chromosomal level and encode genes that are linked by function and are differentially expressed in malignant neoplasia and breast cancer, methods of screening for agents which regulate the activity of a polypeptide or a polynucleotide and antibodies that specifically bind to a full length or partial polypeptide. The method is useful for predicting response to cancer treatment. The methods and compositions are useful for predicting, diagnosing, prognosing, preventing or treating malignant neoplasia including breast cancer, ovarian cancer, gastric cancer, colon cancer, esophageal cancer, mesenchymal cancer, bladder cancer or non-small-cell lung cancer. This sequence represents a human polypeptide used in the scope of the invention.

Sequence 622 AA;

Query Match 100.0%; Score 77; DB 9; Length 622;
Best Local Similarity 100.0%; Pred. No. 0.00011;

```

XX AC ADF91430;
XX DT 26-FEB-2004 (first entry)
XX DE Mouse cytokeatin 18 #SEQ ID 2.
XX KW Antiaethmatic; antiallergic; antiinflammatory; gene therapy;
XX KW bronchial asthma; chronic rhinitis; cytokeatin 18.
XX OS Mus sp.
XX PN WO2003098211-A1.
XX PD 27-NOV-2003.
XX PF 12-MAY-2003; 2003WO-KR000933.
XX PR 15-MAY-2002; 2002KR-00026765.
XX PA (NAHM/) NAHM D.
XX PA (JEON/) JEON S.
XX PI Nahm D, Jeon S;
XX PS WPI; 2004-022911/02.
XX DR
XX XX Diagnosing bronchial asthma and chronic rhinitis comprises detecting
PT autoantibodies to cytokeatin 18 protein in the bodily fluid of a human
PT subject.
XX PS Claim 18; SEQ ID NO 2; 42pp; English.
XX CC The invention relates to a method for diagnosing bronchial asthma and
CC chronic rhinitis comprising detecting autoantibodies to cytokeatin 18
CC protein in the bodily fluid of a human subject. The method or cytokeatin
CC 18 protein is useful in diagnosing, classifying bronchial asthma and
CC chronic rhinitis or for formulating pharmaceutical formulations for
CC protecting or treating patients with or non-allergic patients with
CC bronchial asthma and chronic rhinitis or patients with bronchial asthma
CC and chronic rhinitis associated with autoantibodies to cytokeatin 18.
CC Cytokeatin 18 protein is used as drug target in the production of drugs
CC for treating bronchial asthma and chronic rhinitis. The current sequence
CC represents mouse cytokeatin 18.
XX SQ Sequence 423 AA;
Query Match 85.7%; Score 66; DB 8; Length 423;
Best Local Similarity 86.7%; Pred. No. 0.0067;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TMOELNSRLASYLDK 16
DB 75 TMOQLNDRASYLDK 89
||||| |||||
RESULT 7
AAB43930
ID AAB43930 standard; protein; 167 AA.
XX AC AAB43930;
XX DT 08-FEB-2001 (first entry)
XX DE Human cancer associated protein sequence SEQ ID NO:1375.
XX KW Human; cancer associated gene; cancer antigen; detection; cancer;
XX KW diagnosis; cytostatic; proliferative; vulnerable; immunomodulator;
XX KW antidiabetic; antiaethmatic; antirheumatic; antiarthritic; antiviral;
XX KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
XX KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
XX KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
XX KW immune disorder; haematopoietic cell disorder; autoimmune disorder;

KW KW allergic reaction; graft versus host disease; organ rejection;
KW KW haemostatic; thrombolytic; cardiovascular disorder; infection;
KW OS Homo sapiens.
XX PN WO200055350-A1.
XX XX 21-SEP-2000.
XX PF 08-MAR-2000; 2000WO-US005882.
XX PR 12-MAR-1999; 99US-0124270P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Rosen CA, Ruben SM;
XX XX WPI; 2000-587533/55.
XX DR N-PSDB; AAC78139.
XX XX Novel isolated nucleic acids comprising sequences encoding peptides
PT useful for treating or diagnosing e.g. cancer.
XX PS Claim 11; Page 2040-2041; 2352pp; English.
XX CC AAC77607 to AAC78448 encode the human cancer associated proteins given in
CC AAB43398 to AAB44239. The proteins can have activities based on the
CC tissues and cells the genes are expressed in. Example of activities
CC include: cytostatic; proliferative; vulnerable; immunomodulator;
CC antidiabetic; antiaethmatic; antirheumatic; antiarthritic;
CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
CC nootropic; vasotropic; antipsoriatic and antiangiogenic. The
CC polynucleotides and polypeptides can be used for preventing, treating or
CC ameliorating medical conditions and diagnosing pathological conditions.
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC the present invention may be used to treat immune disorders by activating
CC or inhibiting the proliferation, differentiation or mobilisation of
CC immune cells, to treat disorders of haematopoietic cells, autoimmune
CC disorders, allergic reactions, graft versus host disease and organ
CC rejection, modulate haemostatic or thrombolytic activity, modulate
CC inflammation, cancers, cardiovascular disorders, neurological disease and
CC bacterial or viral infections. The peptides, nucleotides, antibodies,
CC agonists and antagonists may be also be used in drug screens. AAC78449 to
CC AAC78457 and AAB44240 represent sequences used in the exemplification of
CC the present invention
XX SQ Sequence 167 AA;
Query Match 84.4%; Score 65; DB 3; Length 167;
Best Local Similarity 86.7%; Pred. No. 0.0034;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TMOELNSRLASYLDK 16
DB 118 TMOQLNDRASYLDK 132
||||| |||||
RESULT 8
ADT50990
ID ADT50990 standard; protein; 218 AA.
XX AC ADT50990;
XX DT 13-JAN-2005 (first entry)
XX DE Cancer related protein sequence #153.
XX KW Cytostatic; gene therapy; vaccine; diagnosis; breast; colon; lung;
KW KW ovarian; prostate; cancer.
XX OS Homo sapiens.

```

```
XX PN WO2004092338-A2.
XX PD 28-OCT-2004.
XX PF 12-APR-2004; 2004WO-US011104.
XX PR 11-APR-2003; 2003US-0462399P.
XX PR 01-JUL-2003; 2003US-0484333P.
XX PA (DIAD-) DIADEXUS INC.
XX PI Macina RA, Turner LR, Sun Y, Tam A;
XX DR WPI; 2004-766851/75.
XX PT New cancer specific nucleic acid (CaSNA) molecules, useful for
XX PT diagnosing, monitoring the presence of, or treating a patient with
XX PT breast, colon, lung, ovarian, or prostate cancer.
XX PS Claim 12; SEQ ID NO 294; 891pp; English.
XX CC The invention relates to an isolated nucleic acid molecule (I)
XX CC selectively hybridizing to, or comprising at least 95% sequence identity
XX CC to, any of the 362 nucleotide sequences fully defined in the
XX CC specification. The nucleic acid molecules and polypeptides are useful for
XX CC diagnosing, monitoring the presence of, or treating a patient with
XX CC breast, colon, lung, ovarian, or prostate cancer. This sequence
XX CC corresponds to a protein of the invention.
XX CC
XX SQ Sequence 218 AA;
XX
XX Query Match 84.4%; Score 65; DB 8; Length 218;
XX Best Local Similarity 81.2%; Pred. No. 0.0046;
XX Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 STMQELNSRLASYLDK 16
DB :||| ||| ||| ||| |||
47 ATMQLNDRSLASYLDK 62

RESULT 9
ADT50969
ID ADT50969 standard; protein; 247 AA.
XX AC ADT50969;
XX DT 13-JAN-2005 (first entry)
XX DE Cancer related protein sequence #132.
XX KW cytostatic; gene therapy; vaccine; diagnosis; breast; colon; lung;
XX KW ovarian; prostate; cancer.
XX OS Homo sapiens.
XX PN WO2004092338-A2.
XX PD 28-OCT-2004.
XX PF 12-APR-2004; 2004WO-US011104.
XX PR 11-APR-2003; 2003US-0462399P.
XX PR 01-JUL-2003; 2003US-0484333P.
XX PA (DIAD-) DIADEXUS INC.
XX PI Macina RA, Turner LR, Sun Y, Tam A;
XX DR WPI; 2004-766851/75.
XX PT New cancer specific nucleic acid (CaSNA) molecules, useful for
XX PT diagnosing, monitoring the presence of, or treating a patient with
XX PT breast, colon, lung, ovarian, or prostate cancer.
XX OS Homo sapiens.
XX PN WO2004092338-A2.
XX PD 28-OCT-2004.
XX PF 12-APR-2004; 2004WO-US011104.
XX PR 11-APR-2003; 2003US-0462399P.
XX PR 01-JUL-2003; 2003US-0484333P.
XX PA (DIAD-) DIADEXUS INC.
XX PI Macina RA, Turner LR, Sun Y, Tam A;
XX DR WPI; 2004-766851/75.
XX PT New cancer specific nucleic acid (CaSNA) molecules, useful for
XX PT diagnosing, monitoring the presence of, or treating a patient with
```

```
PT breast, colon, lung, ovarian, or prostate cancer.
XX Claim 12; SEQ ID NO 273; 891pp; English.
XX CC The invention relates to an isolated nucleic acid molecule (I)
XX CC selectively hybridizing to, or comprising at least 95% sequence identity
XX CC to, any of the 362 nucleotide sequences fully defined in the
XX CC specification. The nucleic acid molecules and polypeptides are useful for
XX CC diagnosing, monitoring the presence of, or treating a patient with
XX CC breast, colon, lung, ovarian, or prostate cancer. This sequence
XX CC corresponds to a protein of the invention.
XX CC
XX SQ Sequence 247 AA;
XX
XX Query Match 84.4%; Score 65; DB 8; Length 247;
XX Best Local Similarity 81.2%; Pred. No. 0.0054;
XX Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 STMQELNSRLASYLDK 16
DB :||| ||| ||| ||| |||
109 ATMQLNDRSLASYLDK 124

RESULT 10
ADT50968
ID ADT50968 standard; protein; 249 AA.
XX AC ADT50968;
XX DT 13-JAN-2005 (first entry)
XX DE Cancer related protein sequence #131.
XX KW cytostatic; gene therapy; vaccine; diagnosis; breast; colon; lung;
XX KW ovarian; prostate; cancer.
XX OS Homo sapiens.
XX PN WO2004092338-A2.
XX PD 28-OCT-2004.
XX PF 12-APR-2004; 2004WO-US011104.
XX PR 11-APR-2003; 2003US-0462399P.
XX PR 01-JUL-2003; 2003US-0484333P.
XX PA (DIAD-) DIADEXUS INC.
XX PI Macina RA, Turner LR, Sun Y, Tam A;
XX DR WPI; 2004-766851/75.
XX PT New cancer specific nucleic acid (CaSNA) molecules, useful for
XX PT diagnosing, monitoring the presence of, or treating a patient with
XX PT breast, colon, lung, ovarian, or prostate cancer.
XX OS Homo sapiens.
XX PN WO2004092338-A2.
XX PD 28-OCT-2004.
XX PF 12-APR-2004; 2004WO-US011104.
XX PR 11-APR-2003; 2003US-0462399P.
XX PR 01-JUL-2003; 2003US-0484333P.
XX PA (DIAD-) DIADEXUS INC.
XX PI Macina RA, Turner LR, Sun Y, Tam A;
XX DR WPI; 2004-766851/75.
XX PT New cancer specific nucleic acid (CaSNA) molecules, useful for
XX PT diagnosing, monitoring the presence of, or treating a patient with
XX PT breast, colon, lung, ovarian, or prostate cancer.
XX OS Homo sapiens.
XX PN WO2004092338-A2.
XX PD 28-OCT-2004.
XX PF 12-APR-2004; 2004WO-US011104.
XX PR 11-APR-2003; 2003US-0462399P.
XX PR 01-JUL-2003; 2003US-0484333P.
XX PA (DIAD-) DIADEXUS INC.
XX PI Macina RA, Turner LR, Sun Y, Tam A;
XX DR WPI; 2004-766851/75.
XX PT New cancer specific nucleic acid (CaSNA) molecules, useful for
XX PT diagnosing, monitoring the presence of, or treating a patient with
```

```
PT breast, colon, lung, ovarian, or prostate cancer.
XX Claim 12; SEQ ID NO 272; 891pp; English.
XX CC The invention relates to an isolated nucleic acid molecule (I)
XX CC selectively hybridizing to, or comprising at least 95% sequence identity
XX CC to, any of the 362 nucleotide sequences fully defined in the
XX CC specification. The nucleic acid molecules and polypeptides are useful for
XX CC diagnosing, monitoring the presence of, or treating a patient with
XX CC breast, colon, lung, ovarian, or prostate cancer. This sequence
XX CC corresponds to a protein of the invention.
XX CC
XX SQ Sequence 249 AA;
XX
XX Query Match 84.4%; Score 65; DB 8; Length 249;
XX Best Local Similarity 81.2%; Pred. No. 0.0054;
XX Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
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```
QY 1 STMQELNSRLASYLDK 16
Db 86 ATMQLNDRSLASYLDK 101

RESULT 11
ADT50985
ID ADT50985 standard; protein; 262 AA.
XX
AC ADT50985;
XX
DT 13-JAN-2005 (first entry)
XX
DE Cancer related protein sequence #148.
XX
KW cytostatic; gene therapy; vaccine; diagnosis; breast; colon; lung;
KW ovarian; prostate; cancer.
OS Homo sapiens.
XX
PN WO2004092338-A2.
XX
PD 28-OCT-2004.
XX
PF 12-APR-2004; 2004WO-US011104.
XX
PR 11-APR-2003; 2003US-0462399P.
PR 01-JUL-2003; 2003US-0484333P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Macina RA, Turner LR, Sun Y, Tam A;
XX
DR WPI; 2004-766851/75.
XX
PT New cancer specific nucleic acid (CasNA) molecules, useful for
PT diagnosing, monitoring the presence of, or treating a patient with
PT breast, colon, lung, ovarian, or prostate cancer.
XX
PS Claim 12; SEQ ID NO 289; 891pp; English.
XX
SQ Sequence 262 AA;

Query Match 84.4%; Score 65; DB 8; Length 262;
Best Local Similarity 81.2%; Pred. No. 0.0057;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STMQELNSRLASYLDK 16
Db 114 ATMQLNDRSLASYLDK 129

RESULT 12
ADT50991
ID ADT50991 standard; protein; 303 AA.
XX
AC ADT50991;
XX
DT 13-JAN-2005 (first entry)
XX
DE Cancer related protein sequence #154.
XX
KW cytostatic; gene therapy; vaccine; diagnosis; breast; colon; lung;
KW ovarian; prostate; cancer.
XX
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OS Homo sapiens.
XX
PN WO2004092338-A2.
XX
PD 28-OCT-2004.
XX
PF 12-APR-2004; 2004WO-US011104.
XX
PR 11-APR-2003; 2003US-0462399P.
PR 01-JUL-2003; 2003US-0484333P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Macina RA, Turner LR, Sun Y, Tam A;
XX
DR WPI; 2004-766851/75.
XX
PT New cancer specific nucleic acid (CasNA) molecules, useful for
PT diagnosing, monitoring the presence of, or treating a patient with
PT breast, colon, lung, ovarian, or prostate cancer.
XX
PS Claim 12; SEQ ID NO 295; 891pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I)
CC selectively hybridizing to, or comprising at least 95% sequence identity
CC to, any of the 362 nucleotide sequences fully defined in the
CC specification. The nucleic acid molecules and polypeptides are useful for
CC diagnosing, monitoring the presence of, or treating a patient with
CC breast, colon, lung, ovarian, or prostate cancer. This sequence
CC corresponds to a protein of the invention.
XX
SQ Sequence 303 AA;

Query Match 84.4%; Score 65; DB 8; Length 303;
Best Local Similarity 81.2%; Pred. No. 0.0068;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STMQELNSRLASYLDK 16
Db 133 ATMQLNDRSLASYLDK 148

RESULT 13
ADT50984
ID ADT50984 standard; protein; 332 AA.
XX
AC ADT50984;
XX
DT 13-JAN-2005 (first entry)
XX
DE Cancer related protein sequence #147.
XX
KW cytostatic; gene therapy; vaccine; diagnosis; breast; colon; lung;
KW ovarian; prostate; cancer.
XX
OS Homo sapiens.
XX
PN WO2004092338-A2.
XX
PD 28-OCT-2004.
XX
PF 12-APR-2004; 2004WO-US011104.
XX
PR 11-APR-2003; 2003US-0462399P.
PR 01-JUL-2003; 2003US-0484333P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Macina RA, Turner LR, Sun Y, Tam A;
XX
DR WPI; 2004-766851/75.
XX
PT New cancer specific nucleic acid (CasNA) molecules, useful for
```

PT diagnosing, monitoring the presence of, or treating a patient with
PT breast, colon, lung, ovarian, or prostate cancer.
PS Claim 12; SEQ ID NO 288; 891pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I)
CC selectively hybridizing to, or comprising at least 95% sequence identity
CC to, any of the 362 nucleotide sequences fully defined in the
CC specification. The nucleic acid molecules and polypeptides are useful for
CC diagnosing, monitoring the presence of, or treating a patient with
CC breast, colon, lung, ovarian, or prostate cancer. This sequence
CC corresponds to a protein of the invention.
XX
SQ Sequence 332 AA;

Query Match 84.4%; Score 65; DB 8; Length 332;
Best Local Similarity 81.2%; Pred. No. 0.0076; 2; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STMQELNSRLASYLDK 16
Db 117 ATMQLNDRSLASYLDK 132

RESULT 14
AAW54233
ID AAW54233 standard; peptide; 432 AA.
XX
AC AAW54233;
XX
DT 10-AUG-1998 (first entry)
XX
DE Human cytokeatin 17 protein.
XX
KW Cervical cancer-associated protein; Cvc; tryptic peptide; human;
KW detection; treatment; cytokeatin 17; non-chromatin protein.
XX
OS Homo sapiens.
XX
PN WO9809170-A2.
XX
PD 05-MAR-1998.
XX
PF 19-AUG-1997; 97WO-US014526.
XX
PR 30-AUG-1996; 96US-00705660.
XX
PA (MATR-) MATRITTECH INC.
XX
PI Keesee SK, Obar R, Wu Y;
XX
DR WPI; 1998-230271/20.
XX
PT Detection and therapy of cervical cancer - using specific cervical cancer
PT -associated proteins as targets for treatment or as indicators for
PT detection.
PS Claim 10; Page 52-53; 79pp; English.
XX
CC This protein is the human cytokeatin 17 which is used to obtain tryptic
CC peptides which are used in a method for detecting cervical cancer. The
CC method involves detecting the presence of a cervical cancer-associated
CC protein (Cvc) in a tissue or body fluid sample. The Cvc is characterised
CC as having a molecular weight of 44900-69400 Daltons as determined by
CC sodium dodecyl-sulphate (SDS)-PAGE techniques and an isoelectric point
CC (pI) of 5.1-6.6 as determined by standard isoelectric focusing
CC techniques. The protein is further characterised as being a non-chromatin
CC protein which is detectable at a higher level in a human cervical cancer
CC cell than in a normal human cervical cell, as determined by 2D-gel
CC electrophoresis. The methods can be used for the early and rapid
CC detection of cervical cancer, for treating cervical cancers and for
CC monitoring the efficacy of such treatment

SQ Sequence 432 AA;

Query Match 84.4%; Score 65; DB 2; Length 432;
Best Local Similarity 81.2%; Pred. No. 0.01;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STMQELNSRLASYLDK 16
Db 86 ATMQLNDRSLASYLDK 101

RESULT 15
ABG77168
ID ABG77168 standard; protein; 432 AA.
XX
AC ABG77168;
XX
DT 05-NOV-2002 (first entry)
XX
DE Prostate adenocarcinoma associated protein #3.
XX
KW Prostate cancer; differential expression; cancer diagnosis;
KW cancer treatment; cancer monitoring; prostate adenocarcinoma.
XX
OS Homo sapiens.
XX
PN US2002119463-A1.
XX
PD 29-AUG-2002.
XX
PF 30-JUL-2001; 2001US-00919172.
XX
PR 28-JUL-2000; 2000US-0222469P.
XX
PA (FARI/) FARIS M.
PA (TURN/) TURNER C M.
XX
PI Paris M, Turner CM;
XX
DR WPI; 2002-608155/65.
XX
DR N-PSDB; ABS62731.
XX
PT New composition, useful for treating and diagnosing prostate cancer,
PT comprises human cDNAs that are differentially expressed in prostate
PT cancer.
XX
PS Example; Page 29-30; 147pp; English.
XX
CC The invention describes a composition of a number of human cDNAs that are
CC differentially expressed in prostate cancer. The composition of the
CC invention useful for a high-throughput method for detecting differential
CC expression of cDNAs in a nucleic acid containing sample comprising
CC amplifying the nucleic acids of the sample, hybridising the composition
CC with nucleic acids of the sample, detecting the hybridisation complexes
CC and comparing the complexes with those of a standard, where differences
CC indicates differential expression. The sample is from a subject with
CC prostate cancer and comparison with a standard defines an early, mid or
CC late stage of the disease. The composition and or protein encoded by the
CC cDNA's are useful for a high-throughput method to screen molecules or
CC compounds to identify a ligand which specifically binds a cDNA or protein
CC comprising between cDNA/protein and molecule or compound. The molecules and
CC compounds are selected from DNA, RNA, peptide nucleic acid molecules,
CC mimetics, peptides, proteins, (ant)agonists, antibodies, immunoglobulins,
CC inhibitors, drug compounds, pharmaceutical agents, transcription factors,
CC repressors, and regulatory proteins. The composition is useful for
CC diagnosing, treating or monitoring the progression or treatment of
CC prostate cancer. The antibodies are also useful for the diagnosis of
CC disease. This sequence represents a prostate adenocarcinoma protein
XX
SQ Sequence 432 AA;

Query Match 84.4%; Score 65; DB 5; Length 432;

Best Local Similarity 81.2%; Pred. No. 0.01;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 STMQELNSRLASYLDK 16
:|||||
Db 86 ATMQLNDRLASYLDK 101

Search completed: July 5, 2006, 18:43:45
Job time : 141.029 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 5, 2006, 20:38:52 ; Search time 117.126 Seconds
(without alignments)
63.277 Million cell updates/sec

Title: US-10-774-928a-14
Perfect score: 77
Sequence: 1 STMQELNSRLASYLDK 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	16	5	US-10-774-928-14
2	66	85.7	423	4	US-10-080-334-269
3	66	85.7	423	5	US-10-514-932-2
4	65	84.4	167	3	US-09-925-301-1375
5	65	84.4	432	3	US-09-919-172-9
6	65	84.4	432	3	US-09-315-355-18
7	65	84.4	432	5	US-10-752-986-9
8	65	84.4	432	5	US-10-848-572-18
9	65	84.4	432	5	US-10-821-234-1463
10	65	84.4	459	3	US-09-925-298-469
11	65	84.4	459	3	US-10-102-806-469
12	65	84.4	757	5	US-10-450-763-37062
13	65	84.4	887	5	US-10-450-763-54043
14	65	84.4	1113	5	US-10-450-763-37061
15	64	83.1	128	3	US-09-925-300-1730
16	64	83.1	142	3	US-09-738-973-213
17	64	83.1	142	3	US-09-854-133-213
18	64	83.1	142	4	US-10-144-649A-213
19	64	83.1	166	5	US-10-450-763-35705
20	64	83.1	189	4	US-10-029-386-34114
21	64	83.1	221	5	US-10-450-763-54046
22	64	83.1	400	3	US-09-922-217-1115
23	64	83.1	400	4	US-10-025-380-1115
24	64	83.1	400	4	US-10-734-564-118
25	64	83.1	400	5	US-10-733-969A-33
26	64	83.1	400	6	US-11-108-172-1115
27	64	83.1	433	5	US-10-450-763-35709

28 64 83.1 452 5 US-10-631-467-1588 Sequence 1588, Ap
29 64 83.1 456 3 US-09-919-172-31 Sequence 31, Appl
30 64 83.1 456 4 US-10-363-616-310 Sequence 310, App
31 64 83.1 456 5 US-10-752-986-31 Sequence 31, Appl
32 64 83.1 456 5 US-10-631-467-873 Sequence 873, App
33 64 83.1 470 5 US-10-631-467-657 Sequence 657, App
34 64 83.1 472 6 US-11-037-713-35 Sequence 35, Appl
35 64 83.1 494 4 US-10-435-696-51 Sequence 51, Appl
36 64 83.1 558 5 US-10-450-763-54047 Sequence 54047, A
37 64 83.1 593 4 US-10-435-696-50 Sequence 50, Appl
38 64 83.1 618 3 US-09-925-300-1381 Sequence 1381, Ap
39 61 79.2 53 5 US-10-883-020-4 Sequence 4, Appl
40 61 79.2 81 5 US-10-450-763-57390 Sequence 57390, A
41 61 79.2 99 4 US-10-029-386-34091 Sequence 34091, A
42 61 79.2 125 5 US-10-450-763-49053 Sequence 49053, A
43 61 79.2 140 5 US-10-450-763-48990 Sequence 48990, A
44 61 79.2 157 3 US-09-864-761-44299 Sequence 44299, A
45 61 79.2 177 5 US-10-450-763-31405 Sequence 31405, A

ALIGNMENTS

RESULT 1
US-10-774-928-14
; Sequence 14, Application US/10774928
; Publication No. US20040241168A1
; GENERAL INFORMATION:
; APPLICANT: O'Daly, Jose
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Clinical Remission
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 302178
; CURRENT APPLICATION NUMBER: US/10/774,928
; CURRENT FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Leishmania
US-10-774-928-14

Query Match 100.0%; Score 77; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STMQELNSRLASYLDK 16
DB 1 STMQELNSRLASYLDK 16

RESULT 2
US-10-080-334-269
; Sequence 269, Application US/10080334
; Publication No. US20040002584A1
; GENERAL INFORMATION:
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shimkets, Richard A
; APPLICANT: Li, Li
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A
; APPLICANT: Padigar, Muralidhara

```

; APPLICANT: Liu, Xiaohong
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spaderna, Steven K
; APPLICANT: Zerhusen, Bryan D
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-275
; CURRENT APPLICATION NUMBER: US/10/080,334
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/270,523
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/322,712
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/311,980
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/330,307
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/278,796
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/281,521
; PRIOR FILING DATE: 2001-08-04
; PRIOR APPLICATION NUMBER: 60/276,677
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,595
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/270,220
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/274,295
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/318,526
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/286,548
; PRIOR FILING DATE: 2001-08-25
; PRIOR APPLICATION NUMBER: 60/291,765
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/270,797
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/276,400
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/270,810
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 269
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-080-334-269

Query Match      85.7%; Score 66; DB 4; Length 423;
Best Local Similarity 86.7%; Pred. No. 0.014;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TMQELNSRLASYLDK 16
Db 75 TMQDLNDRSLASYLDK 89

RESULT 3
US-10-514-932-2
; Sequence 2, Application US/10514932
; Publication No. US20050208583A1
; GENERAL INFORMATION:
; APPLICANT: NAHM, DONG HO
; APPLICANT: JEON, SOOK YEONG
; TITLE OF INVENTION: DETECTION OF AUTOANTIBODIES TO CYTOKERATIN 18 PROTEIN IN PATIENTS
; TITLE OF INVENTION: WITH BRONCHIAL ASTHMA AND CHRONIC RHINITIS, AND ITS APPLICATIONS
; TITLE OF INVENTION: INCLUDING A KIT FOR DIAGNOSING BRONCHIAL ASTHMA AND CHRONIC
; TITLE OF INVENTION: RHINITIS COMPRISING MAMMALIAN CYTOKERATIN 18 PROTEIN
; FILE REFERENCE: NP03-0002
; CURRENT APPLICATION NUMBER: US/10/514,932
; CURRENT FILING DATE: 2004-11-12

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; PRIOR APPLICATION NUMBER: KR1020020026765
; PRIOR FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 2
; LENGTH: 423
; TYPE: PRT
; ORGANISM: MOUSE
US-10-514-932-2

Query Match      85.7%; Score 66; DB 5; Length 423;
Best Local Similarity 86.7%; Pred. No. 0.014;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TMQELNSRLASYLDK 16
Db 75 TMQDLNDRSLASYLDK 89

RESULT 4
US-09-925-301-1375
; Sequence 1375, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1375
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (157)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (161)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (163)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1375

Query Match      84.4%; Score 65; DB 3; Length 167;
Best Local Similarity 86.7%; Pred. No. 0.0074;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TMQELNSRLASYLDK 16
Db 118 TMQKLNDRSLASYLDK 132

RESULT 5
US-09-919-172-9
; Sequence 9, Application US/09919172
; Patent No. US20020119463A1
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28

```

NUMBER OF SEQ ID NOS: 102
SOFTWARE: PERL Program
SEQ ID NO 9
LENGTH: 432
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020119463A1 1454852CD1
US-09-919-172-9

Query Match 84.4%; Score 65; DB 3; Length 432;
Best Local Similarity 81.2%; Pred. No. 0.02;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STMQELNSRLASYLDK 16
:|||||
DB 86 ATMQLNDRLASYLDK 101

RESULT 6

US-09-315-355-18
Sequence 18, Application US/09315355
Publication No. US20030157482A1
GENERAL INFORMATION:
APPLICANT: KEESEE, SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-JYE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
DETECTION OF CERVICAL CANCER
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,355
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GREENHALGH, DUNCAN A
REGISTRATION NUMBER: 38,678
REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-355-18

Query Match 84.4%; Score 65; DB 3; Length 432;
Best Local Similarity 81.2%; Pred. No. 0.02;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STMQELNSRLASYLDK 16
:|||||
DB 86 ATMQLNDRLASYLDK 101

RESULT 7

US-10-752-986-9
Sequence 9, Application US/10752986
Publication No. US20040253609A1
GENERAL INFORMATION:
APPLICANT: Paris, Mary
APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/10/752,986
CURRENT FILING DATE: 2004-01-06
PRIOR APPLICATION NUMBER: US/09/919,172
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PERL Program
SEQ ID NO 9
LENGTH: 432
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 1454852CD1
US-10-752-986-9

Query Match 84.4%; Score 65; DB 5; Length 432;
Best Local Similarity 81.2%; Pred. No. 0.02;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STMQELNSRLASYLDK 16
:|||||
DB 86 ATMQLNDRLASYLDK 101

RESULT 8

US-10-848-572-18
Sequence 18, Application US/10848572
Publication No. US20050164313A1
GENERAL INFORMATION:
APPLICANT: Keesee, Susan K.
APPLICANT: Obar, Robert
APPLICANT: Wu, Ying-Jye
TITLE OF INVENTION: Methods and Compositions for the Detection of Cervical Cancer
FILE REFERENCE: MTP-023C1
CURRENT APPLICATION NUMBER: US/10/848,572
CURRENT FILING DATE: 2004-05-18
PRIOR APPLICATION NUMBER: US 08/989,045
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: US 08/705,660
PRIOR FILING DATE: 1996-08-30
PRIOR APPLICATION NUMBER: US 09/315,355
PRIOR FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 432
TYPE: PRT
ORGANISM: Homo sapiens
US-10-848-572-18

Query Match 84.4%; Score 65; DB 5; Length 432;
Best Local Similarity 81.2%; Pred. No. 0.02;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STMQELNSRLASYLDK 16
:|||||
DB 86 ATMQLNDRLASYLDK 101

RESULT 9

US-10-821-234-1463
Sequence 1463, Application US/10821234
Publication No. US20050255114A1

; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT FILING DATE: 2004-04-07
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1463
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1463

Query Match 84.4%; Score 65; DB 5; Length 432;
Best Local Similarity 81.2%; Pred. No. 0.02; 2; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 STMQELNSRLASYLDK 16
Db 86 ATMQLNDRSLASYLDK 101
:|||||

RESULT 10

US-09-925-298-469
; Sequence 469, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103
; CURRENT FILING DATE: 2001-08-10
; CURRENT APPLICATION NUMBER: US/09/925,298
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 469
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-298-469

Query Match 84.4%; Score 65; DB 3; Length 459;
Best Local Similarity 81.2%; Pred. No. 0.022; 2; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 STMQELNSRLASYLDK 16
Db 113 ATMQLNDRSLASYLDK 128
:|||||

RESULT 11

US-10-102-806-469
; Sequence 469, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103PIC1
; CURRENT FILING DATE: 2002-03-22
; CURRENT APPLICATION NUMBER: US/10/102,806
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 2000-03-08
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 469
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-102-806-469

; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 469
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-102-806-469

Query Match 84.4%; Score 65; DB 4; Length 459;
Best Local Similarity 81.2%; Pred. No. 0.022; 2; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 STMQELNSRLASYLDK 16
Db 113 ATMQLNDRSLASYLDK 128
:|||||

RESULT 12

US-10-450-763-37062
; Sequence 37062, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 37062
; LENGTH: 757
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: DOMAIN
; LOCATION: (577)..(602)
; OTHER INFORMATION: Vertebrate galactoside-binding lectin proteins domain
; OTHER INFORMATION: identified by eMATRIX, accession number BL00309C, p-value=7.429e-
; OTHER INFORMATION: 22, raw score of 18.65
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (84)..(388)
; OTHER INFORMATION: Intermediate filament proteins domain identified by Pfam,
; OTHER INFORMATION: accession name filament, E-value=2.4e-123, Pfam score of 423.2
US-10-450-763-37062

Query Match 84.4%; Score 65; DB 5; Length 757;
Best Local Similarity 81.2%; Pred. No. 0.037; 2; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 STMQELNSRLASYLDK 16
Db 87 ATMQLNDRSLASYLDK 102
:|||||

RESULT 13

US-10-450-763-54043
; Sequence 54043, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11

;; PRIOR APPLICATION NUMBER: PCT/US01/08631
;; PRIOR FILING DATE: 2001-03-30
;; PRIOR APPLICATION NUMBER: 09/540,217
;; PRIOR FILING DATE: 2000-03-31
;; PRIOR APPLICATION NUMBER: 09/649,167
;; PRIOR FILING DATE: 2000-08-23
;; NUMBER OF SEQ ID NOS: 60736
;; SOFTWARE: Custom
;; SEQ ID NO 54043
;; LENGTH: 887
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: DOMAIN
;; LOCATION: (547)..(567)
;; OTHER INFORMATION: kw ALLERGEN POLLEN CIM1 HOL-LI domain identified by eMATRIX,
;; OTHER INFORMATION: accession number DM01724, p-value=8.091e-11, raw score of 8.14
;; FEATURE:
;; NAME/KEY: DOMAIN
;; LOCATION: (84)..(857)
;; OTHER INFORMATION: Intermediate filament proteins domain identified by Pfam,
;; OTHER INFORMATION: accession name filament, E-value=2e-247, Pfam score of 835.4
US-10-450-763-54043

Query Match 84.4%; Score 65; DB 5; Length 887;
Best Local Similarity 81.2%; Pred. No. 0.044;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 STMQELNSRLASYLDK 16
:|||||
DB 87 ATMQNLNDRASYLDK 102

RESULT 14
US-10-450-763-37061
;; Sequence 37061, Application US/10450763
;; Publication No. US20050196754A1
;; GENERAL INFORMATION:
;; APPLICANT: Hyseq, Inc
;; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;; FILE REFERENCE: 790CIP3/US
;; CURRENT APPLICATION NUMBER: US/10/450,763
;; CURRENT FILING DATE: 2003-06-11
;; PRIOR APPLICATION NUMBER: PCT/US01/08631
;; PRIOR FILING DATE: 2001-03-30
;; PRIOR APPLICATION NUMBER: 09/540,217
;; PRIOR FILING DATE: 2000-03-31
;; PRIOR APPLICATION NUMBER: 09/649,167
;; PRIOR FILING DATE: 2000-08-23
;; NUMBER OF SEQ ID NOS: 60736
;; SOFTWARE: Custom
;; SEQ ID NO 37061
;; LENGTH: 1113
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: DOMAIN
;; LOCATION: (1004)..(1024)
;; OTHER INFORMATION: kw ALLERGEN POLLEN CIM1 HOL-LI domain identified by eMATRIX,
;; OTHER INFORMATION: accession number DM01724, p-value=3.045e-11, raw score of 8.14
;; FEATURE:
;; NAME/KEY: DOMAIN
;; LOCATION: (84)..(1104)
;; OTHER INFORMATION: Intermediate filament proteins domain identified by Pfam,
;; OTHER INFORMATION: accession name filament, E-value=3.3e-277, Pfam score of 934.3
US-10-450-763-37061

Query Match 84.4%; Score 65; DB 5; Length 1113;
Best Local Similarity 81.2%; Pred. No. 0.057;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 STMQELNSRLASYLDK 16
:|||||

DB 87 ATMQNLNDRASYLDK 102

RESULT 15

US-09-925-300-1730
;; Sequence 1730, Application US/09925300
;; Patent No. US20020151681A1
;; GENERAL INFORMATION:
;; APPLICANT: Craig Rosen,
;; APPLICANT: Steve Ruben
;; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;; FILE REFERENCE: PA101
;; CURRENT APPLICATION NUMBER: US/09/925,300
;; CURRENT FILING DATE: 2001-08-10
;; PRIOR APPLICATION NUMBER: PCT/US00/05988
;; PRIOR FILING DATE: 2000-03-08
;; PRIOR APPLICATION NUMBER: 60/124,270
;; PRIOR FILING DATE: 1999-03-12
;; NUMBER OF SEQ ID NOS: 1890
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1730
;; LENGTH: 128
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-925-300-1730

Query Match 83.1%; Score 64; DB 3; Length 128;
Best Local Similarity 86.7%; Pred. No. 0.0082;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TMQELNSRLASYLDK 16
:|||||

DB 100 TMQNLNDRASYLDK 114
:|||||

Search Completed: July 5, 2006, 20:51:56
Job time : 118.126 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 20:39:32 ; Search time 9.16505 Seconds
(without alignments)
46.842 Million cell updates/sec

Title: US-10-774-928A-14

Perfect score: 77

Sequence: 1 STMQELNSRLASYLDK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 112942

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New.*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pap.*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pap.*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	83.1	400	7	US-11-105-233-182
2	61	79.2	430	7	US-11-105-233-181
3	58	75.3	422	7	US-11-105-233-176
4	56	72.7	259	7	US-11-293-697-4615
5	55	71.4	424	7	US-11-105-233-183
6	52	67.5	466	7	US-11-289-102-289
7	52	67.5	551	7	US-11-270-040-4
8	49	63.6	586	6	US-10-505-928-314
9	48	62.3	450	7	US-11-293-697-4090
10	43	55.8	794	6	US-10-449-902-50320
11	43	55.8	969	6	US-10-449-902-47888
12	41	53.2	535	7	US-11-293-697-4336
13	38	49.4	328	7	US-11-293-697-3859
14	38	49.4	422	6	US-10-449-902-53735
15	38	49.4	469	6	US-10-505-928-457
16	38	49.4	483	7	US-11-105-233-180
17	38	49.4	1614	6	US-10-505-928-199
18	37	48.1	93	6	US-10-449-902-33339
19	37	48.1	304	6	US-10-953-349-24282
20	37	48.1	322	6	US-10-953-349-24281
21	37	48.1	322	6	US-10-953-349-24280
22	37	48.1	390	6	US-10-449-902-44395
23	37	48.1	520	7	US-11-293-697-3712
24	37	48.1	955	6	US-10-449-902-42940
25	36.5	47.4	515	6	US-10-953-349-21352

Sequence 21351, A
Sequence 21350, A
Sequence 31278, A
Sequence 1326, Ap
Sequence 396, App
Sequence 33250, A
Sequence 43998, A
Sequence 56574, A
Sequence 39097, A
Sequence 39096, A
Sequence 37830, A
Sequence 51417, A
Sequence 270, App
Sequence 16, Appl
Sequence 15077, A
Sequence 12, Appl
Sequence 27509, A
Sequence 27508, A
Sequence 220, App
Sequence 1, Appl

26 36.5 47.4 516 6 US-10-953-349-21351
27 36.5 47.4 521 6 US-10-953-349-21350
28 36 46.8 121 6 US-10-449-902-31278
29 36 46.8 149 6 US-10-471-571A-1326
30 36 46.8 250 6 US-10-471-571A-396
31 36 46.8 291 6 US-10-449-902-33250
32 36 46.8 291 6 US-10-449-902-43998
33 36 46.8 291 6 US-10-449-902-56574
34 36 46.8 313 6 US-10-953-349-39097
35 36 46.8 316 6 US-10-953-349-39096
36 36 46.8 320 6 US-10-449-902-37830
37 36 46.8 618 6 US-10-449-902-51417
38 36 46.8 1038 7 US-11-289-102-270
39 35 45.5 52 6 US-10-489-730-16
40 35 45.5 54 6 US-10-953-349-15077
41 35 45.5 100 6 US-10-489-730-12
42 35 45.5 131 6 US-10-953-349-27509
43 35 45.5 167 6 US-10-953-349-27508
44 35 45.5 180 7 US-11-251-208-220
45 35 45.5 299 7 US-11-361-788-1

ALIGNMENTS

RESULT 1

US-11-105-233-182
; Sequence 182, Application US/11105233
; Publication No. US20060134653A1
; GENERAL INFORMATION:
; APPLICANT: Thiagalingam et al
; TITLE OF INVENTION: Differential Expression of Genes in MSI
; FILE REFERENCE: 1657/2001
; CURRENT APPLICATION NUMBER: US/11/105,233
; CURRENT FILING DATE: 2005-04-13
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-233-182

Query Match 83.1%; Score 64; DB 7; Length 400;
Best Local Similarity 86.7%; Pred. No. 0.001;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TWOELNSRLASYLDK 16
Db 83 TWOELNSRLASYLDK 97

RESULT 2

US-11-105-233-181
; Sequence 181, Application US/11105233
; Publication No. US20060134653A1
; GENERAL INFORMATION:
; APPLICANT: Thiagalingam et al
; TITLE OF INVENTION: Differential Expression of Genes in MSI
; FILE REFERENCE: 1657/2001
; CURRENT APPLICATION NUMBER: US/11/105,233
; CURRENT FILING DATE: 2005-04-13
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 181
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-233-181

Query Match 79.2%; Score 61; DB 7; Length 430;

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Best Local Similarity 80.0%; Pred. No. 0.0037; Mismatches 1; Indels 2; Gaps 0;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TMQELNSRLASYLDK 16
   |||||
Db 83 TMQSLNDRLASYLDR 97

RESULT 3
US-11-105-233-176
; Sequence 176, Application US/11105233
; Publication No. US20060134653A1
; GENERAL INFORMATION:
; APPLICANT: Thiagalingam et al
; TITLE OF INVENTION: Differential Expression of Genes in MSI
; TITLE OF INVENTION: Tumors
; FILE REFERENCE: 1657/2001
; CURRENT APPLICATION NUMBER: US/11/105,233
; CURRENT FILING DATE: 2005-04-13
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-233-176

Query Match 75.3%; Score 58; DB 7; Length 422;
Best Local Similarity 68.8%; Pred. No. 0.012; Mismatches 3; Indels 2; Gaps 0;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 STMQELNSRLASYLDK 16
   :|||
Db 74 ATMQNLNDRLASYVEK 89

RESULT 4
US-11-293-697-4615
; Sequence 4615, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4615
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4615

Query Match 72.7%; Score 56; DB 7; Length 259;
Best Local Similarity 73.3%; Pred. No. 0.016; Mismatches 1; Indels 3; Gaps 0;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TMQELNSRLASYLDK 16
   |||||
Db 120 TMQSLNDRLASYLDR 134

RESULT 5
US-11-105-233-183
; Sequence 183, Application US/11105233
; Publication No. US20060134653A1
; GENERAL INFORMATION:
; APPLICANT: Thiagalingam et al
; TITLE OF INVENTION: Differential Expression of Genes in MSI
; TITLE OF INVENTION: Tumors
```

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; FILE REFERENCE: 1657/2001
; CURRENT APPLICATION NUMBER: US/11/105,233
; CURRENT FILING DATE: 2005-04-13
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 183
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-233-183

Query Match 71.4%; Score 55; DB 7; Length 424;
Best Local Similarity 78.6%; Pred. No. 0.04; Mismatches 1; Indels 2; Gaps 0;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 MQELNSRLASYLDK 16
   |||||
Db 74 MQNLNDRLASYLEK 87

RESULT 6
US-11-289-102-289
; Sequence 289, Application US/11289102
; Publication No. US20060121511A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Hyerim
; APPLICANT: Shaw, Peter M.
; TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO
; TITLE OF INVENTION: MICROTUBULE-STABILIZING AGENTS
; FILE REFERENCE: 10338 NP
; CURRENT APPLICATION NUMBER: US/11/289,102
; CURRENT FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US 60/631,993
; PRIOR FILING DATE: 2004-11-30
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 289
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-289-102-289

Query Match 67.5%; Score 52; DB 7; Length 466;
Best Local Similarity 64.3%; Pred. No. 0.15; Mismatches 3; Indels 2; Gaps 0;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 MQELNSRLASYLDK 16
   :|||
Db 107 LQELNDRFANYIDK 120

RESULT 7
US-11-270-040-4
; Sequence 4, Application US/11270040
; Publication No. US20060110762A1
; GENERAL INFORMATION:
; APPLICANT: Kapil, Sanjay
; APPLICANT: Kim, Jeong-Ki
; TITLE OF INVENTION: PORCINE REPRODUCTIVE AND RESPIRATORY
; TITLE OF INVENTION: SYNDROME VIRUS RECEPTOR COMPONENTS AND USES THEREOF
; FILE REFERENCE: 14337/004001
; CURRENT APPLICATION NUMBER: US/11/270,040
; CURRENT FILING DATE: 2005-11-09
; PRIOR APPLICATION NUMBER: 60/680,297
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/626,788
; PRIOR FILING DATE: 2004-11-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 551
; TYPE: PRT
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; ORGANISM: Cercopithecus aethiops
US-11-270-040-4
Query Match      67.5%; Score 52; DB 7; Length 551;
Best Local Similarity 64.3%; Pred. No. 0.18;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 MOELNSRLASYLDK 16
Db 87 LQELNDRFANYIDK 100
      :|||||:|:|:|
      :|||||:|:|:|

RESULT 8
US-10-505-928-314
; Sequence 314, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/33178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 314
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-314

Query Match      63.6%; Score 49; DB 6; Length 586;
Best Local Similarity 64.3%; Pred. No. 0.65;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 MOELNSRLASYLDK 16
Db 36 LQELNDRFANYIDK 49
      :|||||:|:|:|
      :|||||:|:|:|

RESULT 9
US-11-293-697-4090
; Sequence 4090, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4090
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4090

Query Match      62.3%; Score 48; DB 7; Length 450;
Best Local Similarity 57.1%; Pred. No. 0.72;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 MOELNSRLASYLDK 16
Db 92 LQELNDRFANYIEK 105
      :|||||:|:|:|
      :|||||:|:|:|

RESULT 10
US-10-449-902-50320
; Sequence 50320, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50320
; LENGTH: 794
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-50320

Query Match      55.8%; Score 43; DB 6; Length 794;
Best Local Similarity 50.0%; Pred. No. 10;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 STMQELNSRLASYLDK 16
Db 318 SAWKELSDNMSSYLDK 333
      :|||||:|:|:|
      :|||||:|:|:|

RESULT 11
US-10-449-902-47888
; Sequence 47888, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47888
; LENGTH: 969
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-47888

Query Match      55.8%; Score 43; DB 6; Length 969;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 STMQELNSRLASYLDK 16
Db 493 SAWKELSDNMSSYLDK 508
      :|||||:|:|:|
      :|||||:|:|:|

RESULT 12
US-11-293-697-4336
; Sequence 4336, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
```

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; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4336
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4336

Query Match      53.2%; Score 41; DB 7; Length 535;
Best Local Similarity 53.8%; Pred. No. 15;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY  4 QELNSRLASYLDK 16
Db   506 EEINFRLRQYMDK 518
      :||: |||: |||:

RESULT 13
US-11-293-697-3859
; Sequence 3859, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; PRIOR FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3859
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3859

Query Match      49.4%; Score 38; DB 7; Length 328;
Best Local Similarity 88.9%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  8 SRLASYLDK 16
Db   299 SRLPSYLDK 307
      ||| |||||

RESULT 14
US-10-449-902-53735
; Sequence 53735, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53735
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Oryza sativa

US-10-449-902-53735
Query Match      49.4%; Score 38; DB 6; Length 422;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY  1 STMQELNSRLASYLDK 16
Db   399 SSTHOLNTELASFVVK 414
      |: |||: |||: |||:

RESULT 15
US-10-505-928-457
; Sequence 457, Application US/10505928
; Publication No. US20060089532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 457
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-457

Query Match      49.4%; Score 38; DB 6; Length 469;
Best Local Similarity 42.9%; Pred. No. 42;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY  3 MOELNSRLASYLDK 16
Db   95 IKALNNKFASFIDK 108
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Search completed: July 5, 2006, 20:53:00
Job time : 9.16505 secs
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Result No.	Score	Query Match	Length	DB	ID	Description	
1	77	100.0	16	2	US-09-809-003A-14	Sequence 14, Appl	
2	65	84.4	432	1	US-08-705-660-18	Sequence 18, Appl	
3	65	84.4	432	2	US-08-989-045-18	Sequence 18, Appl	
4	65	84.4	432	2	US-09-919-172-9	Sequence 9, Appl	
5	65	84.4	432	2	US-09-315-355A-18	Sequence 18, Appl	
6	64	83.1	22	1	US-07-934-656A-2	Sequence 2, Appl	
7	64	83.1	22	1	US-07-934-656A-3	Sequence 3, Appl	
8	64	83.1	22	1	US-07-934-656A-4	Sequence 4, Appl	
9	64	83.1	22	1	US-07-934-656A-6	Sequence 6, Appl	
10	64	83.1	22	1	US-07-934-656A-7	Sequence 7, Appl	
11	64	83.1	142	2	US-09-370-838-213	Sequence 213, App	
12	64	83.1	142	2	US-09-854-133-213	Sequence 213, App	
13	64	83.1	400	1	US-07-730-953-2	Sequence 2, Appl	
14	64	83.1	442	2	US-09-949-016-8625	Sequence 8625, Ap	
15	64	83.1	456	2	US-09-919-172-31	Sequence 31, Appl	
16	64	83.1	471	2	US-09-538-092-837	Sequence 837, App	
17	64	83.1	593	2	US-09-538-092-919	Sequence 919, App	
18	61	79.2	120	2	US-09-621-976-5162	Sequence 5162, Ap	
19	61	79.2	212	2	US-09-949-016-8463	Sequence 8463, Ap	
20	61	79.2	422	1	US-09-067-351-3	Sequence 3, Appl	
21	61	79.2	422	2	US-09-360-490-3	Sequence 3, Appl	
22	61	79.2	430	2	US-09-919-039-105	Sequence 105, App	
23	61	79.2	447	2	US-09-949-016-11032	Sequence 11032, A	
24	60	77.9	22	1	US-07-934-656A-5	Sequence 5, Appl	
25	60	77.9	355	2	US-10-104-047-2943	Sequence 2943, Ap	
26	60	77.9	435	2	US-09-949-016-8415	Sequence 8415, Ap	

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,660
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: GREENHALGH, DUNCAN A
; REGISTRATION NUMBER: 38,678
; REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-705-660-18

```

Query Match 84.4%; Score 65; DB 1; Length 432;
 Best Local Similarity 81.2%; Pred. No. 0.0055;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 STMQELNSRLASYLDK 16
    :||| ||| ||| ||| |||
Db 86 ATMQLNDRSLASYLDK 101

```

```

RESULT 3
; Sequence 18, Application US/08989045
; Patent No. 6027905
; GENERAL INFORMATION:
; APPLICANT: KEESEE, SUSAN
; APPLICANT: OBAR, ROBERT
; APPLICANT: WU, YING-JYE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; DETECTION OF CERVICAL CANCER
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,045
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: GREENHALGH, DUNCAN A
; REGISTRATION NUMBER: 38,678
; REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-989-045-18

```

Query Match 84.4%; Score 65; DB 2; Length 432;
 Best Local Similarity 81.2%; Pred. No. 0.0055;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 STMQELNSRLASYLDK 16
    :||| ||| ||| ||| |||
Db 86 ATMQLNDRSLASYLDK 101

```

```

RESULT 4
; Sequence 9, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 9
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 1454852CD1
; US-09-919-172-9

```

Query Match 84.4%; Score 65; DB 2; Length 432;
 Best Local Similarity 81.2%; Pred. No. 0.0055;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 STMQELNSRLASYLDK 16
    :||| ||| ||| ||| |||
Db 86 ATMQLNDRSLASYLDK 101

```

```

RESULT 5
; Sequence 18, Application US/09315355A
; Patent No. 6803189
; GENERAL INFORMATION:
; APPLICANT: Keesee, Susan
; APPLICANT: Obar, Robert
; APPLICANT: Wu Ying-Jye
; TITLE OF INVENTION: Methods for the Detection of Cervical Cancer
; FILE REFERENCE: MTP-023DV2
; CURRENT APPLICATION NUMBER: US/09/315,355A
; CURRENT FILING DATE: 1999-05-17
; PRIOR FILING DATE: US 08/989,045
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: US 08/705,660
; PRIOR FILING DATE: 1996-08-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-315-355A-18

```

Query Match 84.4%; Score 65; DB 2; Length 432;
 Best Local Similarity 81.2%; Pred. No. 0.0055;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 STMQELNSRLASYLDK 16
    :||| ||| ||| ||| |||

```

Db 86 ATWQNLNRLASYLDK 101

```
RESULT 6
US-07-934-656A-2
; Sequence 2, Application US/07934656A
; Patent No. 5500347
; GENERAL INFORMATION:
; APPLICANT: MOLL, Roland
; APPLICANT: FRANK, Werner W.
; TITLE OF INVENTION: PROCESS FOR THE PURIFICATION OF
; TITLE OF INVENTION: CYTOKERATIN 20 AND ITS USE FOR THE PRODUCTION OF
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,656A
; FILING DATE: 27-JAN-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 40 23 945.4
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Murray, Robert B.
; REGISTRATION NUMBER: 22,980
; REFERENCE/DOCKET NUMBER: P564-3003
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; APPLICATION TYPE: peptide
; US-07-934-656A-2

Query Match 83.1%; Score 64; DB 1; Length 22;
Best Local Similarity 86.7%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TMOELNSRLASYLDK 16
Db 7 TMOQNLNRLASYLDK 21

RESULT 7
US-07-934-656A-3
; Sequence 3, Application US/07934656A
; Patent No. 5500347
; GENERAL INFORMATION:
; APPLICANT: MOLL, Roland
; APPLICANT: FRANK, Werner W.
; TITLE OF INVENTION: PROCESS FOR THE PURIFICATION OF
; TITLE OF INVENTION: CYTOKERATIN 20 AND ITS USE FOR THE PRODUCTION OF
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,656A
; FILING DATE: 27-JAN-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 40 23 945.4
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Murray, Robert B.
; REGISTRATION NUMBER: 22,980
; REFERENCE/DOCKET NUMBER: P564-3003
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; APPLICATION TYPE: peptide
; US-07-934-656A-3

Query Match 83.1%; Score 64; DB 1; Length 22;
Best Local Similarity 86.7%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TMOELNSRLASYLDK 16
Db 7 TMOQNLNRLASYLDK 21

RESULT 8
US-07-934-656A-4
; Sequence 4, Application US/07934656A
; Patent No. 5500347
; GENERAL INFORMATION:
; APPLICANT: MOLL, Roland
; APPLICANT: FRANK, Werner W.
; TITLE OF INVENTION: PROCESS FOR THE PURIFICATION OF
; TITLE OF INVENTION: CYTOKERATIN 20 AND ITS USE FOR THE PRODUCTION OF
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,656A
; FILING DATE: 27-JAN-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 40 23 945.4
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Murray, Robert B.
; REGISTRATION NUMBER: 22,980
; REFERENCE/DOCKET NUMBER: P564-3003
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; APPLICATION TYPE: peptide
; US-07-934-656A-4

Query Match 83.1%; Score 64; DB 1; Length 22;
Best Local Similarity 86.7%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TMOELNSRLASYLDK 16
Db 7 TMOQNLNRLASYLDK 21
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/ TELEPHONE: (202)638-5000
/ TELEFAX: (202)638-4810
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 22 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-07-934-656A-4

Query Match 83.1%; Score 64; DB 1; Length 22;
Best Local Similarity 86.7%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TMOELNSRLASYLDK 16
Db 7 TMOELNSRLASYLDK 21

RESULT 9
US-07-934-656A-6
/ Sequence 6, Application US/07934656A
/ Patent No. 5500347
/ GENERAL INFORMATION:
/ APPLICANT: MOLL, Roland
/ APPLICANT: FRANK, Werner W.
/ TITLE OF INVENTION: PROCESS FOR THE PURIFICATION OF
/ CYCLOKERATIN 20 AND ITS USE FOR THE PRODUCTION OF
/ ANTIBODIES
/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Nikolaide, Marmelstein, Murray & Oram
/ STREET: 655 Fifteenth Street N.W. Suite 330
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005-5701
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/934, 656A
/ FILING DATE: 27-JAN-1993
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: DE P 40 23 945.4
/ FILING DATE: 27-JUL-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Murray, Robert B.
/ REGISTRATION NUMBER: 22,980
/ REFERENCE/DOCKET NUMBER: P564-3003
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)638-5000
/ TELEFAX: (202)638-4810
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 22 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-07-934-656A-6

Query Match 83.1%; Score 64; DB 1; Length 22;
Best Local Similarity 86.7%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TMOELNSRLASYLDK 16
Db 7 TMOELNSRLASYLDK 21

RESULT 10
US-07-934-656A-7
/ Sequence 7, Application US/07934656A
/ Patent No. 5500347
/ GENERAL INFORMATION:
/ APPLICANT: MOLL, Roland
/ APPLICANT: FRANK, Werner W.
/ TITLE OF INVENTION: PROCESS FOR THE PURIFICATION OF
/ CYCLOKERATIN 20 AND ITS USE FOR THE PRODUCTION OF
/ ANTIBODIES
/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Nikolaide, Marmelstein, Murray & Oram
/ STREET: 655 Fifteenth Street N.W. Suite 330
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005-5701
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/934, 656A
/ FILING DATE: 27-JAN-1993
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: DE P 40 23 945.4
/ FILING DATE: 27-JUL-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Murray, Robert B.
/ REGISTRATION NUMBER: 22,980
/ REFERENCE/DOCKET NUMBER: P564-3003
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)638-5000
/ TELEFAX: (202)638-4810
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 22 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-07-934-656A-7
Query Match 83.1%; Score 64; DB 1; Length 22;
Best Local Similarity 86.7%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TMOELNSRLASYLDK 16
Db 7 TMOELNSRLASYLDK 21

RESULT 11
US-09-370-838-213
/ Sequence 213, Application US/09370838
/ Patent No. 644425
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Lodes, Michael J.
/ APPLICANT: Mohamath, Roadoh
/ APPLICANT: Secrist, Heather
/ TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
/ LUNG CANCER AND METHODS FOR THEIR USE
/ FILE REFERENCE: 210121.475C1
/ CURRENT APPLICATION NUMBER: US/09/370,838
/ CURRENT FILING DATE: 1999-08-09
/ EARLIER APPLICATION NUMBER: US 09/285,323
/ EARLIER FILING DATE: 1999-04-02
/ NUMBER OF SEQ ID NOS: 289
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 213

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; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-370-838-213

  Query Match      83.1%; Score 64; DB 2; Length 142;
  Best Local Similarity 86.7%; Pred. No. 0.0025;
  Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TMOELNSRLASYLDK 16
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Db 25 TMQNLNDRSLASYLDK 39

RESULT 12
US-09-854-133-213
; Sequence 213, Application US/09854133
; Patent No. 6759508
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 213
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-854-133-213

  Query Match      83.1%; Score 64; DB 2; Length 142;
  Best Local Similarity 86.7%; Pred. No. 0.0025;
  Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TMOELNSRLASYLDK 16
   ||| ||| ||| ||| |||
Db 25 TMQNLNDRSLASYLDK 39

RESULT 13
US-07-730-953-2
; Sequence 2, Application US/07730953
; Patent No. 5288614
; GENERAL INFORMATION:
; APPLICANT: BODENMULLER, Heinz
; APPLICANT: DESSAUER, Andreas
; TITLE OF INVENTION: METHOD FOR THE DETECTION OF MALIGNANT
; TITLE OF INVENTION: DISEASES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/730,953
; FILING DATE: 19910723
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28

; APPLICATION NUMBER: DE P 39 42 999.7
; FILING DATE: 21-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitts, Monica C.
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P564-1119
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 400 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-730-953-2

  Query Match      83.1%; Score 64; DB 1; Length 400;
  Best Local Similarity 86.7%; Pred. No. 0.0075;
  Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TMOELNSRLASYLDK 16
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Db 83 TMQNLNDRSLASYLDK 97

RESULT 14
US-09-949-016-8625
; Sequence 8625, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8625
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8625

  Query Match      83.1%; Score 64; DB 2; Length 442;
  Best Local Similarity 86.7%; Pred. No. 0.0084;
  Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TMOELNSRLASYLDK 16
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Db 125 TMQNLNDRSLASYLDK 139

RESULT 15
US-09-919-172-31
; Sequence 31, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
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; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 31
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673545 1709387CD1
US-09-919-172-31
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Query Match      83.1%; Score 64; DB 2; Length 456;
Best Local Similarity 86.7%; Pred.No. 0.0087;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Oy      2 TMQELNSRLASYLDK 16
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Db      108 TMQNLNDRSLASYLDK 122
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Search completed: July 5, 2006, 19:24:23
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